

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 202292

TO: Jane Zara

Location: REM-2A59&2C18

Art Unit: 1635

Monday, October 02, 2006

Case Serial Number: 10/642946

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen 1a69

Phone: 571-272-2518

BOB

barbara.obryen@uspto.gov

#### Search Notes

For the score over length search, neither fragment had hits in the EST database, so no EST results are included with the S/L output.

Barb



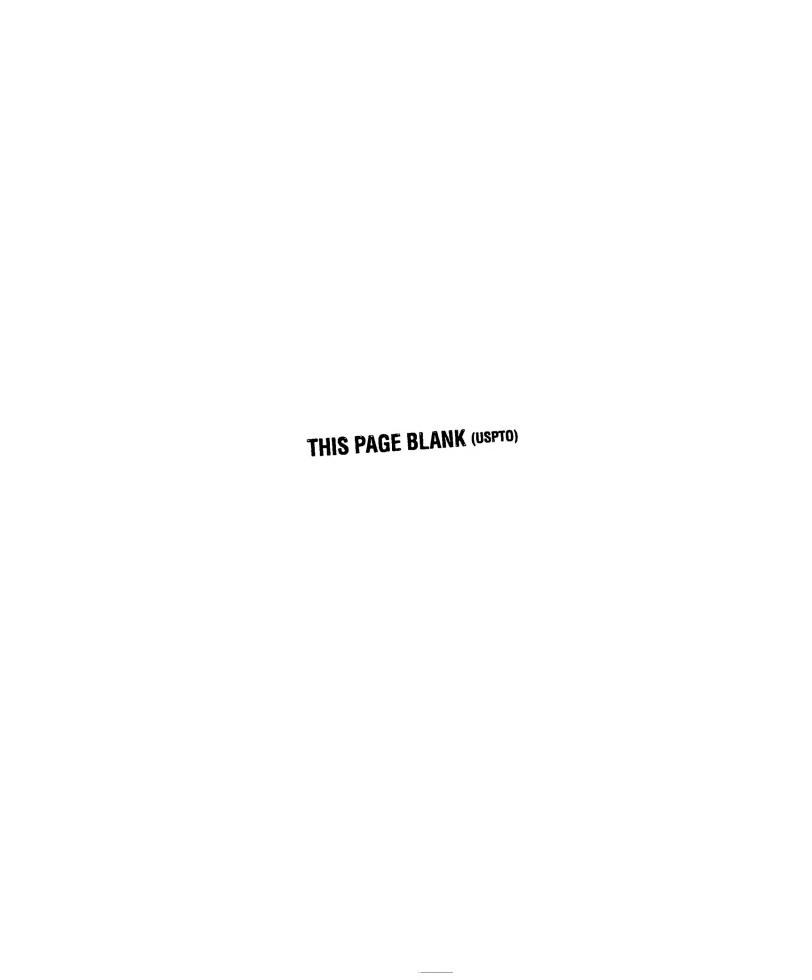
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9-981

Scientific and Technical Information Center

### SEARCH REQUEST FORM

Requester's Full Name: TANE ZARA Examiner #: 77572 Date: 49/19/06
Art Unit: 163C Phone Number: 2-0+61 Serial Number: 707 6 13-176
Location (Bldg/Room#): 2 AS9 (Mailbox #): 2-C18 Results Format Preferred (circle): APER) DISK
LOCATION (DICE) NOOTH, 5 - 1 (1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.
To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:
Title of Invention: Isolated Genonic polynuc's chron +
Inventors (please provide full names): Tw RYAN
Earliest Priority Date: QCR8CBO 9-24-01
Search Topic: Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.
*For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.
O Please Search Des Seg ID No: 3  Nucleic Acid JATA BASES ONLY
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-QB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALICN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=15 -MODE=LOCAL
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-USER=US10642946_@CGN 1_1 10799 @runat_29992006_125308_12402 -NCPU=6 -ICPU=3
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## ALIGNMENTS

Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:	ORIGIN		source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	
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Aventis Pharma S.A. (FR)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluFheLeuGluGly
LysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysLysGly
                                                                                  GluProThrProArgValArgLysAlaGlnAlaGlyGlyLysProGlyLysArgProGly
                       ACGGCCGCAGAAGTGCCTCCGGAAAAGACCAAAGACAAAGGGAAGAAAGGCAAGAAAGAC
                                    ThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLysLysAsp
                                                                     GAGCCCACCCCGCGGGTCCGAAAAAGCCCCAGGCGGGGGCAAGCCAGGGAAGCGGCCAGGG
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/mol_type="unassigned DNA"
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1460 ACCCAGTGGATAGAGGTGGACACCAGGAGGACTACCCGGTTCACAGGCGTCATCACCCAG	
AGTGGATAGAGGTGGACACCAGGAGGAC	ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAspAspAlaArg
LuValAspThrArgArgThrThrArg	luAspAspTyrTyrAspGlyAlaTrt 
ATGATGGTGCGTGGTGTGCCG	YrAspGlyAlaTrpCysAlaG
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laH.	2480 CAGGAGC 801 SerGluA                 2540 TCCGAGG
\laHisLeuThrLeuT 	
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AlaHisLeuThrLeuThrGluProTyrArgGlyGlyCys	
SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 	2480 CAGGAGCAGCTGCTGGCCGAGCCATGCCAGCCAGCCCGGGGGAGGATGAGGACGAGGTC  801 SerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla

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                                 Homo sapiens aortic complete cds. AF053944
                     AF053944.1
                                                                                                                                                              GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158
                                                                                                                                                                                                                                                                      PheGlyThrLy8ValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120
                                                                                                                                              CAGGCATTCCCCTTCACAACAGTAGAGACCTACACAGTGAACTTTGGGGACTTC 3613
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                     GI:3288915
                                                                3935 bp mRNA carboxypeptidase-like
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                                                                ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly
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1 (bases 1 to 3935)

Layne,M.D., Endege,W.O., Jain,M.K., Yet,S.F., Hsieh,C.M., Chin,M.T., Perrella,M.A., Blanar,M.A., Haber,E. and Lee,M.E. Aortic carboxypeptidase-like protein, a novel protein with discoidin and carboxypeptidase-like domains, is up-regulated vascular smooth muscle cell differentiation J. Biol. Chem. 273 (25), 15654-15660 (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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IGATQCNFILARSNWKRIREIMANNGNRPIPHIDPSRPMTDQGRRLQQRRLQQRRLQHLRLR
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VVTEFGTEVEPEFGTKVEPEFETQLEPEFETQLEPEFEEEEEEEEKEEEIATGQAFPFT
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/product="aortic_carboxypeptidase-like
/protein_id="AAC25585.1"
/db_xref="GI:3288916"
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/db_xref="taxon:9606"
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and Lee, M.-E.
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GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158
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                                                                 LeuGluProGluPheGluGluGluGluGluGluLysGluGluGluIleAlaThrGly
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                                                                                                                                                                                                                                                                                         LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGlu
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Klausner, R.D., Colline, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Fermer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villaion, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Vallaion, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl.gov Series: IRAK Plate: 79 Row: p Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4755145.
                                                                                                                                                                                              web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Benjamin,B.,
Akhter,N., Ayele,K., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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Contact: MGC help desk
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Submitted (15-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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1 (bases 1 to 4125)
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/db_xref="deneID:165"
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/tissue_type="Brain, adult, 6 pooled whole
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SerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla 8	11 GlnGluGlnLeuLeuAlaAlaAlaMetAlaAlaArgGlyGluAspGluAspGluVal	1 ABDLEUABDG1yG1yG1UArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 	1 SerThrGluValargAlaileilealaTrpMetGluLysAsnProPheValLeuGlyAla 	1 ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 7	11 AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTrpValProTyr 	SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu 	ArgilehibleuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly (	TyrleuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr	1 ThralaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGln 	1 AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 	CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr 	AspPheArgHisHisSerTyrLysAspMetArgGInLeuMetLysValValAsnGluGlu	SerValAlaBrovalTyrSerTyrAlaGlnAsnGluValValAlaThrAspAspLeu	ArgileTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 5	ValaspLysaspThrProValLeuSerGluLeuProGluProValValalaargPheIle 5	81 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500	61 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480
RESULT 5 AB209744 LOCUS DEFINITION ACCESSION	B 8	B 8	Qy db	B &	dg dg	gg Qy	db Qy	Db Oy	Db Qy	B 65	dg Qy	dg Qy	Db Qy	dg dg	Qy Db	οb Oγ	Db
44 AB209744 4038 bp mRNA linear PRI 31-MAR-2005 TION Homo sapiens mRNA for adipocyte enhancer binding protein 1 precursor variant protein. ION AB209744	1141 GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158 	1121 LeuGluProGluPheGluGluGluGluGluGluGluLysGluGluGluIleAlaThrGly 1140 	1101 PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120 	1081 SerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100 	1061 LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGlu 1080 	1041 ThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrThr 1060	1021 ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla 1040 	1001 ProlleProHislleAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGln 1020 	981 IleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000 	961 ThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe 980 	941 AspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyr 960 	921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThrAlaSerGlyGly 940 	901 MetGluGlnValHisArgGlyIleLy8GlyValValThrAspGluGlnGlyIleProIle 920	881 ProHisGluSerGluLeuProArgGluTrpGluAsnAsnLysGluAlaLeuLeuThrPhe 900 	861 PheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880 	841 GlyGlyMetGlyIleValAsnGlyAlaLysTrpAsnProArgThrGlyThrIleAsnAsp 860 	66

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Librate Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute, Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute, Chiba, 292-0816, Japan (E-mail:cdnainfo@kazusa.or.jp, Chiba, 292-0816, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://protein.gsc.riken.go.jp/, Tel:81-438-52-3930, Fax:81-438-52-3931)

This work was supported in part by the National Project on Protein Structural and Functional Analysis , Ministry of Education, Culture , Sports, Science and Technology of Japan. Totoki Y, Toyoda A, Takeda T, Sakaki Y, Tanaka A, Yokoyama S, RIKEN Genomic Sciences Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan. e-mail: aktanaka@postman.riken.go.jp

URL: http://protein.gsc.riken.go.jp

URL: http://protein.gsc.riken.go.jp/.
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Ohara, O., Nagase, T. and F.Kikuno,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                      KTKDKKGKUNGEKUPKGELEGSPRD PKKGKEKPPKATKKPKEKP
PKATKKPKKGKUNGERDE PKOKKERPPKATKKPKEKP
PKATKKPKEKPKATKKPSKEKP
PKATKKPKEKPPKATKKPPKOKRE
NWQNRGEETHVEAREHQPE PEEETEQPTLDVNDQI EREDYEDFEYI RRQKQPRPPPSR
RRPERVWPEDPEEKAPAPAPERRI LDVNDQI EREDYEDFEYI RRQKQPRPPPSR
RRPERVWPEDPEEKAPAPAPERRI EPVKPLLPPLPDYGDGYV I PNYDDMDYY FGP
PPPQKPDAERQTDEEKEELKKPKKEDSSPKEFTDKWAVEKKCHKEPKKGEELEEWT
PTEKVKCPPIGMESHRI EDNQI RASSMLRHLGLAQRGRLNMQTGATEDDYYDGAMCAE
DDARTQMI EVUTRATTRETGVI TQGRDSSIHDDEVTTFFVGFSNDSQTWYMYTNGYEE
MTFHANVDKOTPVLSELPEPVJARFI RI YPLTWNGSLCMELEULGCSVAPVYSYYAQN
EVVATDDLDFRHHSYKMMRQLMKVVNEECPTI TRTYSLGKSSRGLKI YAMEI SDNPGE
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HELGBE PER YTAG HIGNEVLGRELLLLLMYSLCREYRDGNPRVBSLVQOTTRI HJVPSL
NPDGYEVAAQMGSEFGNWALGLWTEEGFDI FEDFPLASHLTLTFREWENNKEALLTF
MGGVHRAARGEDEDEUSGAQFTEDHAI FRILAISFTSAHLTLTLTEPYRGGCQADYTGG
MGI VNGAKWNPRTGTINDFSYLHTNCLELSFYLGCDKFPHESELPREWENNKEALLTF
MEQVHRGI KGVVTDEGGI PI ANATI SVSGINHGVKTASGODYWRLINDFGSYRVTAHAE
GYTPSAKTCNVDYDIGATOCNFI LARSMKKI REIMAMNGNRFI PHI DPSR PWTPQQR
RLQQRLQHRLGLKRAQWRLRRLAATTTLGPHTVPFTL PAAPATTLSTTI EPWGLI PT
TAGMGESSETETYTEVTEFFGTTEVEPEFGTKVEPPEFETQLEPFETQLEPFFEEEEEEE
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/translation="PPAPSPEPPARAAAMAAVRGAPLLSCLLALLALCPGGRPQTVLT
DDEIEEFLEGFLSELEPEPREDDVEAPPPPEPTPRVRKAQAGGKPGKRFGTAAEVPPE
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details_recorded"
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/note="This clone is also named as hsk003002098
vector:pBluescriptII SK plus"
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variant"
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/db_xref="taxon:9606"
/clone="ej00975"
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/mol_type="mRNA"
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                                                               ProAlaProGluGluArgIleGluProProValLy8ProLeuLeuProProLeuProPro
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uGlnLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGluAspGluAs 	mGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThr 	Alail        GCCA1	)AsnAsnAsnLeul           ;AACAATAACTTG(	OASpLeuAsnSerValLeuTrpGlyAlaGluGluArgLySTrpVal 	reGlyAsnTrpAlsLeuGlyLeuTrpThrGluGluGlyPheAsp 	isLeuValProSer]            ACCTGGTGCCCTCA	xLeuCybArgGluTyrArgAbpGlyAbnProArgVal                     CTGTGCCGAGAGTACCGCGATGGGAACCCACGTGTG	TleHisGlyAsn(            ATCCATGCCAAC	4==	:lleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLys 	H18H1	ProVa	ProLe	AspThi        GACACI	ThrTrpValMet'           3ACATGGGTGATG	pSerSerIleHis:             CTCCAGCATCCAT	ThrGlnTrpIleGluValAgpThrArgArgThrThrArgPheThrGlyVal 
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Direct Submission
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                                                         AsnMetGlnThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAsp
                                                                                                    AACCAGATCCGTGCCTTCTCCATGCTGCGCCACGGCCTTGGAGCCCAGGGGGGCCGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-SEP-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Preparation: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
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Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://genome.uiowa.edu
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                              /mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="MGC:100139 IMAGE:30648530"
/tissue_type="Eye"
/clone_lib="NIH BMAP_HB0"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
/note="Vector: pYX-ASC"
                                                                                                                                                                                                                                                           organism="Mus musculus"
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(ValAspLysAspT)	AspSerGlnThrT:	IleThrGlnGlyArgAspSerSerIleHisAspAspPheValThrThrPhePheVa 	AspAlaArgThrGlnTrpIleGluValAspThrArgArgThrThrArgPheThrGlyVa	AsnMetGlnThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAs           	AsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLe		AACAAGGACCACA	GlyLysAspHisL	.ProlyslysGluAspSerSerProlysGluGluThr             CCAAAAAGGAGGGTAGTAGCCCCAAGGAGACACAGAG	lyProProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGl                        CCACCCTCCACCGCAGAAGCCTGATGTTGGACAAGAGGTGGATGAGGAAAAGGAAGA	TyrglyaspglyT           TATGGGGATAGCT	ProAlaProAlaProGluGluArgIleGluProProVally8P 	ACACCCAGCAGGAGGAGGCTCTGGCCAGAGCGCCCTGAGGAGAAGAC	:ArgArgArgArgP	IleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgPr       :::	GluHisGlnProGluProGluGluGluGluThrGluGlnProThrLeuAppTyrAsnAspGln:::	GACACACCTTCCCAAATGCCTGGCAAGGTCAAGGAGAAGAGACCCAGGTGGAGGC	)LeuSerAsnAsnT	LeuGluTrpProLeuProProProProSerProGlyProGluGluLeuProGl     :::	LysAlaThrLysLysProProSerGlyLysArgProProIleLeuAlaPr.          :::	ThrLysLysProLysGluGluProProLysAlaThrLysLysProLysGluLy 
pThrProValLeuSerG	pSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMet	rIleHisAspAsp             CATCCATGACGAC	.uValAspThrArg            GGTGGACACCCGA	.uAspaspTyrTyr            AGATGACTACTAT	TLeuArgHisGly	CCACCTATTGGG	AGGGCCCCGGAAG	pHisLysGluProArgLysGlyGluGluLeuGluGluGluTrp	PSerSerProLys	COASPAlaGluArg	rGlyAspGlyTyrVallleProAsnTyrAspAspMet.           rGGGGATAGCTACGTGATCCCCAACTATGATGACTATG	rgIleGluProPro 	AGGCTCTGG	coGluArqValTrp	ppPheGluTyrIle	luGluThrGluGln           aggagaCTGagaTG	 	rpGlnAsnProGly	roProSerProGly	erGlyLysArgPro ::     ::: CAGGAAAGAAGTTC	roProLysAlaThr             ACCCAAGGCCACC
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ValAla 51	rphe 4	ePheValGly 477	C 45	C 43	gGlyArgLeu 417           GGCCGGCTC 143	∩—	. G-	ω 7	-AspLysTrpAla 35.          GGACAAGTGGACC 12!	u 33	LABPTYrTyrPhe 318           GACTATTATTTC 113	roLeu 29     CrG 10	T 10	a 27	9—0 0 25	91	CAAG 85	uAlaGln 21	nGluGly 19  ::: Gaagaga 79	OSerGluThr 17            CTTGGAAACG 73	uLysProPro 15           AAGCCACCC 67
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AF053943 3790 bp mRNA Mus musculus aortic carboxypeptidase-like complete cds.
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1 (bases 1 to 3790)
Layne,M.D., Endege,W.O., Jain,M.K., Yet,S.F., Hsieh,C.M., Chin,M.T., Perrella,M.A., Blanar,M.A., Haber,E. and Lee,M.E. Aportic carboxypeptidase-like protein, a novel protein with discoidin and carboxypeptidase-like domaine, is up-regulated vascular smooth muscle cell differentiation J. Biol. Chem. 273 (25), 15654-15660 (1998)
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RS Kawai, S., Takeshita, A., Okazaki, M. and Aman, E.

BONE-RELATED CARBOXYPEPTIDASE-LIE PROTEIN AND ITS PRODUCTION

PAtent: JP 1994121682-A 1 06-MAY-1994;

HOECIST JAPAN LTD

OS Mus sp. (mouse)
PN JP 1994121682-A/1
PD 06-MAY-1994
PF 03-DEC-1992 JP 1992324033
PR 28-AUG-1992 JP 92P 230029
PI KAWAI SHINUI, TAKESHITA ATSUSHI, OKAZAKI MAKOTO, AMAN EGON PC C12N9/48, A61K37/02, A61K37/02, A61K39/395, A61K39/395, C07K13/00, PC C07K15/04,
PC C07K15/06, C12N15/57, C12P21/08, G01N33/53, G01N33/577; CC strandedness: Double;
PC C07K15/04,
PC C07K15/06, C12N15/57, C12P21/08, G01N33/53, G01N33/577; CC strandedness: Double;
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PC C07K15/06, C12N15/06, C12N1
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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JP 1994121682-A/1.
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wai,S., Takeshita,A.,
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encoding bone-related carboxypeptidase-like protein,OSF-5.
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378 ThrProThrGluLy8ValLy8Cy8ProProIleGlyMetGluSerHi8ArgIleGluA8p 397 	358 ValGluLysGlyLysAspHisLysGluProArgLysGlyGluGluLeuGluGluGluGluTrp 377 		GlyProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGlu 3	299 ProProAspTyrGlyAspGlyTyrVallleProAsnTyrAspAspMetAspTyrTyrPhe 318	ProAlaProAlaProGluGluArgIleGluProProValLysProLeuLeuProProLeu 2		IleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgPro ;       :::		199 GlyAlaProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHisValGluAlaGln 218	79 LeuGluTrpProLeuProProProProSerProGlyProGluGluLeuProGlnGluGly	159 LysalaThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThr 178	ThrLysLysProLysGluGluProProLysAlaThrLysLysProLysGluLysProPro	119 LysGlyLysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAla 138 	99 LyahapLyaGlyProLyaValProLyaGluSerLeuGluGlySerProArgProProLya 118	79 ProGlyThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysGlyLysGlyLys 98	59 ProProGluProThrProArgValArgLysAlaGlnAlaGlyGlyLysArgGlyLysArg 78	129 CCTGAGGGGAACCCACAGACGGTGCTGACGGACGACGAGGATCGAGGAGTTCCTCGAAGGC 188 41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProPro 58
Oy 738 AlafhrValSerfhrGluValArgAlaIleIleAlafrpHetGluLy8AenProPheVal 757	718 ValProTyrArgValProAsnAsnAsnLeuProTleProGluArgTyrLeuSerProAsp 7	698 IlePheGluAspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTrp	678 GlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAsp 	Qy 658 GlnAspThrArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAla 677	638 LeuMetGlnTyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuVal 	Qy 618 PheArgTyrThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeu 637	Qy 598 LysileTyrAlaMetGluIleSerAspAsnProGlyGluHi8GluLeuGlyGluProGlu 617	Qy 578 AsnGluGluCysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeu 597	Qy 558 AspAspLeuAspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValVal 577		Qy 518 ArgPheIleArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluVal 537	HisGlyAsnValAspLysAspThrProValLeuSerGluLeuProGluProValValAla :::	Qy 478 PheSerAsnAspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPhe 497	IleThrGlnGlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGly	438 As :: 1353 GA	418 ASIMEEGLITTATSGLYALATTATGLIABASDTYTTYTASPGLYALATTATCYSALAGILABD	398 AsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeu 

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                                                                                           CTCAATTCTACCGCA-----GGCCCTGCCACAAGCCCCACTCCTGCCCTTATGCCTCCC
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Sequence
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Patent: US 5460951-A 1 24-OCT-1995;
LOCATION/Qualifiers
1. .3728
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Unknown.
Unclassified.
1 (bases 1 to 3728)
1 (bases 1 to 3728)
Kawai,S., Takeshita,S., Okazaki,M.
Bone-related carboxypeptidase-like
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                                                                                                                  LysaspLysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLys
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458 IleThrGlnGlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGly 477	<b>чече</b>	319 GlyProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGlu	239 IleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgPro 258	159 LysalaThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThr 178
2493 838 2553 858 2613	Cy 7-58 LeuGyALAAABHLEUAASHGLYGLUVAISETTYFFTOTYFABPMETALAATG LEUGYALAAABHLEUAASHGLYGLUVAISETTYFFTOTYFABPMETALAATG Db 2313 CTGGGTGCAAATCTGAACGGTGGTGAGGCGGCTTTGTGTCTTATCCCTATGACATGGCCCGG  CY 778 ThrProThrGlnGlnLeuLeuAlaAlaAlaAlaAlaAlaArgGlyGluAspGlu CY 778 ThrProThrGlnGlnGlnLeuLeuAlaAlaAlaAlaAlaAlaArgGlyGluAspGlu CY 78 ThrProThrGlnGlnGlnCluThrProAspHisAlaIlePheArgTTpLeuAlaIIle Db 2373 ACACCTAGCCAGGAGCAGCTGTTGGCCGAGGAGCAATGAT CY 798 AspGluValSerGluAlaGlnGluThrProAspHisAlaIlePheArgTTpLeuAlaIle Db 2433 GACGGGTTCTGAGGCCCAGGAGACTCCAGATCAGCTATTTTCCGCTGGCTG	Db 2073 CAGATGGGCTCAGAGTTTGGGAACTGGGGCTGTGGACTGAGGAGGGCTTTGAC  Qy 698 IlePheGluAspPheProAspLeuAsnSerValLeuTrpGlyAlaGluArgLysTrp	1833 618 1893 638 1953 658 2013	Qy  \$18 ArgPheIleArgIleTyrProLeuThrTrpAsnGlySerLeuCygMetArgLeuGluVal

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Sequence 8 from Patent WO0224741.
AX473127 AX473127.1 GI:22207848
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                             Homo sapiens (human)
 Ryan, J.W
                     Hominidae; Homo.
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AUTHORS
                                  COMMENT
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                                                                                                                                                                                                      Direct Submission
Submitted (30-SEP-2000) I
University, 4444 Forest E
6 (bases 1 to 153203)
Waterston, R.H.
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Feb 6, 2003 this sequence version replaced gi:5732182.
                                                                                                                                                 Direct Submission
Submitted (06-FEB-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                             MO 63108, USA
5 (bases 1 to 153203)
Waterston, R.
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Monitred (13-AUG-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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Submitted (28-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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AC006454
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The sequence of Homo sapiens
                                                                                                     Wilson, R.
                                                                                                                          MO 63108,
7 (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sulston, J.E. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                        USA
                                                                                                                                                                                                                                         Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
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complete sequence.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu ----- Summary Statistics Center project name: H\_DJ0852P06

Center: Washington University Genome Sequencing Center Center code: WUGSC

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at http://www.chori.org using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994)

The library is from one male donor.
The clone may be obtained either from Genome Systems, Inc. (http://www.resgen.com); or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert o
overlapped by ACO17116 and ACO93086.
Location Qualifiers

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the clone. This clone

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FEATURES

source

repeat\_region /rpt\_fami 29857. .3 /rpt\_family="AT\_rich" 19637. .19720 /rpt\_family="(TG)n" 6111. .6203 /rpt\_family="CT-rich" 24962. .25829 rpt\_family="(TATG)n" /rpt\_family="(TTCC)n"
|6480..16578 rpt\_family="(TG)n" rpt\_family="Alu" /rpt\_family="C-rich" L773: .2072 /clone\_lib="RPCI-5" 10. .177 clone="RP5-852P6" /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" /chromosome="7" \_famil \_family="Alu" family="L1" 7. .37467 \_family="Alu" \_family="(CTG)n" family="MER1\_type" family="(TG)n" family="C-rich" \_family="CT-rich" \_family="CT-rich" .4852 .30160 .16613 24852 y="MER1\_type" .y=" (TG) n"

Alignment Scores:  0	repeat_region 570357210  /rpt_family="Alu"  repeat_region 5810858532  /rpt_family="MaLR"  repeat_region 5965360200  /rpt_family="ERNI"  repeat_region 6039260455  /rpt_family="MIR"	t_region t_region t_region t_region t_region t_region t_region t_region	t_region
84	Db 147154 CACTGAAGCATTTAACCCACGGCCTCTTGCATAATCATGTTGTCAGTAAATCTTAGCTGTT 147095  Qy 84	84	21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly

2/9 roalarroalabroglusculte	Qy       178 rLeuGluTrpProLeuProProProProSerProGluGluLeuProGlnGluGl 198       Qy
55 CCCCAAGCAGGAGGAGGACCCGAGCGGGTCTGGCCAGAGCCCCCTGAGGAGAAGGCCCC	Qy 158 oLysalaThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluTh 178
15 ACTCTGAGCCAGCCTCCCCCTCAGTTGAGTACATTCGGCGCCAGAAGCAACCCAGGCCAC 15 ACTCTGAGCCAGCCTCCCCCTCAGTTGAGTACATTCGGCGCCCAGAAGCAACCCAGGCCAC	Qy         138 aThrLysLysBroLysGluGluProProLysAlaThrLysLysBroLysGluLysBroPr 158         7
75 CCTGGGTCGGACCCCTGGCCTGGGGGATGTGCCAATGGGCCCATCCCAGCCTTGGGCCCC	Qy         118 % SLYSGLYLYSGLULYSPTOPYOLYSALATHYLYSLYSPTOLYSGLULYSPTOPYOLYSAL 138         7
235 YIASINADGIIII IEGIMAI GGIMAID YIGIMAD YIGIMAD 11   1   1   1   1   1   1   1   1   1	Oy         98         SLYSASPLYSGIYPTOLYSVAIDTOLYSGIUSETLEUGIUGIYSETPTOATGPTOLY         118
95 CAGCTACCAGCGCTTTCCCCTCAGAGCCGGAGGAGGAGGAGCCGAGCAACCCACACTGGACT	Oy 85ValProProGluLysThrLysAspLysGlyLysGlyLy 98
145055 GCTGCCCTGGCTGGTTGGACTGAGGGCTTCCCCAGAGTAGGCCTGGGTGGG	Db 146134 GTTCTGGGCATCTAGAGAGGGGCCTCATGGGGGCACAGAGCTGGCTCTGTTCATTTGACA 146075
222	146194 TGACTTAACCTCTCAGTTTGCTGATCCGCACTGGGAACTGACAAGAGTCCCTGTGCCCAG
214	84 84
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199GlyAlaProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHi 214	Db 146314 CTCCCCCTGGGAACTGGGAACCCTACGCTCAGTCTTTAGAGAGGTTGAGATTGGTGGTCA 146255 Oy
198	Qy 84
TTGGAGTGAGCTCGGCCTCAGGAGGGTGTCCACAGGCTCTGTGTGGGCTCTATGGGTGGC	146374 GTGGAGGAGTGGATAGTAAGGAACCCCTATTGAGGTTTTGGCAGGTGGGGGGATGAGGGC 146315
198 198	2
54 AGCTCTCTGGCCCCATGAGATGCCAGCAGGATGCTGAAGGCCAGAGGAGCTCAGGCCTCC	146424 (1970) (19
198	Db 146494 GGGAAGGTCTTGGGCCCATGTCCCTTTGTATGGCAGTTGGCAGGGATGACCAGATG 146435
98	84 84
145474 GCCCCTGCCCAGATGTCCCTGGGCTCTGAGCCCCATGGAGTTCCCCTCCTGCCTTCTCCCCGC 145415	Db 146554 TTCAATACTCAACCAACTGTCCTTTTCTTTGAAGCTTTTCTTTGCCCCCGTAGGAGACCAG 146495
98	146614 CTTCCAATCAATTCCAAACCCCTTACTTCTCGAAAGGAGACCACTTCCTCTTCTTTGGGC 146555
34 AGCCTCTTTTGGGTAGGGAGAGGCTTTGGCAGCCTTTTGGGTGGG	Qy 84 84 Db
145594 TGGGAACCTCACTTTTGCTATAAATTTCACAATTTGATTGGTGGGCTCCCTCAGTGCTGT 145535	146674 GCTCCCTACCTGTCTTTTCTGTCCTCTGTGTGATCCCTGAACCCCCCAGGACTCCCTATC 146615
98	84 84
145654 GGGAGTGGGAGGCAGGTTTCTGGGGCCCTGCTTCCTATAGACCTTCAGCTCCCCACTGGA 145595	Db 146734 AATCCTCACAACCAGTCCCTGCTCCCCTGCTCCCAGACTCTGAAATGAGTGTGCAGCCACAA 146675
198 198	140/74 AILANGITUTAAKAGAALITUKAGGITUTIAGGGITUTIAGGGITUTIAGGGITUTUAGAGITUTUATIGGG
	84 84

142475 GTGGGCATTGGGATGGGCCCATCTCCCAACTGGGATAAGGGACTCCTCCGCCCATGCTCA 142416	143555 CCCACATGGTCCTCAAAGCCCAGAGCCAGGCTGACTGGCCCCTCCTACCTTGCACCTTCC
419 419	339
	Qy 339 339 Db 143615 GBCCABGACCTTTCCCACACCCTTGABAGGCCACCTTGCACGCCTTGAATCCACC 143556
::: 5 GCGTCCTCAGAG 1 ArgAlaSerSer	Oy 323 ProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGluLeu 339
142655 CCTTGGTTCTGGGTTTGGTGGAGGGAAGGATGGAGCTAGTGAGCCACCATTCTGGGGTAC 142596 384Ly8-Cy8ProProIleGlyMetGluSerHi8ArgIleGluAspAsnGlnIle 400	143735 CAGGCCAGCCTCAGCTGGCTCCCCCCCCATAGTGGACTATTACTTTGGGCCTCCTCCG 143676
383 383	Db 143795 GGCGCGGTCCTGTCCTGCTGAGCTCCTGTGGACCCAGGAGCTGAGGCCCCGCAGCAGCAGGGT 143736 Qy  Qy 314
142715 CAGCTGACCAGAGCTGCCCTCTGACTGTGCCCCCGATGTGCCGGGAGTGGGCTCTGGGCT 142656	313 313
142775 GCTCCTGGCCTGGCTTTGAGTCGATTCCAGGTGGGCTGGTGCAGGCACCAGGGAGCCAC 142/16	Db 143855 GACTCCTGCAAGACCCTCTCCCAACTCAGCTGTCCCCATCTCCCGTCCTCCTCTCT 143796 Qy
	Oy 313 313 Oy
5 GTTCTCCAGATGGGGCAGCTGAGGCCCAGGGAGGGGAAGCACAGGCTGGGATTGGAAACA	313 313
142895 CIGGGGGAGCICIACCIGIGATIICACGIGIGCCCCIGAGAGCIGGGCAIGGCAI	Db 143975 TCCAGGCCTTTCCCCATGCCCTGGGCCTCGAGTCCTTTCCCCCAGGCCAGATGCTCCTGGAA 143916 Ov
	Oy 313 313 Oy
S GTATCCCTGCAGGGCCATTGTGCAGACGGTCCCCATCTGGATGACATCTGTGGCTGCGCC	144035 CCAATGTCTCCCCATCTCACCCCCAGCCCGCAACCCCCAGGCACAGGTGCCAGGTTGTCCC 143976
383 383	DD 144095 CUTCUIGGITGCAGCCCGTIGCATCCCCCAGGTCCCCATCAGTGCCT 144036 QY
143015 CGTGGTAGGGGGAGGACCTGGGGGCCTTGGTGGGGAGTGAGGACCTCAGGTACCTTCACAG 142956	313 313
	Db 144155 AGGGCTTTTGCCTCCTGTTGCTCATGCCCCTGCGTCCCTTGAGGCCCTCAGGTTCCCTTT 144096 Oy
GGACCCCAGGCTGGCTTCAGGAGGGTGGCAGCTCCCCAGGGCCCCTAGTGGCTGGG	Qy 313 313 pb
	Db 144215 GTGCTCTAACTGGCTTCCCGCTGGCTCGTGGCCACTGCCCCACTCTCTTCAGGGAGCCCG 144156
143175 GABACCCABACCCACCACCACCACATACCCACCATACCCTTCCCTTCCCTCCCCACCCCT 143076	Qy 313 313 Ph
143195 CTGGCCCAATGTCACAAACAGGACCCAGGTCCCCGGAACCCTTTCCTACTCAGATTCTTG 143136	Db 144275 GGTGTCCCTAGGCACACTCTGCCCTGTCACCCCATGTGGGTTCCAGCCCTCCCAGTCCT 144216
	Oy 313 313
; AGTGGGGGCACAAGGGGTGAGGGTGGGGGCCACAGGATGGGGGTGCTGGGACAAGTGA	144335 CTCAGGCTGGTCTTTCCTTGGCCGCTTCCCTGGTTCCTGCTTGGCTGTGACCCCCACAGG 144276
383 383	313
H	Qy         313
GluProArgLysGlyGluGluLeuGluGluGluTrpThrProThrGluLysVal	Db 144455 GTGGTCAGGAGCCAGCTGGGGCAACTCACCCACCTTGCAACCCCACCTGTGCCCGTGGTT 144396 Qy
GOARCTGAACTCCTGATTGCCTCCCGGGCCCTTGGTGCCATGTCCTCCCTTCATTGTCCC	Oy 313 313 nh
	Db 144515 GTGAGTACCCAGCACCCCAGAGTCTGAGGGACATAGGCAGGTGGGGGTCGGGGCTGGGGT 144456
	Oy 313 313
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340 Lys-LysProLysLysGluAspSerSerProLysGluGluThrAspLysTrpAlaValGl 359	144635 CCACGGCGCTCTGGCCCCCTCCTAACCTCCCCGCCTCCCCAGAGCCTCCTGTGAAGCCTC

740 740	571 571
140315 GCCATCCCTGAACGCTACCTTTCGCCAGATGCCACGGT-GAGGCTACAGCCTGGCTGAA	Qy       561 spPheArgHisHisSerTyrLysAspMetArg
140375 TGTGCTCTGGGGAGCTGAGGAGGAGAATGGGTCCCCTACCGGGTCCCCAACAATAACTT	Qy 543AlaProValTyrSerTyrTyrAlaGlnAsnGluValValAlaThrAspAspLeuA 561
140435 707	Db 141515 TGAGTGGAGGTGGGGTGAGGGTGGGCCAGCCGGCACCCCAGCTAAAGACAACCCCGGCCT 141456 Oy
140495 GTGGGTAGCCGATGCCTACCCTGCTGGCTCCCCACAGGCTCAGAGTTTGGGAACTGGGC	533 etArgLeuGluValLeuGlyCy8SerVal
678 GLIRMEC  140555 CAGATGGTGGGTTGAAGGGTGAGGCTGGCCAGGGTCC	Oy 513 luProValValAlaArgPheIleArgIleTyrProLeuThrTrpAsnGlySerLeuCysM 533
658 GlnAspThrArg1leHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAla	QY 496ThrPheHisGlyAsnValAspLysAspThrProValLeuSerGluLeuProG 513
140675 CTCATGCAGTACCTGTGCCGAGAGTACCGCGATGGGAACCCACGTGTGCGCAGCCTGGTG	QY 495495  Db 141755 ATTGTCTGGGCGAGGGGCTCTCAGAGGGGCTGGCAGTACTGCTCTGAGGCCTGCCT
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140795 CCCTGGGCCTCGGGAGACTGAGTGCTCACTGAGGCTCCCGCCCTTGCAGGGAGCCCGAG	Qy         468 -AspAspPheValThrThrPhePheValGlyPheSerAsnAspSerGlnThrTrpValMe 487
140855 GAGCCCCAGCTGTCCCCCAGACCCTCGGGTATGAGGTGGGTCTGGGTC	141935 AGGCCACCTGAGGGCCTGGGAGGGGAAGACCCCTTGCTCTGACCACTGTCCACCACAG 141876
613	467 467
140915 CTGCCTCCCGCCTGTTCCGGAGCCTCTCTGGGGATTCTGGCTTGTCTTACAGGGGCCCTAG	Db 141995 GGGCCGTGCAGCACCCTGCTAGCTCTTAAATTCTTGGGGCTCGGAAGAGGGGCTC 141936
140975 AACTGGGTGAGGGTCTGTGGGGGGCCAGCAGCTGGCTGCTGCTGATGTGCAGAGCTCA 140916	Db 142055 TTAGGGACAGATCACCTGCCCATGGCTATGTGACGGGCATAGGACCCCAGGCTCAACACCT 141996 OY
612 luLeu 613	Oy 467
92 ysSerSerArgGlyLeuLysIleTyrAlaMetGluIleSerAspAsnProGlyGluHisG 612	467 467
141095	OY 467 467  Db 142175 CCAGTGGGCCCTTCTTTGGCCCAAGCCAAAGAAGGCCCAAAAAAGATCAGTGAGGGACTCACC 142116
141155 GGGGCATGGTCAGCGGGGGGACGGATTGCATGATTGATTCCACGTCCTCCCCCCTCTGCCCC	GGATAGTTGGCAGAGGGGAGTGGCTACATAGGCATGGCTCTGTGTCCCATTAAGGAGATT 142176
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571 571	453
141275 AGTCCCTACTGGTTCCAGGGATGCTGGCTGTCCCTCACCTTAGGAAGGA	Qy         433 pCysAlaGluAspAspAlaArgThrGlnTrpIleGluValAspThrArgArgThrThrAr 453
141335 GGGGTGGGACCTGTCTGTGGCTGACGGGAGTGTGTGCCTGGTGCTTCTGTCACTGGGCCC	QY 420GlmThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTr 433

20	139177 ACTCAGCGAGCAGGTAGAGTCTGGGGAGCCTGGGGGGGGAAATTCAGAGAGGGAGG	망
JOURNAL Biochem. Biophys. Res. Commun. 228 (2), 411-414 (1996)	937 937	Ş
cDNA cloning of	139237 GCACACCTTTACCCCATCTTTCTGAGGGAGGACCCCGCCAGAGAGGGTGGGGGGCTTGAGGA 139178	망
AUTHORS Ohno, I., Hashimoto, J., Shimizu, K., Takaoka, K., Ochi, T., Marsuhara K and Okubo K	937 937	Ş
Mam Hom	921 laAsnAleThrIleSerValSerClyIleAsnHisGlyValLysThrAla 937 	음 성
Homo sapiens (human)	139356 TTCCCTAGGTGCACCGCGCATTAAGGGGGTGGTGACGGACG	멍
VERSION: D86479.1 GI:1468942 KEYWONDS AEBP1.	904ValHisArgGlyIleLysGlyValValThrAspGluGlnGlyIleProIleA 921	Ş
LOCUS D86479. 2839 bp mRNA 11near PRI 07-FEB-1999 DEFINITION Homo sapiens mRNA for AEBP1, complete cds.	139416 GGGCGGGAGGGAGCAGCGGACCACATTGGACCTTCCTGAGGACCAGCAGCCCTCACCTGC 139357	Дb
9 14	903	S
138397	901 tGluGln 903	음 성
1140	139536 TCATGAGAGTGAGCTGCCCCGCGAGTGGGAGAACAACAAGGAGGCGCTGCTCACCTTCAT	밁
Cy 1120 InLengineroginerneging ing ing ing ing ing ing ing ing ing	881 oHisGluSerGluLeuProArgGluTrpGluAsnAsnLysGluAlaLeuLeuThrPheMe 901	ફ
138517 AGTTTGGGACCAAGGTGGAGCCCGAGTTTGAGACCCAGTTGGAGCCCTGAGTTTGAGACCC	139596 CAGTTACCTGCATACCAACTGCCTGGAGCTCTTCTTACCTGGGCTGTGACAAGTTCCCC	당
Qy 1100 luPheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrG 1120	13988 1681CV96A9A9A9GGC16AC1116GG1C161A1C191CCCGGCCAGC1A1CAA119AC11	Q 5
138577	130656	}
1080 luSerGluThrGluThrTyrThrGluValThrGluPheGlyThrGluValGluProG 1100	139716 GGCCAAGTGGAACCCCCGGACCGGGAGTGAGTCAGCCTGGGAGGGGCTGTGGGCGGGGCC 139657	망
Oy 1060 hrteuserThtThrileGluProTryGiyLeulleProFroThrintAldyFyTabdiug 1080	848	Ş
138697 CCACCACCCTAGGCCCCACACTGCCCCCCCCCTGCCCCCCGCCACCACCACCCTGCCCCCTGCCACCACCACCACCCTGCCACCACCACCACCACCACCACCACCACCACCACCACCA	139776 GCCCTACCGCGAGGCTGCCAAGCCCAGGACTACACCGGCGGCATGGCCATCGTCAACGG 139717	문 성
Qy 1040 laThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrT 1060	139836 CCACGCCATCTTCCGGTGGCTTGCCATCTCCTTCGCCTTCGCACCTTATCTTGTTTGACCGA	} 5
757 AGCGACGCCTACAACACCGCCTGCGGCTTCGGGCACAGATGCGGCTGCGGCGCCTCAACG	808 phisAlaIlePheArgTrpLeuAlaIleSerPheAlaSerAlaHisLeuThrLeuThrGl	\$ \&
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138877 1	768 uValSerTyrProTyrAspMetAlaArgThrProThrclnGluGlnLeuLeuAlaAlaAl 788 	B 성
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Direct Submission

Direct Submission

Submitted (11-JUL-1996) Ikko Ohno, Institute for Molecular and Submitted (11-JUL-1996) Ikko Ohno, Institute for Molecular and Cellular Biology, Osaka University, Molecular Genetics; 1-3 Yamada-oka, Suita, Osaka 565, Japan (E-mail:kousaku@imcb.osaka-u.ac.jp, Tel:81-6-879-7992, Fax:81-6-877-1922)
                                                                                                                                                                                                                                                                                                                                                                              MetAspTyrTyrPheGlyProProProGlnLysProAspAlaGluArgGlnThrAsp
Cy8AlaGluAspAspAlaArgThrGlnTrpIleGluValAspThrArgArgThrThrArg
                                              GluGluGluTrpThrProThrGluLysValLysCysProProIleGlyMetGluSerHis
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                                                                                                                                                                                                                                                                                                                  GluGluLysGluGluLeuLysLysProLysGluAspSerSerProLysGluGluThr
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Hering, T.M., Flory, D.M.,
Direct Submission
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Flory,D.M., Kollar,J., Huynh,T.D. and Hering,T.M.
Transcription factor AEBP1 expression during chondrocyte
differentiation and phenotypic modulation
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ValGluLysGlyLysAspHisLysGluProArgLysGlyGluGluLeuGluGluGluTrp
                                                                                    LysLysProLysGluAspSerSerProLysGluGlu-----ThrAspLysTrpAla
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                                                          AAGAAACCCAAAAAAGGAGGCAGCAGCCCCAAGGAAGAGAGAGACAGATGACAAATGGACT
                                                                                                                                        CCTCCCAAGCCCCAGAAGCCCCGACACTGGCCTGGAAACAGATGAAGAGAAGAAGAGCTG
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GFDIYEDFPDVNSVLWGAEERKWVPYRVPNNNLPIPERVLSPDATVSTEVRAIIAME
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IFRWLAISPASTHLTWTEPYRGGCQAQDYTGGMGIVNGAKWKPRGGTINDFSYLHTNC
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5: /BMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

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Sequence 9, Appli
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Sequence 20, Appl
Sequence 584, App
Sequence 210, App
Sequence 4246, Ap
Sequence 4412, Ap
Sequence 1437, Ap
Sequence 249, Appli
Sequence 2249, Ap
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PCT-US93-04384-21	US-09-972-484-50	US-09-494-151-50	US-08-331-625A-50	US-09-551-737C-66	US-09-551-737C-65	US-09-721-543A-17	US-10-131-831-2354	US-10-131-827-2354	US-09-270-767-25514	US-10-131-831-5658	US-10-131-827-5658	US-09-422-978-2579	US-09-422-978-1100	US-09-422-978-2714	PCT-US91-01750-10	PCT-US91-01746-39	US-09-182-145-152	US-08-471-791-39	US-10-131-831-2060	US-10-131-827-2060	US-09-371-489-4
Sequence 21, Appl	50,	Sequence 50, Appl	Sequence 50, Appl	66,	Sequence 65, Appl	Sequence 17, Appl	Sequence 2354, Ap	Sequence 2354, Ap	25514,	Sequence 5658, Ap	Sequence 5658, Ap	Sequence 2579, Ap	Sequence 1100, Ap	Sequence 2714, Ap	Sequence 10, Appl	Sequence 39, Appl	Sequence 152, App	Sequence 39, Appl	•	Sequence 2060, Ap	Sequence 4, Appli

## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Ronald R. Breaker
ITITLE OF INVENTION: Bioreactive Allosteric Polymucleotides
FILE REFERENCE: OCR-794.CIP
CURRENT APPLICATION NUMBER: US/09/849,069
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 09/331,809
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 57
SOFTWARE: MS-DOS
SEQ ID NO 9
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WS-09-849-069-9/c
US-09-849-069-9/c
; Sequence 9, Application US/09849069
; Patent No. 6630306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: G8 DNA US-09-849-069-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: artificial sequence
                                                                                            APPLICANT: NOONBERG, SARAH B.
APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
OLIGONUCLEOTIDES DERIVED THEREFROM
                                                                                                                                                                                                                                                                                                                                                                                                                          100 CCCCCTCTCATTCTCCTGCTCCCACTCTTGCATG 133
                                                                                                                                                                                                                                                                                                                                                                              35 CCGCCTGTCATCCTCCAGCTCCTACCCTTGGCTG
: 755 PAGE MILL PALO ALTO
                                                                                                                                                                                                                                                                   Application US/08324001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                    MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21.2; DB 3;
Pred. No. 2.5e+03;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 49;
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,
                                                                                                                                 OF TRIPLEX FORMING
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COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 CACCTGCTCCCCTTCTCCTTCTGCCATGATT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20, Application US/08324001
5. 5624803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 CTCCTCCACCTCCTCCTTCTCTGATT 41
                                                                                                                                                                                                                                                                                                                                                                                              E: MORRISON & FOERSTER
755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN VIVO OLIGONUCLECTIDE GENERATOR, AND METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING OLIGONUCLECTIDES DERIVED THEREFROM
                                                                                                                                                                                              US/08/324,001
                                                                                         22000-20544.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.8; DB 2;
Pred. No. 3.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 43;
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                                              GENERAL INFORMATION:

APPLICANT: Wohlgemuth, Jay
APPLICANT: Wry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TRANSPLANT REJECTION
FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
NUMBER OF SEQ ID NOS: 9190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-584
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Par
SEQ ID NO 584
SOFTWARE: PatentIn version 3.1
SEQ ID NO 584
LENGTH: 50
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LY, NGOC
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-6-08
RUMBER OF SEQ ID NOWS 9990
NUMBER OF SEQ ID NOS: 9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wohlgemuth, Jay APPLICANT: Fry, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 CACCTGCTCCCCTTCTCCTTCTGCCATGATT 168
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10. 702612
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o. 6905827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 GTGAGAGCTGGTTTGTTTGAAAGAGCCTGGCCCCCTCTCATTC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CTCCTCCTCCACCTCCTCCTCTCTCTGATT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGACCCTGTTTGTTTTAAATATTCTGTTCCCATGTCAATC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Woodward, Robert
                                                                                                                                                                                                                                                                                                                                            Application US/10131831
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Pred. No. 8.1e+03;
0; Mismatches 14;
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Pred. No. 3.
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Gaps

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US-08-324-001-19

STRANDEDNESS:

linear

H: 43 base pairs nucleic acid NDEDNESS: double

TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSN FOERSSFO
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH:

Matches

25;

Conservative

Query Match Best Local Similarity

8.8%;

US-08-324-001-20/c

Sequence 20 Patent No.

GENERAL INFORMATION:

APPLICANT: NOONBERG, SARAH B.
APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: UTIVO OLI
TITLE OF INVENTION: METHODS OF
TITLE OF INVENTION: OLIGONUCLEC
NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

STREET:

CITY: PALO ALTO ADDRESSEE:

CA

COUNTRY:

USA

APPLICATION NUMBER: US/08/324, FILING DATE: 13-OCT-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: MONROY, GLADYS H. REGISTRATION NUMBER: 32,430 REFERENCE/DOCKET NUMBER: 2200 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600 TELEPHONE: (415) 494-0792 TELEX: 706141 MRSN FOERSSFO INFORMATION FOR SEQ ID NO: 20:

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; MOLECULE TYPE: 1
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-480-640A-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-480-640A-210/c
; Sequence 210, Application US/08480640A
; Patent No. 6033904
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; ORGANISM: Homo sapiens
US-10-131-831-584
                                                                                                                                     RESULT 7
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                                                                                                                US-08-686-968C-210/c
          Sequence 210, Application US/08686968C Patent No. 6221361
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION UMBER: US/08/480,640A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
FILE REFERENCE: 39119-H/JML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cochran, Mark D. APPLICANT: Junker, David E. TITLE OF INVENTION: Recombi
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                  199 ATGCTAACGCCATGCTTCTTGTTCTGTCTGCAAAACT 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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66.7%;
                                                                                                                                                                                                                                                                      8.2%;
                                                                                                                                                                                                                                                                                                                                                                        (genomic)
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              Swinepox Virus
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                      DB 3; Length 45;
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                                           Query Match
Best Local Similarity
Thes 26; Conserva
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US-08-488-237A-210/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 210
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 210, Application US/08488237A Patent No. 6251403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/686,968C CURRENT FILING DATE: 1996-07-25 NUMBER OF SEQ ID NOS: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 210:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Homology OTHER INFORMATION: vector 752-22.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                         MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,237A
FILING DATE: 07-UN-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cochran, Mark D. APPLICANT: Junker, David E.
                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 8.2%;
Local Similarity 70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                      ENGTH:
                              199
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41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10036
                                                                                                                                                                                                                     nucleic acid
                    ATGCTAACGCCATGCTTCTTGTTCTGTCTGCAAAACT 235
ATGATTACGCCAAGCTTCTAGTACAGTATTTACGACT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1185 Avenue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                               Conservative
                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                                                       double
                                                                           8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Swinepox Virus
                                                            <u>,</u>
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                                                            Score 19.4; DB 3; Length Pred. No. 9e+03; Indels 0; Mismatches 11; Indels
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                                                              11; Indels
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                                                               Gaps
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US-08-375-992A-210/c
; Sequence 210, Application US/08375992A
; Patent No. 6328975
; Patent No. 6328976
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Sequence 210, Application US/08472679H
Patent No. 6497882
GENERAL INFORMATION:
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NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAC: (212) 391-0525
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,992A
FILING DATE: Herewith
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
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       COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

COMPUTER: PSYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0,
                                                                                                                                                                         NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salkeld
STREET: 2000 Galloping Hill F
                                                                                                                                                                                                                                               APPLICANT: Cochran, Mark D.
Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
   CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 ATGCTAACGCCATGCTTCTTGTTCTGTCTGCAAAACT 235
                                                                                                                                                                                                                                                                                                                                                                                                                              41 ATGATTACGCCAAGCTTCTAGTACAGTATTTACGACT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
DEDNESS: double
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                                                                                                                                          STATE: New Jersey
                                                                                                                           COUNTRY: USA
                                                                                                                                                            CITY: Kenilworth
   APPLICATION DATA:
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220
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                                                                                                                                                                            Hill Road
                    Version #1.25
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                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4246
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Best Local Similarity
Matches 26; Conserv
                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
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APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
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                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
MOLECULE TYPE: DN
HYPOTHETICAL: NO
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RESULT 12
US-10-131-827-4412
; Sequence 4412, Application US/10131827
; Patent No. 6905827
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4246
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE DESCRIPTION: SEQ ID NO: 210:
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                                                                                                                                                          104 CTCTCATTCTCCTGCTCCCACTCTTGCAT 132
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5. 6905827
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                                                                                                                      CCCTCATCCTTCTGCTCACTCTCTTCCAT 50
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Pred. No. 9.4e+03;
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Pred. No. 9e+03;
                                                                                                                                                                                               Mismatches
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; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4246
; LENGTH: 50
; TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-831-4246
                                                                                                                                                                                     RESULT 14
US-10-131-831-4412
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US-10-131-831-4246
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; ORGANISM: Homo Bapiens
US-10-131-827-4412
                                                                                                                          Sequence 4412, Application US/10131831 Patent No. 7026121 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
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                                                           APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WOOdward, Robert
APPLICANT: LY, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
TITLE OF INVENTION: TRANSPLANT REJECTION
FILE REFERENCE: 506612000121
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
TITLE OF INVENTION: TRANSPLANT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILLING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LY, NGOC
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNI
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                 104 CTCTCATTCTCCTGCTCCCACTCTTGCAT 132
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Pred. No. 9.4e+03;
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Search completed: October Job time : 112.569 secs

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US-10-131-827-1437
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-4412
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
SEQ ID NO 1437
LENGTH: 50
TYPE: DNA
                                                                              Matches
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1437, Application US/10131827 Patent No. 6905827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.2%;
Best Local Similarity 79.3%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1 SEQ ID NO 4412
                                                                                                Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNITIED OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/296,764 PRIOR FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/131,8:
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 TTCTCCTGCTCCCACTCTTGCATGAGACA 138
46 TTCTCCTCAGCACTGGTGGTAAGAAGCCCCTTGCTCTCT 7
                                     66 TTCACGTGAGAGCTGGTTGTTTGAAAGAGCCTGGCCCCCT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 TTATCCTGCTTCCACTATAGCATGAATCA 41
                                                                              27;
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Similarity 67.5%;
                                                                              Conservative
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                                                                          Score 19.2; DB 3;
Pred. No. 1.1e+04;
0; Mismatches 13
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Pred. No. 9.4e+03;
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Maximum Match 100%
Listing first 45 summaries
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seq length: 50
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/AE_COMB.seq:*
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Match Length
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242
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-08-503-730-37
US-10-131-837-1159
US-08-644-664B-35
US-08-761-277A-35
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US-08-741-931-25
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US-08-123-936-904
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US-08-475-228A-504
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Sequence 7899, Ap
Sequence 20, Appl
Sequence 20, Appl
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Sequence 1159, Ap
Sequence 1159, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 6394, Ap
Sequence 6784, Ap
Sequence 5784, Ap
Sequence 5784, Appl
Sequence 5784, Appl
Sequence 5784, Appl
Sequence 504, Appl
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US-10-131-827-7899
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Sequence 313, App	313,	•	•	Sequence 313, App	•	Sequence 313, App	•	•	•	•	•	•		Sequence 26, Appl	Sequence 1005, Ap	Sequence 1005, Ap	Seguence 18892, A	Sequence 12, Appl	Sequence 504, App	٠

## ALIGNMENTS

```
APPLICANT: Wohlgemuth, Jay

APPLICANT: Wohlgemuth, Jay

APPLICANT: Woodward, Robert

APPLICANT: Ly, Ngoc

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND

CURRENT OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE REFRENCE: 506612000120

CURRENT APPLICATION NUMBER: US/10/131,827

CURRENT FILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: US 10/006,290

PRIOR APPLICATION NUMBER: US 10/006,290

PRIOR APPLICATION NUMBER: US 60/296,764

PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 9090

SOFTWARE: Patentin version 3.1

SEQ ID NO 7899

LENGTH: 50

TYPE: DNA

ORGANISM: Homo sapiens
US-10-131-831-7899

Sequence 7899, Application US/10131831

PATENT NO. 7026121

GENERAL INFORMATION:

APPLICANT: Wohlgemuth, Jay

APPLICANT: Woodward, Robert

APPLICANT: Ly, Ngoc

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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70.0%; Pred. No. 1.7e
tive 0; Mismatches
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                           FOR DIAGNOSING AND MONITORING
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CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US/10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: PACENTIN VERSION 3.1
SEQ ID NO 7899
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PCT-US94-14106-20/c
commence 20, Application PC/TUS9414106
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                            Sequence 37, Application US/08503730 Patent No. 5780269
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
TITLE OF INVENTION: Process for Gen
NUMBER OF SEQUENCES: 61
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
                                         APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: NEW HYBRID MOLECULES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
COUNTRY:
                                CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US94/14106
                                                                                                                                                                                                                                                                                                                                    177 TTAAGCCCACCGTGTCTGTTAGGGTTGTCTAGGCTGTATCAG 218
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                                                                                                                                                                                                                                                                                                         42 TTGAGCCCAGCGGCCCACTAGTGATATCTGGGCCGAACCAG 1
                                                                                                                                                                                                                                                                                                                                                                               28;
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               PA
USA
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Pred. No. 4.2e
0; Mismatches
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Pred. No. 1.7e+03;
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US-10-131-827-1159/c
; Sequence 1159, Application US/10131827
; Patent No. 6905827
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Best Local Similarity 66.7
28; Conservative
                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1 SEQ ID NO 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                         Matches
                                                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                    APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-106-08
NUMBER: OF SEQ ID NOS: 9090
NUMBER: OF SEQ ID NOS: 9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                             LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Weiser, Gerard J.
REGISTARENE 19,763
REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/503,730
FILING DATE: 18-UUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/817,430
FILING DATE: 06-UAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 GCTCCACCTCCCCAGCTGCTGCCTCACCTGCTTTTCCAAACC 82
                                                                         28;
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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                                                                         Conservative
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Pred. No. 4.5e+03;
0; Mismatches 14;
                                                                       Score 19.6; DB 3
Pred. No. 4.5e+03
0; Mismatches 1:
                                                                                                             DB 3;
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                                                                                                           Length 50;
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RESULT 6

Sequence 1159,

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US-08-644-664B-35/c
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; ORGANISM: Homo sapiens
US-10-131-831-1159
                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: GENT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 9190
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/08644664B Patent No. 5776746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
TITLE OF INVENTION: TRANSPLANT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                SOFTWARE: PATENTIN Release #1.0, VICURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/644,664B
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Gene Amplication Methods NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Denney Jr., Dan W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 01-MAN
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                                                                       nucleic acid
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                                                                                            39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10131831
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                DNA (genomic)
                                                       single
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
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                                                                                                                                                    US-08-391-000-25
                                                                                                                                                                            RESULT 9
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Best Local Similarity
Matches 24; Conserv
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Best Local Similarity 75.0
Matches 24; Conservative
                                                                                                               Patent No.
                                                                                            GENERAL INFORMATION:
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                APPLICANT: HOUTZ, ROTITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: sir
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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NUMBER OF SEQUENCES:
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STATE: California
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Patent No.

COUNTRY: U

TOPOLOGY:

ENGTH:

Matches

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Sequence 25, Application US/08391000 Patent No. 5723752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/761,277A
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/644,664
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MACKHISHL, KAMPIN T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Denney Jr., Dan W
TITLE OF INVENTION: Vaccines
TITLE OF INVENTION: Leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 TGTATCAGATACCCAACTAAAACTGGATTCAC 242
                                                                                                                                                                                                                                                                         211 TGTATCAGATACCCAACTAAAACTGGATTCAC 242
                                                                                                                                                                                                                                    37 TGAAACAGATACGAACCTAAACTTGGATCCAC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Denney Jr., Dan W.
MENTION: Vaccines For Treatment Of Lymphoma And
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
ROBERT L.

1: CLONING AND DEVELOPMENTAL EXPRESSION OF

1: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE

9: SUBUNIT N-METHYLTRANSFERASE
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75.0%; Pred. No. 5.6e+03;
vative 0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                  Score 19.2; DB 2;
Pred. No. 5.6e+03;
                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                     Length 39;
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CORRESPONDENCE ADDRESS:

ADDRESSEE: STREET: P

P.O. Box 1404

Burns, Doane, Swecker & Mathis

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US-08-741-931-25
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NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 028750-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHAX: (703) 836-6620
TELEPHAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08741931 Patent No. 5866394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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APPLICANT: HOUTZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CLOITITLE OF INVENTION: PEA TITLE OF INVENTION: SUBJECT OF SEQUENCES: 411 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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STRANDEDNESS: Bingle
TOPOLOGY: linear
(OLEFORM
                                            APPLICATION NUMBER: US/08/741,931
FILING DATE: 31-OCT-1996
CLASSIFICATION: 45
PRIOR APPLICATION DATA:
APPLICATION UNDATA:
APPLICATION UNDATA:
FILING DATE: 21-FEB-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 GAGCTCCACCTCCCCAGCTGCTGCCTCACCTG 70
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7: United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States
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Pred. No. 5.8e+03
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                                                                                                                                                                                                                                                                                                                        Version #1.30
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APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Hun
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 43
LENGTH: 39
TYPE: DNA
ORGANISM: human
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US-09-475-947A-43
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                                                                                                                                                                                                                                                                                                                                                                                                 US-10-131-827-6394/c
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Best Local Similarity 75.0%;
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                        Sequence 6394, Application US/10131827 Patent No. 6905827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
SEQ ID NO 6394
LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                   APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-10-06-08
NUMBER: OF SEQ ID NOS: 9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 836-20 INFORMATION FOR SEQ ID NO:
                                     SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 836-66. TELEFAX: (703) 836-2021
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100.0%; Pred. No.
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Pred. No. 5
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; ORGANISM: Homo sapiens
US-10-131-827-6784
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US-10-131-827-6784
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; ORGANISM: Homo sapiens
US-10-131-827-6394
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 6784
                                                          NUMBER OF SEQ ID NOS: 9190
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6394
LENGTH: 50
                                                                                                              APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
TITLE OF INVENTION: TRANSPLANT REJECTION
TILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6394, Application US/10131831 Patent No. 7026121
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Best Local Similarity
Matches 25; Conserv
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Best Local Similarity 71.4%;
Matches 25; Conservative
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TYPE: DNA ORGANISM: Homo sapiens -10-131-831-6394
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APPLICANT: Ly, NGCC
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
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APPLICANT:
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APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
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APPLICANT: Fry, Kirk
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Pred. No. 7.3e+0
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APPLICANT: LY, NGOC
TITLE OF INVENTION: TRANSPLANT REJECTION
FILE OF INVENTION: TRANSPLANT REJECTION
FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 06/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: Patentin version 3.1
SEQ ID NO 6784
US-10-131-831-6784
US-10-131-831-6784
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Job time : 116.431 secs
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US-10-131-831-6784
                                                                                                                          Query Match 7.9%;
Best Local Similarity 71.4%;
Matches 25; Conservative
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APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6784,
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Matches :
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APPLICANT:
APPLICANT:
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Woodward, Robert
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Pred. No. 7.3e
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Pred. No. 7.3e+03;
0; Mismatches 10
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Result
No.
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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/abbs/ABSSWEB gpool/US10642946/runat_29092006_125312_12565/app_query.fasta_1
-Q=/abbs/ABSSWEB gpool/US10642946/runat_29092006_125312_12565/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap_-SUFFIX=p2n.mii -MINMATCH=0.1 -LOODCL=0
-LOODEXT=0 -UNITS-blts -START=1 =ND=-1 -MATRIX=blosum62 -TRANS=human10.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR:MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abbs05h -USER=US10642946_@CGN 1 1 315 @runat 29092006 125312 12565
-NCPU=6 -ICPU-3 -NO MAAP -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       6272
6264
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1: /EMC_Celerra_SIDS
2: /EMC_Celerra_SIDS
3: /EMC_Celerra_SIDS
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                                       IleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg
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Sequence 2722 Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-41

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2722

LENGTH: 4092

TYPE: DNA

ORGANISM: Human

US-09-949-016-2722
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Best Local Similarity:
Query Match:
DB:
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                   ThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLysLysAsp
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2707 TCCGAGGCCCAGGAGACTCCAGACCACGCCATCTTCCGGTGGCTTGCCATCTCCTTCGCC	CPT CASE CONTROL CASE CASE CASE CASE CASE CASE CASE CASE	441 ThrGlnTrpTleGluValAspThrArgArgThrThrArgPheThrGlyValIl	당 성
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75. AsnleuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780	C 1506	381 GluLysValLysCysProProTleGlyMetGluSerHisArgTleGluAspAsnGlnI1 	g Q
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	1206	281 ProAlaProGluGluArgIleGluProProValLysProLeuLeuProProLeuProPro	B 8
2167 ACTGCTGGGATCCATGGCAACGAGGTGCTGGGCCGAGAGCTGTTGCTGCTCATGCAG 2221 641 TvrLeuCvsArgGluTvrArgAspGlvAspProArgValArgSerLeuValGlnAspThr 660	280 1146	261 SerArgArgArgArgProGluArgValTrpProGluProProGluGluLysAlaProAla	95 S
	1086	241 ArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgProProPro 	95 9
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GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158
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NAME/KBY:
LOCATION:
US-08-111-939-1
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Best Local Similarity:
Query Match:
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FILING DATE: 26-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 324033/92
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: JP 230029/92
PRIOR APPLICATION UMBER: JP 230029/92
APPLICATION NUMBER: JP 230029/92
APPLICATION NUMBER: JP 230029/92
APPLICATION NUMBER: JP 230029/92
APPLICATION DATA:
APPLICA
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3728 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 0248
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPAX: 202-408-4000
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APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like
TITLE OF INVENTION: Protein and Process for its Production
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
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STRAIN: osteoblastic ce
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STRANDEDNESS: doub
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ProProGluProThrProArgValArgLysAlaGlnAlaGlyGlyLysProGlyLysArg
                                                           TTCCTTTCGGAGTTGGAGACCCAGTCCCCGCCCCGGGAAGACGACGTGGAAGTCCAGCCG
                                                                                              PheLeuSerGluLeuGluProGlu-----ProArgGluAspAspValGluAlaProPro
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RESULT 3
US-08-111-939-1
; Sequence 1, Application US/081119:
; Sequence No. 5460951
; Patent No. 5460951
; GENERAL INFORMATION:
; APPLICANT: Kawai, Shinji
; APPLICANT: Takeshita, Sunao

US/08111939

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Sequence 14464, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Best Local Similarity:
Query Match:
DB:
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SEQ ID NO 14464
LENGTH: 14205
TYPE: DNA
ORGANISM: Human
US-09-949-016-14464
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8906 GGGGGTGGGACCTGTCTGTGGCTGACGGGAGTGTGTGCCTGGTGCTTCTGTCACTGGGCC 8965	420	ક
GAT TI COGGCACCACAGC	7766 GGTGGGCATTGGGATGGGCCCATCTCCCAACTGGGATAAGGGACTCCTCCGCCCATGCTC 7825	뮻
TORGODITO OTRATATADA GORDOTTO A CONTROLA CANTROLA CANTROL	419 419 Oy	ş
8786 TCCCTTGCGCTGTCTACAGCTACGCACAGAATGAGGTGGCCACCGATGACCTG	400 eArgA.aSerserMetLeuArgH18G4YLEUG4HA.aGLIMATGG4YArgLeUASHM8C 419	B 8
543AlaProValTyrSerTyrTyrAlaGlnAsnGluValValAlaThrAspAspLeu	46 CGCGTCCTCAGAGTGTCCCCCCATTGGGATGGAGTCACACCGTATTGAGGACAACCAGAT 7705	В
8726 CTGAGTGGAGGTGGGGTGCTAGGGTGGGCCAGCCGGCACCCAGCTAAAGACAACCCCGCC	384Lys-CysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnI1 400	ş
	7586 TCCTTGGTTCTGGGTTTGGTGGAGGGAAGGATGGAGCTAGTGAGCCACCATTCTGGGGTA 7645	Ď
8666 ATGCCCTGGAAGTGCTGGGCTCCTGTGGCCCCGTGAGTGTGGAAGGGCTGGCAGGGGCT	383 383 Db	Ş
	7526 CCAGCTGACCAGAGCTGCCCTCTGACTGTGCCCCCGGATGTGCCGGGGAGTGGGCTCTGGGC 7585	DЬ
	383 383	ş
	7466 AGCTCCTGGCCTTGAGTCGATTCCAGGTGGGCTGGTGCAGGGCACCAGGGAGCCA 7525	망
	383 383	Ş
CATTGICIE	7406 CGTTCTCCAGATGGGGCAGCTGAGGCCCAGGGAGGGGAAGCACAGGCTGGGATTGGAAAC 7465	ఠ
	383 383 Pr	φ
	7346 CCTGGGGGAGCTCTACCTGTGATTTCACGTGTGTCCCCTGAGAGCTGGGCATGGTCAGCC 7405	망
8436 TGTBACGCTBTGAGGABATGCTGGGCACGATGCCAGGCTCTTGGCTCCC	383 383	Ş
	7286 GGTATCCCTGCAGGGCCATTGTGCAGACGGTCCCCATCTGGATGACATCTGTGGCTGCGC 7345	망
	383 383	ş
	7226 GCGTGGTAGGGGGACCTGGGGGCCTTGGTGGGGAGTGAGGACCTCAGGTACCTTCACA 7285	뮹
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767	7166 TGGACCCCAGGCTGGCTTCAGGAGGGTGGCAGCTCCCCAGGGCCCCTAGTGGCTGG 7225	đ

848	Qy           spHisAlaIlePheArgTrpLeuAlaIleSerPheAlaSerAlaHisLeuThrLeuThrG 828	808	Qy euValSerTyrProTyrAspMetAlaArgThrProThrGlnGlnGlnLeuLeuAlaAlaA 788	768 10285		GGTGTGAAGCTTCATGGAGGGTGATCGGGCTAGGTTGGGGATAGTGGCCGGAGGC	QY	AGGGCAGGAGCAGCTGGACCCTGGGGTCCTGGTGTTCTGGGGCTTGGGGGTGGGGGCT 10045	TGCCCATCCCTGAACGCTACCTTTCGCCAGATGCCACGGTGAGGCTACAGCCTGGCTGAA 9985  Oy	9925	laLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGluAspPheProAspLeuAsnS 707	TGTGGGTAGCCGATGCCTGCTGGCTCCCACAGGGCTCAGAGTTTGGGAACTGGG 9805	aGlnMet679               GCAGATGGTGGGTTGAAGGGTGAGGCTGGGGTTCTGGGGGGG 9745	QY   GlnAspThrArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAl 677	Qy   ULeuMetGlnTyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuVa 657	UPheArgTyrThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLe 637	GCCCTGGGCCTCGGGAGACTGAGTGCTCACTGAGGCTCCCCGCCCTTGCAGGGGAGACCCGA 9505	GGAGCCCCAGCTGTCCCCCAGACCCTCGGGTATGAGGTGGGTCTGGGTCCTTCCT
1039 nAlaThrThrTeuGlyProHisThrValProProThrLeuProProAlaProAlaTh 1059	1019 nGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAs 1039 	999 nArgProIleProHisIleAspProSerArgProMetThrProGlnGlnArgArgLeuGl 1019 	979 nPheIleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAs 999 	YTYTThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAs 	939 yGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGl 959 	937Alasergl 939	936 936 11126 GCCTGGGGGGAACTCAGAGGGGGGAGGGGAGGGCCTGGGGGCAGGACTGAGTGGGAAGG 11185	ACTCAGCGAGCAGGTAGAGTCTGGGGAGCCTGGGGGGGGG	11006 GCACACCTTTACCCCCATCTTTCTGAGGGAGGGACCCCGCCAGAGAGGGGTGGGGGGCTTGAGGA 11065		CTTCCCTAGGTGCACCGCGCATTAAGGGGGTGGTGACGGACG	TGGGCGGGAGGGAGCAGCGGACCACATTGGACCTTCCTGAGGACCAGCAGCAGCCTCACCTG	10766 TGGAGCAGGTGGGGTAGGGCAATGCCTGGGGAAGGAGGCTGCACAGGCTCCTGGA 10825	TOHISGLUSERGLULeuProArgGluTrpGluAsnAsnLysGluAlaLeuLeuThrPheM		58		10486 AGCCCTACCGCGGAGGCTGCCAAGGCCCAGGACTACACCGGCGGCATCGGCATCGTCAACG 10525

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucl
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC53
CURRENT PELICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR PPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-03-20
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; Patent NO. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P
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DR APPLICATION NUMBER: 60/075945

DR FILING DATE: 1998-02-25

DR APPLICATION NUMBER: 60/078910

DR FILING DATE: 1998-03-20

DR APPLICATION NUMBER: 60/083322

DR FILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/084600
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Baker, Kevin P.
Botstein, David
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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Godowski, Paul
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Ferrara, Napoleone
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OR APPLICATION NUMBER: 60/088810
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OR APPLICATION NUMBER: 60/088626
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088658
OR FILING DATE: 1998-06-11
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252

APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948

FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908

APPLICATION NUMBER: 60/089952

FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

APPLICATION NUMBER: 60/089653

NUMBER: 60/089801

FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23

APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23

APPLICATION NUMBER: 60/090431

1998-06-24

FILING DATE:

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Best Local Similarity:
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09 .
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                                                                                         uLysAlaProAlaProAlaProGluGluArgIleGluProProValLysProLeuLeuPr
                                             oProLeuProProAspTyrGlyAspGlyTyrValIleProAsnTyrAspAspMetAspTy
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Matches:
Conservative:
Mismatches:
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696

APPLICATION NUMBER: 60/090694

APPLICATION NUMBER: 60/090676 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690

FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540

FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472

FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090435

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FILING DATE:
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NUMBER: 60/091633

NUMBER: 60/ : 1998-07-02

60/091626

APPLICATION NUMBER: 60/091544
PILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02

APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02

APPLICATION NUMBER: 60/091360 APPLICATION NUMBER: 60/090863

FILING DATE: APPLICATION NUMBER: FILING DATE:

1998-06-26 1998-06-25

60/090862

FILING DATE:

1998-07-01

673 rGluValAlaAlaGlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGl 693	ArgSerLeuValGlnAspThrArgIleHisLeuValProSerLeuAsnProAspGlyTy	uLeuLeuLeuLeuMetGlnTyrLeuCysArgGluTyrArgAspGlyAsnPy                   -:::    :::    :::	uglygluproglupheArgTyrThrAlaglyIleHisglyAsnGluValLeuGlyArgGl	SerArgGlyLeuLysIleTyrAlaMetGluIleSerAspAsnProGlyGluHisGluLe	UMELLYSVALVALASIGLUGLUCYSProThrIleThrArgThrTyrSerLeuGlyLysSe	ValValAlaThrAspAspLeuAspPheArgHisHisSerTyrLysAspMetArgGlnLe   :::	GLeuGluValLeuGlyCysSerValAlaProValTyrSerTyrTyrAlaGlnAsnGl	AlaargPheIleArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetAr 	rPheHisGlyAsnValAspLysAspThrProValLeuSerGluLeuProGluProValVa 	IGLyPheSerAsnAspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetTh 		6 UASPASPAIAATGTHTGINTTPIIEGLUVALASPTHTATGATGTHTTHTATGPHETHTGI		6 uAspAsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyAr 41	76 uTrpThrProThrGluLysValLysCysProProIleGlyMetGluSerHisArgIleGl         :::   ::: :::    28AGTTGCCCACCTCTTGGTCTGGAAACCTTAAAAATCAC	pAlaValGluLysGlyLysAspHisLysGluProArgLysGlyGluGluLeuGluGluGluGluGluGluGluGluGluGluGluGluGlu	617GGCCTCCACCA
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1033 tArgLeuArgArgLeuAsnAlaThrThrThrLeuGlyProHisThrValProProThr 1052	1013 oGlnGlnArgArgLeuGlnGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMe 1033	993 eMetAlaMetAsnGlyAsnArgProlleProHisIleAspProSerArgProMetTnrPr 1013       :::   ::: 2512 CATGGAGAAGTTTGGGAAGCAGCCCGTC	eGlyAlaThrGInCysAsnPheIleLeuAlaArgSerAsnTrpLysArgIleArgGluIl	953 lThralaHisAlaGluGlyTyrThrProSerAlaLysThrCysAsnValAspTyrAspIl 973	933 yValLysThrAlaSerGlyGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArgVa 953 	913 rAspGluGlnGlyIleProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHisGl 933	893 nLysGluAlaLeuLeuThrPheMetGluGlnValHisArgGlyIleLysGlyValValTh 913	873 eTyrLeuGlyCysAspLysPheProHisGluSerGluLeuProArgGluTrpGluAsnAs 893	oArgThrGlyThrIleAsnAspPheSerTyrLouHisThrAsnCysLeuGluLeuSerPh    ::::::	833 YCYSGlnAlaGlnAspTyrThrGlyGlyMetGlyTleValAsnGlyAlaLysTrpAsnPr 853	GTrpLeuAlaIleSerbheAlaSerAlaHisLeuThrLeuThrGluProTyrArgGlyG1           	793 gGlyGluAspGluValSerGluAlaGlnGluThrProAspHisAlaIlePheAr 813					

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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/073920
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
                                                               APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
                                                                                                                                           FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
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APPLICATION !
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087827
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Stewart, Timothy A.
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Kljavin, Ivar J
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Grimaldi, J.Christopher
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Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60/087106
                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR TILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR APPLICATION NUMBER: 60/089947
OR FILING DATE: 1998-06-19
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OR APPLICATION NUMBER: 60/089952
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OR APPLICATION NUMBER: 60/090246
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090252
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OR FILING DATE: 1998-06-22
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BR APPLICATION NUMBER: 60/089538

DR FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089598

DR FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089599
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DR APPLICATION NUMBER: 60/088876

DR FILING DATE: 1998-06-11

DR APPLICATION NUMBER: 60/089105

DR FILING DATE: 1998-06-12

DR APPLICATION NUMBER: 60/089440

DR APPLICATION NUMBER: 60/089512

DR FILING DATE: 1998-06-16

DR APPLICATION NUMBER: 60/089512

DR FILING DATE: 1998-06-16
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OR APPLICATION NUMBER: 60/088217
OR APPLICATION NUMBER: 60/088655
OR APPLICATION NUMBER: 60/088655
OR FILING DATE: 1998-06-09
OR APPLICATION NUMBER: 60/088734
OR PILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088738
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088742
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OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088033
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088326
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088167
OR FILING DATE: 1998-06-05
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Db 728AGTTGCCCACCTCTTGGTCTGAAAACCTTAAAAATCAC 765  Oy 396 uAspAsmGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyAr 416  Oy 11	US-10-642-946-3 (1-1158) x US-09-990-444-61 (1-3772)  Qy
728AGTTGCCCACCTCTTGGTCTGAAACCTTAAAAATCAC 396 uAspAsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyAr	-10-642-946-3 (1-1158) x US-09-990-444-61 (1-3772) 80 GlyThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLysLys 
376 ULLDHILFLUHIGHUNDSVALLDVONDER DE DE DESCRIPCIONES EN LES EN L	10-642-946-3
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376 wTroThrDroThrCluivsVallvsCvsDroDroIleGlvMetGluSerHisArdIleGl	cal Similarity: 45.7% atch: 34.6%
Db 689GATCACAGTGTCCGTGTGGCCCGTGAAGATGTCAGAGAG 727	nt Similarity: 58.3% Conservative:
Qy 356 pAlaValGluLysGlyLysAspHisLysGluProArgLysGlyGluGluLeuGluGluGl 376	lignment Scores: 3.01e-135 Length:
Db 634 ACACAGCAACAAAAAAAGTTATGAGAACCAAGAGCTCTGAGAAGGCTGCCAACGAT 688	FRIOR FILING DAID: 1990-0/-
Qy 336 gGluGluLeuLysLysProLysLysGluAspSerSerProLysGluGluThrAspLysTr 356	APPLICATION
Db 617CCGCCTCCACCA	R APPLICATION NUMBER
Oy 316 rTyrPheGlyProProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLy 336	APPLICATION NUMBER
Db 616 616	R APPLICATION NUMBER
Qy 296 oProLeuProProAspTyrGlyAspGlyTyrVallleProAsnTyrAspAspMetAspTy 316	APPLICATION N
Db 601 GAAGTCG GCTCCGGAG 616	APPLICATION N
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Db 553 CÁGGCCGCCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCCCAAGAGGGA 600	PRIOR FILING NATE: 1998.07-02
Oy 256 oArgProProSerArgArgArgProGluArgValTrpProGluProProGluG1 276	APPLICATION NUMBER: 60/091360
Db 517 GCCCGGGGAGGAGTGGGAGCGGCGCGCAGGAGCC 552	APPLICATION
Oy 236 nAspGlnIleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnPr 256	FRIOR STITUS DATE: 1596-705-25  DETOR STITUS DATE: 1698-76-26
Db 457 GCCCTACTACGCGCGCCCGGAGCCCGAGACCTTCTCTCCCGCCGCTGCCTGC	APPLICATION NUMBER: 60/090696
Qy 216 uAlaGlnGluHisGlnProGluBroGluGluGluGlnProThrLeuAspTyrAs 236	U
Db 397 AGCCCAGGGCGCAGCCCTCGAGGACCCTGATTATTACGGGCAGGAGATCTGGAGCCGGGÁ 456	APPLICATION NUMBER: 60/090694
Qy 216Gl 216	
Db 337 GGGGACCGCTACCCCAGCGCTGGCCCTGGTGCTCCTGGCAGTGACCCTGGCCGGGGTCGG 396	APPLICATION NUMBER: 60/090678
Qy 209 oGlyGluGluThrHisVal 215	APPLICATION NUMBER: 60/090676
pb 289 GACCGTGACCCTGGGCGGGGGGGGGGGGGGGAGGCATGTCCCGCCC 336	APPLICATION NUMBER: 60/090557
Qy 191 ProGluGlu-LeuProGlnGluGlyGlyAlaProLeuSerAsnAsnTrpGlnAsnPr 209	APPLICATION NUMBER: 60/090542
pb 238cccrrrdccccscsccacgccagcccscagacccsccacacccccccc	APPLICATION NUMBER: 60/090540
Qy 179 LeuGluTrpProLeuPro	APPLICATION NUMBER: 60/090535
Db 199	APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24
Qy 159 LysAlaThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThr 178	APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24
Db 154 CCAGCCCAGCCCGGGGCCGGTCACACGCGCAGCCGGCCGG	APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24
Qy 139 ThrLysLysProLysGluGluProProLysAlaThrLysLysProLysGluLysProPro 158	PRIICATION NUMBER: 60/090435 TLING DATE: 1998-06-24
Db 109CGCCCGCCCCGCCCTCTGCGCGCCCCTGTCCGCCCCAGC	APPLICATION NUMBER: 60/090431
Qy 120 GlyLysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAla 138	RILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 ETITING DATE: 1008-06-24
Db 86 108	1998-06-23 1000BER: 60/090355

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|GATCGACAGAATGTCCCCAGGAAAGTTCCCCAATCACTATATTGCAATCCCTGAGTGGTT
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    CGACCTGGTGCGGTCCCCCTGGAAGACGCAG---
                                                                                sAsnProPheValLeuGlyAlaAsnLeuAsnGlyGlyGluArgLeuValSerTyrProTy
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                                rAspMetAlaArgThrProThrGlnGlnGlnLeuLeuAlaAlaAlaMetAlaAlaAlaAr
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Mary E
APPLICANT: Geritsen, Mary E
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kljavin, Ivar J.
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Patent No. 6953836
GENERAL INFORMATION:
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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CACAGCAAAGGCCGAAGGTTTCACTGCATCCACCAAGAACTGTATGGTTGGCTATGACAT
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CCGGGAATCTCTGATCGTGTTCATGGAGCAGGTTCATCGTGGCATTAAAGGCTTGGTGAG
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Ferrara, Napoleone
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CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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                                       eTyrLeuGlyCysAspLysPheProHisGluSerGluLeuProArgGluTrpGluAsnAs
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                                                 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembra

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PLC20

CURRENT APPLICATION UNMBER: US/09/992,598

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

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PRIOR FILING DATE: 1997-06-16

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PRIOR FILING DATE: 1997-06-16
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Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
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Watanabe, Colin K.
Williams, P. Mickey
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Kljavin, Ivar J.
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PREDICATION NUMBER: 60/06770
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                                                         CATCCGAACAGCCAACGATGGGGATTAC
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                                                                                                                                                                                                                                                                                                                                   CCGGGAATCTCTGATCGTGTTCATGGAGCAGGTTCATCGTGGCATTAAAGGCTTGGTGAG
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                                      GGGGGCCACAAGGTGTGACTTCACACTTAGCAAAACCAACATGGCCAGGATCCGAGAGAT
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TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/06770
PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/08106
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PRIOR APPLICATION NUMBER: 60/087609
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OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087759
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087827
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Kljavin, Ivar J.
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Gerritsen, Mary E
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art, Timothy A.
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APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04

60/088025 60/088021

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R FILING DATE: 1998-06R APPLICATION NUMBER: 6
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NUMBER: 60/088029

1998-06-04

60/088028

1998-06-04

NUMBER: 60/

60/088033 60/088030

PRIOR PRIOR PRIOR

FILING DATE: 1998-06
APPLICATION NUMBER:
FILING DATE: 1998-06

1998-06-04 1998-06-04

60/088326

APPLICATION NUMBER: FILING DATE: 1998-00 APPLICATION NUMBER:

FILING DATE: APPLICATION 1

NUMBER:

60/088212

1998-06-05 1998-06-05

60/088202 60/088167

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Alignment 9
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OR APPLICATION NUMBER: 60/090254
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OR APPLICATION NUMBER: 60/090429
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090431
OR APPLICATION NUMBER: 60/090431
OR APPLICATION NUMBER: 60/090435
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OR APPLICATION NUMBER: 60/090444
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DR FILING DATE: 1998-06-16

PR APPLICATION NUMBER: 60/089514

PR FILING DATE: 1998-06-16

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PR FILING DATE: 1998-06-17

PR APPLICATION NUMBER: 60/089598

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PR APPLICATION NUMBER: 60/089599

PR FILING DATE: 1998-06-17

PR APPLICATION NUMBER: 60/089600

PR FILING DATE: 1998-06-17

PR APPLICATION NUMBER: 60/089653

PR FILING DATE: 1998-06-18

PR APPLICATION NUMBER: 60/089801

PR APPLICATION NUMBER: 60/089801

PR APPLICATION NUMBER: 60/089907

PR APPLICATION NUMBER: 60/089908

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3.01e-135 2171.50 58.3% 45.7%

Length:
Matches:
Conservative:
Mismatches:

Score:

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NUMBER: 60/089440

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733 rLeuSerProAspAlaThrValSerThrGluValArgAlaIleIleAlaTrpMetGluLy 753		,	9
1726 GGATCGACAGAATGTCCCCAGGAAAGTTCCCAATCACTATATTGCAATCCCTGAGTGGTT 1785	CATCTCACACAC 3/0  Db  -::::: Db	######################################	g (
713 uGluArgLysTrpValProTyrArgValProAsnAsnAsnLeuProIleProGluArgTy 733		72£	3 8
	356	336	\$ 5
	GGTAA 633 Qy	617CCGCCTCCACCA	ğ
673 rGluValAlaAlaGlmMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGl 693	rAspGluGluLy 336   Qy		र्
:        :::::::	316	296 oProLeuProProAspTyrGlyAspGlyTyrVallleProAsnTyrAspAspMetAspTy	음 중
1486 GCTGCTGCTGCTGCTGCAGTTCGTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCAT 1545 653 lArgSerLeuValGlnAspThrArgIleHisLeuValProSerLeuAsnProAspGlvTv 673	616 Ov	601	뭕
633 uLeuLeuLeuLeuLeuMetGlnTyrLeuCysArgGluTyrArgAspGlyAsnProArgVa 653	BProleuleuPr 296	276 uLyshlaProAlaProAlaProGluGluArgIleGluProProValLy	8 1
1426 CGGTGAGCCCGAGTTCCACTACATCGCGGGGGCCCACGGCAATGAGGTGCTGGGCCGGGA 1485		256 oArgProProProSerArgArgArgArgProGluArgValTrpProGl	3 8
CCACCAGGGCCTGAAGCTGTATGCTGTGGGAGATCTCAGCCCTGGGGAGCATGAAGT	CGGCGCCGCAGGAGCC 552	517 GCCCGGGGAGGAGTGGGAG	밁
3 rSerArgGlyLeuLysIleTyrAlaMetGluIleSerAspAsnProGlyGluHisGluLe	256	236 nAspGlnIleGluArgGlı	Ş
1306 GATGAAAGTTGTGAATGAAATGTGTCCCCAATATCACCAGAATTTACAACATTGGAAAAAG 1365		457	문 5
573 uMetLysValValAsnGluGluCysProThrIleThrArgThrTyrSerLeuGlyLysSe 593		216	5 1
1246 GATGACCACCACTGATGACCTGGATTTTAAGCACCACAATTATAAGGAAATGCGCCAGTT 1305	CTGGAGCCGGA 456		B 8
553 uValValAlaThrAspAspLeuAspPheArgHisHisSerTyrLysAspMetArgGlnLe 573		٠	9 9
		777	3 5
534 qLeuGluValLeuGlyCysSerValAlaProValTyrSerTyrTyrAlaGlnAsnGl 553	Að	200	8
	209	191	\$ 5
6 lAlaArqPheIleArqIleTvrProLeuThrTrpAanGlvSerLeuCvsMetAr	288	238cccrrreccccacecaactrerecaccaacccdcccaacaccccccar	밁
496 THEREADANACAGE AND THE	-ProProProSerProGly 190	179 LeuGluTrp	ঠ
o CAIGGIGAGCAAIGACAGACACAGIGGICACIGIIAAGAAIGGAICIGGAGACAIGAI	237	199	밁
6  GlyPheSerAsnAspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetTh	178	159 LysalaThrLysLysProProSerGlyLysArgProProIl	ð
946 TGTCATCACTCAAGGGAGGAACTCCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGT 1005		154	8
456 yVallleThrGlnGlyArgAspSerSerIleHisAspAspPheValThrThrPhePheVa 476		139 ThrLysLysProLysGluGluProProLysAlaThrLysL	Ş
886 AAGAAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGG 945		109	B 8
436 uAspAspAlaArgThrGlnTrpIleGluValAspThrArgArgThrThrArgPheThrGl 456	**************************************	<b>.</b>	5 5
826 ACTCAACATCCAGGCGGCATTAATGAAAATGATTTTTATGACGGAGCGTGGTGCGCGGG 885		ysys	3 5
416 gLeuAsnMetGlnThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGl 436		4. c	} 5
6 AGACTICCAGCTCCATGCCTCCACGTGAAGCGCTATGGCCTGGGGGGACACATCGAGGAG	99	80 GlyThrAlaAlaGluValProProGluLysThrLysAspL	<b>\$</b>
396 uAspAsnGlnIleArdAlaSerSerMetLeuArdHisGlvLeuGlvAlaGlnArdGlvAr 416	0	US-10-642-946-3 (1-1158) x US-09-989-735-61 (1-3772)	ĕ
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376 uTrpThrProThrGluLysValLysCysProProIleGlyMetGluSerHisArqIleGl 396	o <sub>v</sub>	34.6% Indels:	õ

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Sequence 61, Application US/09989726
Patent No. 7018811
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers Luc
APPLICANT: Desnoyers Luc
APPLICANT: Eaton, Dan L.
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US-09-989-726-61
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C6
CURRENT APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/08322
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/088021
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PRIOR APPLICATION NUMBER: 60/088026
PRIOR PILING DATE: 1998-06-04
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Grimaldi, J. Christopher
Gurney, Austin_L.
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Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
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1998-06-05

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APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742

APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: 1998-0 FILING DATE: 1998-06-APPLICATION NUMBER: 6 FILING DATE: 1998-06-

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Best Local Similarity:
Query Match:
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OR APPLICATION NUMBER: 60/090696
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090862
OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091478
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/090676
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Matches:
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Mismatches:
Indels:
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JR FILING DATE: 1998-06-17

JR APPLICATION NUMBER: 60/089598

JR FILING DATE: 1998-06-17

JR APPLICATION NUMBER: 60/089599

JR FILING DATE: 1998-06-17

JR APPLICATION NUMBER: 60/089600

JR FILING DATE: 1998-06-17

JR APPLICATION NUMBER: 60/089653

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FILING DATE: FILING DATE:

1998-06-17

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APPLICATION NUMBER: 60/089532

1998-06-1

APPLICATION NUMBER:

60/089514 60/089512

APPLICATION FILING DATE:

NUMBER: NUMBER:

1998-06-16 1998-06-1 FILING DATE:

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APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089105

APPLICATION

NUMBER:

60/088861

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APPLICATION NUMBER: 60/088858

FILING DATE:

FILING DATE: APPLICATION 1

NUMBER:

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1998-06-10

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DR FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089801

DR FILING DATE: 1998-06-18

DR APPLICATION NUMBER: 60/089907

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DR FILING DATE: 1998-06-18
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DR APPLICATION NUMBER: 60/090246
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436 UASDASDALBARGTHRGINTTPILEGIUVALASDTHRARGARGTHRTHRARGPHETHRGI 456 :::	376 uTrpThrProThrGluLysValLysCysProProIleGlyMetGluSerHisArgIleGl 396  728	rTyrPheGlyProProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLy	517 GCCCGGGGAGGAGTGGGAG	337 deddaccectractccaececraececraerecrecreerecre	159 LysalaThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThr 178
Qy  813 GTTPLEUNABPGIUMASPGIUMASECTICACACCCCCACCCCCGATGACCACGTGTTCCG 1971  Qy  813 GTTPLEUNALAILESErPheAlaSerAlaHisLeuThrLeuThrGluProTyrArgGlyGl 833	1786 TCTGTCGAAAATGCCACGGTGGCTGCCGAGACCAGAGCAGTCATAGCCTGGATGAAAA  753 SASDProPheValLeuGlyAlaAsnLeuAsnGlyGlyGluArgLeuValSerTyrProTy	673 × 1606 c 693 u 713 u 1726 g	CACCAGGGCTIGAAGCTIGTATGCTGTGGAAGTTCAGGTTACCCTGGGGACCATGAAGCTCAAGGTCTCAGGTTACCCTGGGGACCATGAAGGTGTATGAGGTTACCCTGGGGACCATGAAGGTGTAAGGTGTACAGGTGGTGGTGGTGGGGGGGG	553 UVAIVAIAIATHTASPASPLEUASPPHEATGHISHISSETTYTLYSASPMETATGGITLE  :::	Db 1006 CATGGTGAGCAATGACAGCCACACGTGGGTCACTGTTAAGAATGGATCTGGAGACATGAT 1065  Qy 496 rPheHisglyAsnValAspLysAspThrProValLeuSerGluLeuProGluProValVa 516

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APPLICANT:
APPLICANT:
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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     INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tArgLeuArgArgLeuAsnAlaThrThrThrLeuGlyProHisThrValProProThr 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oGlnGlnArgArgLeuGlnGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMe 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eMetAlaMetAsnGlyAsnArgProIleProHisIleAspProSerArgProMetThrPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACAGCAAAGGCCGAAGGTTTCACTGCATCCACCAAGAACTGTATGGTTGGCTATGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ThrAlaHisAlaGluGlyTyrThrProSerAlaLysThrCysAsnValAspTyrAspI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yValLysThrAlaSerGlyGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArgVa
                                                                                                                                                                                                                                                                        Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGGAGAAGTTTGGGAAGCAGCCCGTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rAspGluGlnGlyIleProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHisGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCCGAGGAGTGGGAGAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eTyrLeuGlyCysAspLysPheProHisGluSerGluLeuProArgGluTrpGluAsnAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OArgThrGlyThrIleAsnAspPheSerTyrLeuHisThrAsnCysLeuGluLeuSerPh 873
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                                                                         Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
                                                                                                                         Roy, Margaret Ann
Stewart, Timothy A.
                                                    Wood, William I.
                                                                                                                                                                 Paoni, Nicholas F.
                                                                                                                                                                                                    Napier, Mary A.
                                                                                                                                                                                                                     Grimaldi, J.Christopher Gurney, Austin L. Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                 Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                   Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- AGCCTGCCAGCCAGGCGGCTGAAGCTGCGGGGGGGGGAAGAGACGACAGCG 2589
Secreted and Transmembrane Polypeptides Acids Encoding the Same
                      and
                      Nucleic
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CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
OR APPLICATION NUMBER: 60/087609
OR APPLICATION NUMBER: 60/087759
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                    FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/089810
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/075945
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FILING DATE: 1997-11-12
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FILING DATE: 1997-10-17
                                                                                           APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/ FILING DATE: 1998-06-11

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APPLICATION NUMBER: 60/089514

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OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/092182
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OR APPLICATION NUMBER: 60/090863

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APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
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uAlaGlnGluHisGlnProGluProGluGluGluThrGluGlnProThrLeuAspTyrAs
                                                                                                                                                                                                                                                                  LysAlaThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThr
                                                                                                                                                                                                                                                                                                                       ThrLysLysProLysGluGluProProLysAlaThrLysLysProLysGluLysProPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AspLysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysLys
                          AGCCCAGGGCGCAGCCCTCGAGGACCCCTGATTATTACGGGCAGGAGATCTGGAGCCGGGA
                                                                                                                                                                                                                  LeuGluTrpProLeuPro------
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                                                                               GGGGACCGCTACCCCAGCGCTGGCCCTGGTGCTCCTGGCAGTGACCCTGGCCGGGGTCGG
                                                                                                      oGlyGluGluThrHisVal---
                                                                                                                                   GACCGTGACCCTGCCCTGGGCGCGCGGGGCGAGCAGGCATGTCC-----
                                                                                                                                                            ProGluGlu-LeuPro---GlnGluGlyGlyAlaProLeuSerAsnAsnTrpGlnAsnPr
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Matches:
Conservative:
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Indels:
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DR FILING DATE: 1998-06-22

R FILING DATE: 1998-06-22

R FILLING DATE: 1998-06-22

DR FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090355

R APPLICATION NUMBER: 60/09035

R APPLICATION NUMBER: 60/090429

FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 PRIOR PRIOR PRIOR PRIOR PRIOR

FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952

FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252

PRIOR PRIOR

FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18

APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948

APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653

APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17

FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801

PRIOR

DR FILING DATE: 1998-06-24

PR APPLICATION NUMBER: 60/090435

PR FILING DATE: 1998-06-24

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NUMBER: 60/090694

1998-06-25

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73 uMetLysValValAsnGluGluCysProThrIleThrArgThrTyrSerLeuGlyLysSe 593   Db	Oy 553 uValValAlaThrAspAspLeuAspPheArgHisHisSerTyrLysAspMetArgGlnLe 573	534 GLeuGluValLeuGlyCysSerValAlaProValTyrSerTyrTyrAlaGlnAsnGl 553	534			456 yVallleThrGlnGlyArgAspSerSerIleHisAspAspPheValThrThrPhePheVa 476	Oy 436 UASDASDALAARGThrGlnTrpIleGluValASDThrArgArgThrThrArgPheThrGl 456 :::	416 gLeuAenMetGlnThrGlyAlaThrGluAepAepTyrTyrAepGlyAlaTrpCyeAlaGl 436	Oy  396 uAspAsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyAr 416	376 uTrpThrProThrGluLy8ValLy8Cy8ProProIleGlyMetGluSerHi8ArgIleGl 396	356 pAlaValGluLysGlyLysAspHisLysGluProArgLysGlyGluGluLeuGluGluGl 376	336 sGluGluLeuLysLysProLysLysGluAspSerSerProLysGluGluThrAspLysTr 356   Oy	rTyrPheGlyProProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLy	OProLeuProProAspTyrGlyAspGlyTyrValIleProAsnTyrAspAspMetAspTy	Qy 276 uLysAlaProAlaProAlaProGluGluArgIleGluProProValLysProLeuLeuPr 296	OY 256 OArgProProSerArgArgArgProGluArgValTrpProGluProProGluG1 276	236 nAspGlnIleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnPr 256	457 GCCCTACTACGCGCGCGCGGAGCCTCGAGACCTTCTCTCCGCCGCTGCCTGC
933 YValLysThrAlaSerGlyGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArgVa 953 ::::::      :::        :::	TASPGINGINGIYII BTOILEALAARAAIATATILESETVA ISETGIYTIEASHISGI	nLysGluAlaLeuLeuThrPheMetGluGlnValHisArgGlyIleLysGlyValValTh  :::  :::  :::    CCGGAATCTCTGATCGTGTTCATGGAGCAGGTTCATCGTGGCATTAAAGGCTTGGTGAG	eTyrleuGlyCysAsplysPheProH1sGluSerGluLeuProArgGluTrpGluAsnAs    :::         ::        ::      ::	853 oArgThrGlyThrIleAsnAspPheSerTyrLeuHisThrAsnCysLeuGluLeuSerPh 873	833 yCysGlnAlaGlnAspTyrThrGlyGlyMetGlyIleValAsnGlyAlaLysTrpAsnPr	813 gTrpLeuAlaIleSerPheAlaSerAlaHisLeuThrLeuThrGluProTyrArgGlyGl 833	793 gGlyGluAspGluAspGluValSerGluAlaGlnGluThrProAspHisAlaIlePheAr 813	TABPMETALARYTHRPYOTHROLNGLUGINLEULEUALAALAALAALAALAALAALAALAALAALAALAALAALA		날… 변	დ—ლ	693 uGluGlyPheAspIlePheGluAspPheProAspLeuAsnSerValLeuTrpGlyAlaGl 713	673 rGluValAlaAlaGlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrG1 693	653 lArgSerLeuValGlnAspThrArgIleHisLeuValProSerLeuAsnProAspGlyTy	633 uLeuLeuLeuLeuHeuGelnTyrLeuCysArgGluTyrArgAspGlyAsnProArgVa 653	Ö É	Q-5	g p

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PRIOR APPLICATION NUMBER: 60/06250
PRIOR TILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR PELICATION NUMBER: 60/075945
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APPLICANT: ABNREASZI.AVI J.
ADDLICANT: Baker, Kevin P.
ADDLICANT: Baker, Tavid
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CURRENT FILING DATE: 2001-11-20
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C72
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Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Roy, Margaret Ann
Stewart, Timothy A
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Gerritsen, Mary E.
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Best Local Similarity:
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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316 rTyrPheGlyProProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLy
                                                                                                               276 uLysAlaProAlaProAlaProGluGluArgIleGluProProValLysProLeuLeuPr
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Matches:
Conservative:
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Indels:
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R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/990472

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090535

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090540

R FILING DATE: 1998-06-24

APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445

APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24

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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090678

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APPLICATION NUMBER: 60/090695

APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24

DR FILING DATE: 1998-06-26

DR APPLICATION NUMBER: 60/090863

DR FILING DATE: 1998-06-26

DR APPLICATION NUMBER: 60/091360

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091478

DR FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091544

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091519

DR APPLICATION NUMBER: 60/091626

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091633

FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090862

B & B & B & B

GGCCCGCTACATCCGCATAAACCCTCAGTCCTGGTTTGATAATGGAGATCTGCATGAG  GLEUGluValLeuGlyCysSerValAlaProValTyrSerTyrTyrAlaGlnAsnGl AATTGGAGATCCTGGCTGCCCACTGCCAGTCCTAATAATTATTATTATCACACCACGAACCA  LVAlValAlaThrAspAspLeuAspPheArgHisHisSerTyrLysAspMetArgGlnLe  :::	336 #GCluGluLeuLysLysProLysGluAspSerSerProLysGluGluThrAspLySTr 356  #GCluGluLeuLysLysProLysGluAspSerSerProLysGluGluThrAspLySTr 356  #GCLUGLULysGlyLysAspHislysGluProArgLysGluGluThrAspLySTr 356  #GACACGCAACAAAAAGTTATGAGAAACCAAGAGCTCTGACAACAGCTGCCAACGAT
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APPLICANT: Klavin, Tvar J.

APPLICANT: Napler, Mary A.

APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.

APPLICANT: Stewart, Timothy A.

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, D. Mickey
APPLICANT: Williams, D. Mickey
APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C37
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Patent No. 7034106
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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US-09-997-349-61
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CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/075945
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                                                                                                                                                                           NR FILING DATE: 1998-06-02
NR APPLICATION NUMBER: 60/087759
NR FILING DATE: 1998-06-02
NR APPLICATION NUMBER: 60/087827
NR APPLICATION NUMBER: 60/088021
NR APPLICATION NUMBER: 60/088021
DR PETLING DATE: 1998-06-04
DR PETLING DATE: 1998-06-04
OR FILING DATE: 1998-06-04
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R APPLICATION NUMBER: 60/0,
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FILING DATE: 1998-02-25
APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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Kljavin, Ivar J.
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Godowski, Paul J.
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PRIOR EPILIAG DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08803
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PRIOR PILIAG DATE: 1998-06-11
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PRIOR PILIAG DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/08959
PRIOR PILIAG DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
PRIOR PILIAG DATE: 1998-06-18
PRIOR PILIAG DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/08950
PRIOR PILIAG DATE: 1998-

Qy 100 AspLysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysLys 119	Oy 80 GlyThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLysLys 99	US-10-642-946-3 (1-1158) x US-09-997-349-61 (1-3772)	5 Gaps:	Vocal Similarity: 45.7% Mismatches:  March: 34.6% Indels:	o.: 3.01e-135 Length: 2171.50 Matches:	nment Scores:	PRIOR APPLICATION NUMBER: 60/092182  PRIOR FILING DATE: 1998-07-09	APPLICATION NUMBER:	; PRIOR ETLING DATE: 1996-07-07 : PRIOR ETLING DATE: 1996-07-07	APPLICATION NUMBER: 6	APPLICATION NUMBER: 6	R FILING DATE: 1998-0 R APPLICATION NUMBER:	z "	APPLICATION NUMBER:	APPLICATION NUMBER:	1998-06-26 NUMBER: 60/	FILING DATE: 1998-0 APPLICATION NUMBER:	20 20		20 20			; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090676	FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/	R FII	; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090540	; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090535	APPLICATION N	APPLICATION NUMBER		APPLICATION N	APPLICATION NUMBER: 60/	ILING DATE: 1998-06 PPLICATION NUMBER:	APPLICATION NUMBER: 6
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GGATCGACAGAATGTCCCCAGGAAAGTTCCCAATCACTATATTGCAATCCCTGAGTGGTT
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                                CGACCTGGTGCGGTCCCCCTGGAAGACGCAG-
                                                                           rAspMetAlaArgThrProThrGlnGluGlnLeuLeuAlaAlaAlaMetAlaAlaAlaAr
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Sequence 61, Application US/09
Patent No. 7034122
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Javid
APPLICANT: Baten, Dan L.
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Mapoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gomaldi, J. Christ
APPLICANT: Gurney, Austin L.
APPLICANT: Napole, Mary A.
APPLICANT: Napole, Mary A.
APPLICANT: Rapplicant J.
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Ferrara, Napoleone
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Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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                      Gurney, Austin L. Kljavin, Ivar J. Napier, Mary A.
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CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
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OR FILING DATE: 1997-06-16
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/065186
OR APPLICATION NUMBER: 60/065311
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Roy, Margaret Ann
Stewart, Timothy
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Williams, P. Mickey
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GCTGCTGCTGCTGGTGCAGTTCGTGTCAGGAGTACTTGGCCCGGAATGCGCGCAT 1545
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                                      eTyrLeuGlyCy8AspLysPheProHisGluSerGluLeuProArgGluTrpGluAsnAs
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: U9/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13 APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David INFORMATION: Watanabe, Colin K. Williams, P. Mickey Wood, William I. Goddard, Audrey Godowski, Paul J. Grimaldi, J.Christopher Application US/09989293A Tumas, Daniel Roy, Margaret Ann Stewart, Timothy A. Gurney, Austin L. Kljavin, Ivar J. Gerber, Hanspeter Gerritsen, Mary E. Fong, Sherman Ferrara, Napoleone Eaton, Dan L. Pan, James Napier, Mary A. Desnoyers, Luc Paoni,Nicholas F. Colin K.

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OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR APPLICATION NUMBER: 60/078910
OR PILING DATE: 1998-02-25
OR APPLICATION NUMBER: 60/08322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
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OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
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                                    uGlyGluProGluPheArgTyrThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGl
                                                                        rSerArgGlyLeuLysIleTyrAlaMetGluIleSerAspAsnProGlyGluHisGluLe
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| CCACCAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATCACCCTGGGGAGCATGAAGT
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Search completed: October 1, 2006, 00:05:10 Job time : 696 secs

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Run on:

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Minimum DB
Maximum DB
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-Q=/Abss/RBsSRBs spool/US10642946/runat 29092006 125315 12622/app_query.fasta_1
-DB=Published Applications NA main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH-01 -LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
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-HEADSIZE=500 -NINLEN-0 -MAXLEN-200000000 -HOST=abss03p
-USER=US10642946 @CCN 1 12530 @runat 2999206 125315 12622 -NCPU=6 -ICPU=3
-NORMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WAEN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prir and is derived by analysis of the total score distribution.
                                    Score
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seq length: 2000000000
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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Ygapop 10.0 , X
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                            Sequence 1, Application US/10238876

Publication No. US2030084464A1

GENERAL INFORMATION:

APPLICANT: Lee, Mu-En

APPLICANT: Lee, Mu-En

APPLICANT: Lee, Matthew D.

APPLICANT: Yet, Shaw-Fang

FITLE OF INVENTION: AORTIC CARDOXYPEPTIDASE-LIKE POLYPEPTIDE

FITLE REFERENCE: 21509-036CIPCON

CURRENT APPLICATION NUMBER: US/10/238,876

CURRENT FILING DATE: 2002-09-10

PRIOR APPLICATION NUMBER: US 09/060,482

PRIOR APPLICATION NUMBER: US 08/818,009

PRIOR APPLICATION NUMBER: US 08/818,009

PRIOR APPLICATION NUMBER: US 60\013,439

PRIOR APPLICATION NUMBER: US 60\013,439

PRIOR FILING DATE: 1996-03-15

NUMBER OF SEQ ID NOS: 8

SOPTWARE: FastSEQ for Windows Version 3.0

LENGTH: 3935
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Sequence 1, Appli
Sequence 288, App
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Sequence 1128, App
Sequence 128, App
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Sequence 128, App
Sequence 198, App
Sequence 198, App
Sequence 198, App
Sequence 196, Appli
Sequence 8, Appli
Sequence 196, Appli
Sequence 53, Appli
Sequence 53, Appli
Sequence 53, Appl
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Alignment Scores:
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Query Match:
DB:
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; LOCATION: (140)...
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                                                                                                              ArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys
                                                                                                                                ValAspLysAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIle
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                                                          CysProThr11eThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLys11eTyr
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     ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla 1040
                                                                                                                                                                               IleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg
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                                                                                                                             APPLICANT: HOTCOMSY', GADILEL N.

APPLICANT: Meric, Punda
APPLICANT: Meric, Punda
APPLICANT: Meric, Punda
APPLICANT: Meric, Punda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSE.
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/305,501
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-05-04
PRIOR FILING DATE: 2002-05-14
NUMBERS OF SEO TD NOSE: 506.
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Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Clatt, Karen
APPLICANT: Clatt, Karen
APPLICANT: Chao, Xumei
APPLICANT: Gannavarpu, Manjula
APPLICANT: Mertens, Maureen
APPLICANT: Mertens, Maureen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wondhan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobgyi, Gabriel N.
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NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FASTSEQ for Wir
; SEQ ID NO 1
; LENGTH: 3935
TYPE: DNA
; ORGANISM: Homo sapiens
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Monahan, John
Meyers, Rachel E.
Bast Jr., Robert C.
Hortobagyi, Gabriel N
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APPLICANT: Ringner, Markus
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Markus
APPLICANT: Reterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
TILE REFERENCE: 11613.56USI1
CURRENT APPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION UNMBER: US 10/133,937
PRIOR APPLICATION UNMBER: US 10/133,937
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SOCTWARE: Patentin version 3.1
SEQ ID NO 288
LENGTH: 3935
TYPE: NA
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Sequence 194, Application US/10775920

Publication No. US20040175744A1

GENERAL INFORMATION:
APPLICANT: Mergen Ltd
APPLICANT: Mergen Ltd
INTILE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCORTITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROFITILE OF INVENTION: IN CERTAIN CANCERS

FILE REFERENCE: Mergen - 0010B
CURRENT APPLICATION NUMBER: US/10/775,920
CURRENT APPLICATION NUMBER: US/04-02-10
PRIOR APPLICATION NUMBER: US 60/447,900
PRIOR APPLICATION NUMBER: US 60/447,900
PRIOR APPLICATION NUMBER: US 60/447,900
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Best Local Similarity:
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APPLICANT: Mergen Ltd

ITITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCORPTION OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PRO?

ITITLE OF INVENTION: IN CERTAIN CANCERS

FILE REFERENCE: Mergen - 0010B

CURRENT APPLICATION NUMBER: US/10/775,920

CURRENT APPLICATION NUMBER: US 60/447,900

PRIOR APPLICATION NUMBER: US 60/447,900

PRIOR APPLICATION NUMBER: US 60/447,900

PRIOR FILING DATE: 2003-02-13

NUMBER OF SEQ ID NOS: 385

SOFTWARE: Patentin version 3.2

SEQ ID NO 195

LENGTH: 3935

TYPE: DNA

ORGANISM: Homo sapiens
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Best Local Similarity:
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STrDValProTyr 720              argggTcccctac 2299	ePheGlu 700         CTTTGAA 2239	aGlnMetGly 680           CAGATGGGC 2179	r 660     2119	2059	r 620 C 1999	r 600     1939	luGlu 580        AGGAG 1879	aThrAspAspLeu 560 	8 540     C 1759	1699	n 500     1639	1579	1519	1459	nMetGln 420          CATGCAG 1399	e 400 C 1339	UTIPThrProThr 380              TGGACGCCTACG 1279	1219
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260 T 61 G 81 T	ArgGlyAlaProLeuleuSerCysLeuleuAlaLeuleuAlaLeuCys 20	Pred. No.: 0 Length: 3935 Score: 6272.00 Matches: 1158 Percent Similarity: 100.0\$ Conservative: 0 Best Local Similarity: 100.0\$ Mismarches: 0 Query Match: 9 Indels: 0 DB: 9 Gaps: 0 US-10-642-946-3 (1-1158) x US-10-473-974-128 (1-3935)	; SEQ ID NO 128 ; LENCTH: 3935 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-473-974-128	PRIOR FILING DATE: 2002-04-05 PRIOR APPLICATION NUMBER: 60/281,400 PRIOR FILING DATE: 2001-04-05 PRIOR FILING DATE: 201-04-05 PRIOR FILING DATE: 301-04-05	FILE REFERENCE: 37991-0023  CURRENT APPLICATION NUMBER: US/10/473,974  CURRENT FILING DATE: 2003-10-03  PRIOR APPLICATION NUMBER: PCT/IB02/02211	APPLICANT: JACKSON, AMANDA APPLICANT: BUGHNELL, STEVEN APPLICANT: RAWADI, GEORGES TITLE OF INVENTION: GENES INVOLVED IN	APPLICANT: BARON, ROLAND APPLICANT: CALL, KATHERINE APPLICANT: THEILHABER, JOACHIM APPLICANT: THEILHABER, JOACHIM	Publication No. US20040265808A1  GENERAL INFORMATION: APPLICANT: GARCIA, TERESA APPLICANT: GARCIA, TERESA	ESULT 6 S-10-473-974-128 Sequence 128. Application US/10473974	GInAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158	Qy 1121 LeuGluPheGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluG	Qy 1101 PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120	Qy 1081 SerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100
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APPLICANT: Wyeth
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APPLICANT: MOUNTE, William
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ITITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 561
LENGTH: 3935
TYPE: DNA
ORGANISM: Homo sapiens
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                    CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr 600
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941 ThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe 980		01 11. Cordi.: T1. 00. Cordinates and C1.
Alignment Scores:  Pred. No.:  6272.00  Matches:  Percent Similarity:  100.0*  Best Local Similarity:  100.0*  Conservative:  Mismatches:  Query Match:  100.0*  Indels:  0	Db 3020 ACCCCAGCARGACCTCCAACTGCAACTGCAACTCCAGGCCCAACTCCAGGCCACCTCCAGGCCAACTCCCAGGCCAACTCCCAGGCCCAACTCCAGGCCCAACTCCAGGCCCAACTCCAGGCCCCAACTCCAGGCCCCCAACCCCAGGCCCCCAACCCCCAGGCCCCCAACCCCCAGGCCCCCAACCCCCC	

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             LeuSerThrThr11eGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGlu
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APPLICANT: THEILHABER, JOACHIM
APPLICANT: CONNOLLY, TIMOTHY
APPLICANT: CONNOLLY, TIMOTHY
APPLICANT: JACKSON, AMANDA
APPLICANT: JACKSON, AMANDA
APPLICANT: BUSHNELL, STEVEN
APPLICANT: RAWADI, GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
FILE REFERENCE: 37991-0023
CURRENT FILING DATE: 2005-10-07
PRIOR APPLICATION NUMBER: US/11/245,147
CURRENT FILING DATE: 2005-10-07
PRIOR APPLICATION NUMBER: PCT/IB02/02211
PRIOR APPLICATION NUMBER: PCT/IB02/02211
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
SOFTWARE: PALENTIN Ver. 3.2
SEQ ID NO 128
LENGTH: 3935
TYPE: DNA
CRGANISM: Homo Sapiens
US-11-245-147-128
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APPLICANT: ROWAN R.
APPLICANT: BARON, I
APPLICANT: CALL, K
APPLICANT: THEILHAL
APPLICANT: CONNOLL.
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; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Myeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSC
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (Am 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5213
; SEQ ID NO 5213
; LENGTH: 3914
; TYDE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-5213
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Best Local Similarity:
Query Match:
DB:
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RESULT 11  US-10-775-920-198  Sequence 196, Application US/10775920  Publication No. US20040175744A1  GENERAL INFORMATION:  APPLICANT: Mergen Ltd  TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES  TITLE OF INVENTION: OP PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED  TITLE OF INVENTION: IN CERTAIN CANCERS  FULL REFERENCE: Mergen - 0010B  CURRENT APPLICATION NUMBER: US/10/775,920  CURRENT APPLICATION NUMBER: US/10/775,920  CURRENT FILING DATE: 2003-02-13  NUMBER OF SEQ ID NOS: 385  SOFTWARE: PATENTIN VERSION 3.2  SEC ID NO 198  LENGTH: 4125  TYPE: DNA  NORGANISM: Homo sapiens  US-10-775-920-198  Alignment Scores:  Percent Similarity: 100.0%  Best Local Similarity: 99.8%  Ouery Match: 99.9%  Ouery Match: 99.9%  US-10-642-946-3 (1-1158) x US-10-775-920-198 (1-4125)  US-10-642-946-3 (1-1158) x US-10-775-920-198 (1-4125)	9961 ThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe 980
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             CTCCCCCCAGAAGCCCGATGCTGAGCGCCAGACGACGAAGAAGAAGAAGGAGCAGCTGAAGA
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APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND
FILE REFERENCE: 15117.0012
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
UNMER OF SEQ ID NOS: 805
SOFTWARE: PATENTIN DATE: 2011-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 345
LENGTH: 3170
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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roProProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGluLeuLysL
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	Q Db	Oy 641 yrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThrA 661
	OV D	Qy 621 hrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuLeuMetGlnT 641
	δ β <sub>τ</sub>	Qy 601 laMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyrT 621
	S B 7	Oy 581 ysDroThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyrA 601
2147 CCAACGCCACCATCTCTGTGAGTGGCATTAATCACGGCGTGAAGACAGCCAGTGGTGGTG 2206	Q B 4	Qy 561 spPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValValAsnGluGluC 581
2087 TGGAGCAGGTGCCACCGTGGCATTAAGGGGGTGGTGACGGACG	S & 4	Oy 541 ervalalaprovalTyrSerTyrTyrAlaGlnAsnGluvalValAlaIThrAspAspLeuA 561
2027 CTCATGAGAGTGAGCTGCCCCCCGCGAGTGGGAGAACAACAAGGAGGCGCTGCTCCACCTTCA 2086 2027 CTCATGAGAGTGAGCTGCCCCCCGCGAGTGGGAGAACAACAAGGAGGCGCTGCTCACCTTCA 2086	S B 1	Qy 521 rglleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCysS 541
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761 SDLEUASNGLYGLYGLUKTGLEUWALSETTYTEFOLYTASDMECKALAKIGINIFFOLITIG 761 1667 ATCTGAACGGCGAGCGAGCGAGTATCCTACCCCTACGCTATATGGCCCGCACGCCTACCC 1726 1781 INGINIFENI-NANAANAANAANAANAANAANAANAANAANAANAANAAN	S B S	01
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<b>.</b>	84	Db 10653 ACGGCCGCAGAAGGTAAGAGCCCCAGGGCCAGGGCGGGGGGTGTGGGGGGGCTGGCATCTCAGG 10594	Oy 81 ThralaalaGlu84	10713 GAGCCCACCCGCGGGTCCGAAAAGCCCAGGGGGGGGGAAGCCAGGGAAGCCGCCAGGG 1	61 GluProThrProArqValArqLvsAlaGlnAlaGlvGlvLvsProGlvLvsArqProGlv 80	10773 TTCCTGTCAGAGCTAGAACCTGAGCCCCGGGAGGACGACGTGGAGGCCCCGCCGCCGCCTCCC 1	41 PheLeuSerGluLeuGluProGluBroArgGluAspAspValGluAlaProProProPro 60	10833 CCTGGAGGGCGCCGCAGAACGGTGCTGACCGACGAGAATCGAGGAGTTCCTCCAAGGGC 1	21 ProGlyGlyBraproGlyThrValiestThrBenBenGl;;IleGl;;GhelenGl;;Gly 40	Db 10893 ATGGCGGCCGTGCGCGCGCCCCTGCTCACCTGCCTGCCTG	1 Motalaalavalarogivalaprojenijengarovejenijelanjajenijelanjajetenove 2	.642-946-3 (1-1158) x US-09-957-956-8 (1-16161)	76.4% Indels:	milarity: 36.0% Conservative:	0 4791.00	Scor	; ORGANISM: Homo sapiens US-09-957-956-8		SOFTWARE: PatentIn version 3.1	PRIOR FILING DATE: 2001-09-21 NUMBER OF SEO ID NOS: 8	CURRENT FILING DATE: 2001-09-21 PRIOR APPLICATION NUMBER: US 60/234.422	FILE REFERENCE: JR-14,000-US CURRENT APPLICATION NUMBER: US/09/957.956	APPLICANT: Ryan, James W. TITLE OF INVENTION: Genomic Polynucleotide Fragments From Chromosome 7	Publication No. US20030130215A1 GENERAL INFORMATION:	US-09-957-956-8/c : Seguence 8. Application US/09957956	15	2807 AGGCATTCCCCCTTCACAAGAAGAACCTACAACAGTGAACTTTTCCGGGAACTTTC	1141 lnAlaPheDroPheThrThrValGluThrTvrThrValAsnDheGlvAsnDhe 1158		1121 euGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluTleAlaThrGlvG 114	2687 TTGGGACCAAGGTGGAGCCCGAGTTTGAGACCCCAGTTGGAGACCCTGAGTTTGAGACCCAGC	1101 heGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGlnL 112	2627 CGGAGACTGAGACCTACACAGAGGTTGGTGACAGAGTTTGGGACCGAGGTTGGAGACCGAGTT	Db 2567 TGAGCACTACCATAGAGCCCTGGGGCCTCATACCGCCAACCACCGCTGGCTG
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Db 7294 CTCAGGCTGGTCTTTCCTTGGCCGCTTCCCTGGTTCCTGGCTGTGACCCCCACAGG 7235	313	4 ACCTCGCTGTCCCTGCTGTCCCTGCGTGCCCACCCCAGCCACTGCCCTGTCTCCTCTGCC	313	TALA GTGGTCAGGAGCTGGGGCAACTTCACCCACCTTGCAACCCCACCTGTGCCAGGTT 7355	74/4 GTGAGTACCCAGCACCACAGASTCTGAGGGACATAGGCAGGATGGGGGGTCGGGGGT	313	7534 TGCTGCCCCGCTGCCCCTGACTATGGTGATGGTTACGTGATCCCCGAACTACGATGACA	Qy 294 euLeuProProLeuProProAspTyrGlyAspGlyTyrValIleProAsnTyrAspAsp- 313	7594 CCACGGCGCTCTGGCCCCTCCTAACCTCCCCGCCTCCCCAGAGCCTCCTGTGAAGCCTC	Db 7654 CGGCCCCAGCCCCGGAGGAGGAGGATTGGTAGGATTGGGGGGGCAGGAGAGGAGGAGGTGCCATGG 7595	279 roAlaProAlaProGluGluArgIle	Db 7714 CCCCAAGCAGAAGGAGGAGGCCGAGGCGGGTCTGGCCAGAGCCCCCTGAGGAGAAAGGCCC 7655	7774 A	Db 7834 CCTGGGTCGGACCCCTGGCCTGGGGGATGTGCCAATGGGCCCATCCCAGCCTTGGGCCCC 7775  Qy 248	Qy 247 247	7894 ACMATGACCAGATCGAGAGGGAGGACTATGAGTAGGGTAGG	Db 7954 CAGCTACCAGCGCTTTCCCCTCAGAGCCGGAGGAGGAGAGCCGAGCAACTGGACT 7895 Ov 235 VrAsnAspGlnIleGluArqGluAspTyrGluAspPhe	Qy 223GluProGluGluThrGluGlnProThrLeuAspT 235	æ	222		214 eValGluAlaGluGluGluGluFro	### ##################################	100C1vAlagettccxxxygtggtcxgggtxgggcxggcttcccxccttcttcttcttcttcttcttcttcttcttct	01.03 ポンクラではアンクラックでは、そのでは、そのでは、そのでは、そのでは、そのでは、そのでは、そのでは、その	~		8313 AGCTCTCTGGCCCCATGAGATGCCAGCAGGATGCTGAAGGCCAGAGGAGCTCAGGCCTCC	Qy 198 198

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5374 GCCTCCCCTGCCCCTGGACAGACCGGTGCCACTGAGGACGACTACTATGATGGTGCGTG 5315	6454 AGAGAAAACCCAAAAAAGGAGACAGCACCCCAAAGAAGAGAGACCGACAAGTGGGCAGTGGA 63	문 :
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GCGTCCTCAGAGTGTCCCCCCATTGGGATGGAGTCACACCCGTATTGAGGACCAACCA	6634 CCCCAGAAGCCCGATGCTGAGCGCCAGACGAACGAAGAAAAGGAGGAGTGAGT	문
384Lys-CysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle 400	323 ProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGluLeu 339	Ş
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5734 GCTCCTGGCCTGGCTTTGAGTCGATTCCAGGTGGGCTGGTGCAGGGCACCAGGGAGCCAC 5675	6814 GACTCCTGCAAGACCCTCTCCCAACTCAGCTGTCCCCCATCTCCCGTCCTCCCCCTCT 6755	망
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5974 CGTGGTAGGGGGAGCCTGGGGGCCTTGGTGGGGAGTGAGGACCTCAGGTACCTTCACAG 5915	7054 CCTCCTGGGTGGCAGCCCGTGCATCGCCATTTCCCCTGCCCCAAGGTCCCCATCAGTGCCT	문 .
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6094 GGACCCAGAAGGGAGGCCCCGGGAGCCCAGGATAGCCTCGCTTGGCTGCCCCAGCCCT 6035	b 7174 GTGCTCTAACTGGCTTCCCGCTGGCTCGTGGCCACTGCCCCACTCTCTTCAGGGAGCCCG 7115	밁
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035 GCAGCCCTGGCCTCACACGTGCTGGCCACTCCAGGT 748 eAlaTrpMetGluLysaanProPheValLeuGlyAl	- C - C - C - C - C - C - C - C - C - C	8 B 8
3095 GTACTGGTGTGAAGCTTCATGGAGGGTGATCGGGCTAGGTTGGGGATAGTGGCCGGAGCT 741SerThrGluValArgAlaIleIl	GGGGGCTGCGTGAAGGGGTCATGCCCGTCCCCTCGCCATAGAGCAGGCCCCTGGAAGTGGAA	운 문
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3215 AGGGCAGGAGGAGCAGCTGGACCCTGGGGTCCTGGTGTTCTGGGGCTTGGGGGTGGGGCT	570 570 Db 4294 GGGGTGGGACCTGTCTGTGGCTGACGGGAGTGTGTGTGTG	용 성
3274 GCCCATCCCTGAACGCTACCTTTCGCCAGATGCCACGGT-GAGGCTACAGCCTGGCTGAA	561 spPheArgHisHisSerTyrLy8AspMet	ρ γ
3334 TGTGCTCTGGGGAGCTGAGGAGAGGAAATGGGTCCCCTACCGGGTCCCCCAACAATAACTT 727 uProIleProGluArgTyrLeuSerProAspAlaThrVal	143	р Q
3394 GCTGGGACTGTGGACTGAGGAGGGCTTTGACATCTTTGAAGA 707 rValLeuTrpGlyAlaGluGluArgLy8TrpValProTyrAr	4 TGAGTGGAGGTGGGTGCTAGGGTGGGCCAGCCGGCACCCAGCTAAAGACAACCCCGCCT 4	dg .
3454 GTGGGTAGCCGATGCCTACCCTGCTGGCTCCCACAGGGCTCAGAGTTTGGGAACTGGGC 687 aLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGluAspPheProAspLeuAsnSe 		Q B
680	94 AGCCGGTGGCTCGCTTTCATCCGCATCTACCCACTCACCTGGAATGGCAGCCTGTGCA 4535	S B
678 Glmmet	513 luProValValAlaArgPheIleArgIleTyrProLeuThrTrpAsnGlySerLeuCysM 533	8
3574 CAGGACACGCATCCACCTGGTGCCCTCACTGAACCCTGATGGCTACGAGGTGGCAGCG	496ThrPheHisGlyAsnValAspLysAspThrProValLeuSerGluLeuProG 513	용 왕
	4714 ATTGTCTGGGCGAGGGGTGGGCTCTCAGAGGGGCTGGCAGGACTCTGAGGGCCTGCCT	8 8
638	4 GTACACCAACGGCTATGAGGAAATGGTGGGCACCATGCCCAGGCTCTTGGCTCTCCC 4715	융
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	1777	980 nelleLeuAllaArgSerAenTrpLysArgIleArgGluIleWetAlaMetAenGlyAenA 	
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	1957	CGCTCTGGGGCAGCCGGATCGTTCTCCCTCCGCAGC	
	2 2	76 GCTGGGGGCCGGAACTCAGAGGGGGAGGGCGGGGCTGGGGGCAGGACTGAGTGG	
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	402	901 tGluGln	
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	2556	858IleAsnAspPh             2615 TGGTCCGGAGAGGGGCTGACTTTGGGTCTGTATCTGTCCCCGGCCAGCTATCAATGACTT	
	8	75 GGCCAAGTGGAACCCCCGGACCGGGAGTGAGTCAGCCTGGGAGGGGGCT	
•	857	848 YAlaLysTrpAsnProArgThrGlyThr	
	2676	828 UPFOTYFAIGGIYGIYCYGGIDAIAGIDABDTYFTDIGIYGIYMEIGIYIIEVAIABDGI 	
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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB spool/US10642946/runat 29092006 125317_12677/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10642946/runat 29092006 125317_12677/app_query.fasta_1
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-DOPCL=0 -LOOPEXT=0 -UNITS=bIts -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALION=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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2. /EMC_Celerra_SIDS3/ptcdata/1/pubpna/US07_NEW_PUB.seq:*

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## ALIGNMENTS

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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22822, Application US/11266748A Publication No. US20060134663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Johnston, Patrick APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harkin,
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Qy 261 SerArgArgArgProGluArgValTrpProGluProProGluGluLysAlaProAla 280	QY 241 ArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgProProPro 260	Oy 221 GlnProGluProGluGluGluGlnProThrLeuAspTyrAsnAspGlnIleGlu 240	Qy 201 ProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHisValGluAlaGlnGluHis 220	Qy 181 TrpProLeuProProProProSerProGlyProGluGluLeuProGlnGluGlyGlyAla 200	OY 161 ThrLysLysBroProSerGlyLysArgProProIleLeuAlaProSerGluThrLeuGlu 180	QY 141 LyseroLysGluGluProProLysAlaThrLysLysEroLysGluLysEroProLysAla 160	QY 121 LYBGluLYBProProLyBAlaThrLyBLYBProLyBGluLyBProProLyBAlaThrLyB 140	Qy 101 LysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysLysGly 120	QY 81 ThralaalaGluValProProGluLysThrLysAspLysGlyLysLysGlyLysLysAsp 100	QY 61 GluProThrProArgValArgLysAlaGlnAlaGlyGlyLysProGlyLysArgProGly 80	Qy 41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProProPro 60	Qy 21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly 40	QY 1 MetAlaAlaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys 20	8 Gaps:  2-946-3 (1-1158) x US-11-266-748A-22822 (1-393	Pred. No.:  1.55e-305 Length:  Score: Score: 6272.00 Matches: Percent Similarity: 100.0% Monservative: Best Local Similarity: 100.0% Mismatches: Query Match: 0 Universe 100.0% Mismatches: 0 Universe 100.0% Mismatches	NISM: H	; SEQ ID NO 22822 ; LENGTH: 3935
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                                                                        IleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg
                                                                                                                  ACCCCGAGCGCCAAGACCTGCAATGTTGACTATGACATCGGGGCCACTCAGTGCAACTTC
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               Alignment Scores: Pred. No.:
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US-11-266-748A-184697
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US-11-266-748A-184697

Sequence 184697, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Karl

ITILE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION UNMEER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION UNMEER: EP 04105479.2

PRIOR APPLICATION UNMEER: EP 04105483.4

PRIOR APPLICATION UNMEER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION UNMEER: EP 04105483.4

PRIOR APPLICATION UNMEER: EP 04105483.9

PRIOR APPLICATION UNMEER: EP 04105483.9

PRIOR APPLICATION UNMEER: EP 04105483.9

PRIOR APPLICATION UNMEER: US 04105483.9

PRIOR APPLICATION UNMEER: US 04105484.2

PRIOR APPLICATION UNMEER: US 04105484.2

PRIOR APPLICATION UNMEER: US 04062,276

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION UNMEER: US 06/662,276

PRIOR PRILING DATE: 2005-03-14

PRIOR APPLICATION UNMEER: US 60/662,276

PRIOR APPLICATION UNMEER: US 60/662,276

PRIOR PRILING DATE: 2005-03-14

PRIOR APPLICATION UNMEER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PRATURE:

NAME/KEY: misc_feature

LOCATION: (94):.(149)

COTRER INFORMATION: n is a, c, g, or t

US-11-266-748A-184697
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4.26e-179 3744.00

Length: Matches:

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Qy 321 ProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGluLeuLy	QY 301 AspTyrGlyAspGlyTyrVallleProAsnTyrAspAspMetAspTyrTyrPheo	Qy 281 ProAlaProGluGluArgIleGluProProValLy8ProLeuLeuProProLeuLeuProProLeuLeuProProLeuLeuProProLeuLeuProProLeuLeuProProLeuLeuProProLeuLeuProProLeuLeuProProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuL	Qy 261 SerArgArgArgArgProGluArgValTrpProGluProProGluGluLysAlai	Oy 241 ArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgProI	uAspTyrAsnAspGl              GGACTACAATGACCA	201 ProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHisValGluA 	181 TrpProLeuProProProProSerProGlyProGluGluLeuProGlnGluG 	Qy 161 ThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThrLeuGl	GluLysProPr           GAGAAGCCACC	Qy 121 LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAla:	ArgProProLys            AGGCCGCCCAAC	Qy 81 ThralaalaGluValProProGluLysThrLysAspLysGlyLysGlyLysGlyLysLysGlyLysGlyLysGlyLysGlyLysGlyLysLysGlyLysLysGlyLysGlyLysGlyLysGlyLysLysGlyLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysLysGlyLysLysLysGlyLysLysLysGlyLysLysLysGlyLysLysLysGlyLysLysLysGlyLysLysLysGlyLysLysLysGlyLysLysLysLysGlyLysLysLysLysLysGlyLysLysLysLysLysLysLysLysLysLysLysLysLys	Qy 61 GluProThrProArgValArgLysAlaGlnAlaGlyGlyLysProGlyLysArgL 	luAspAspValGluAlaProPro                 \GGACGACGTGGAGGCCCCGCCG	Qy 21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuCluPhe	Oy 1 MetAlaAlaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaI 	59.7% Indels: 8 Gaps: -1158) x US-11-266-748A-184697	ocal Similarity: 99.6% Conservative:  Nismatches:
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SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 192181
LENGTH: 2268
TYPE: DNA
ORGANISM: HOMO Sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (94):.(149)
OTHER INFORMATION: n is a, c, g
US-11-266-748A-192181
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
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PRIOR PRILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER: OS 580 ID NOS: 483996
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US-11-266-748A-192181
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; Sequence 192181, Application US/11266748A
; Publication No. US20060134663A1
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APPLICANT: HARKIN, Paul
APPLICANT: Mulligan, Patrick
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
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US-11-266-748A-184695
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; SOFTWARE: PatentIn version 3; SEQ ID NO 192179; LENGTH: 2065; TYPE: DNA; OTGANISM: Homo Sapiens; FEATURE: MAME/KEY: misc_feature; LOCATION: (1822)..(1884); OTHER INFORMATION: n is a, CUS-11-266-748A-192179
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APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
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CURRENT APPLICATION NUMBER: ED 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105482.6
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105485.9
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US-11-266-748A-192179
; Sequence 192179, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
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; Sequence 98157, Application US/11266748A
; Publication No. US20060134663A1
; Publication No. US20060134663A1
; Publication No. US20060134663A1
; Publication No. US20060134663A1
; Partication Notation, Patrick
APPLICANT: Holigan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT APPLICATION NUMBER: EP 04105479.2
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PRIOR DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PRIOR DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PRIOR DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
CONTACT SEQ ID NOS: 483996
SOFTWARE: DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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SOFTWARE: DATE: 2005-07-18
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                          AlaGlnArgGlyArgLeuAsnMetGlnThrGlyAlaThrGluAspAspTyrTyrAspGly
                                                                                                                           SerHisArgIleGluAspAsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGly
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publication No. US20060134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-150968
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                 ThrargPheThrGlyValIleThrGlnGlyArgAspSerSerIleHisAspAspPheVal
                                                                     GCACAGCGCGGCCGGCTCAACATGCAGACCGGTGCCACTGAGGACGACTACTATGATGGT
                                                                                            AlaGlnArgGlyArgLeuAsnMetGlnThrGlyAlaThrGluAspAspTyrTyrAspGly
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331 GlnThrAspGluGluLysGluGluLeuLysLysProLysGluAspSerSerProLys 350    :::    :::	253 CTCTGGCGGCGCGCTATTATGGGCATCCGGAGCCTGAGCCGGAGCCGGAGCTC 309		305309 305309 305309 305	288 GluProProValLysProLeuLeuProProLeuProProAspTyrGlyAsp 304	2-946-3 (1-1198) X US-11-376-989-1 (1-2490) 273 ProProGluGluLyBAlaProAlaProAlaProGluGluArg	Scores: 5.57e-95 Length: 2066.00 Matches: milarity: 61.9\$ Conservati Similarity: 48.3\$ Mismatches h: 32.9\$ Gaps:	SULT 8 :-11-376-589-1 :-11-376-589-1 Sequence 1, Application US/11376589 Publication No. US20060154368A1 GENERAL INFORMATION: APPLICANT: Allen, Keith D. APPLICANT: Zhang, Qin TITLE OF INVENTION: DISRUPTIONS FILE REFERENCE: R-716 FILING DATE: 2006-03-14 CURRENT APPLICATION NUMBER: US/11/376,589 CURRENT FILING DATE: 2006-03-14 PRIOR APPLICATION NUMBER: US/09/900,518 PRIOR FILING DATE: 2001-07-06 PRIOR FILING DATE: 2000-07-06 PRIOR FILING DATE: 2000-07-06 RINGER OF SEQ ID NOS: 4 SOCTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 2490 TYPE: DNA ORGANISM: Mus mussculus :-11-376-589-1	591 y-LysSerSerArgGlyLeuLysIleTyrAlaMetGluIleSerAspAsn 607 	571 gGlnLeuMetLysValValAsnGluGluCysProThrIleThrArgThrTyrSerLeuGl 591	552 ABRGIUVAIVAIAIATHYABPABPLEUABPPHEAYGHIBHIBSEYTYYLYB-ABPMELAY 571 	532 CyBMetArgLeuGluValLeuGlyCysSerValAlaProValTyrSerTyrTyrAlaGln 551

2383	Db 49	658 GlnAspThrArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAla 677 :::::           :::::	σ <
Symmateriolierichisileasprosexateriomecunirroginginargarg	g	638 LeuMetGlnTyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuVal 657     ::: :::      ::            :::	σ <
CYSASHPREILELEUNIAKYSERASHTYPLYSATGILEAGGIULIEMETAIAMETASH 	) B &	618 PheArgTyrThrAlaGly1leHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeu 637 	σ <
8 GluGlyTyrThrProSerAlaLysThrCysAsnValAspTYrAspIleGlyAlaThrGln	y dd Y	598 LysileTyrAlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGlu 617	0 <
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8 IleProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThrAla	Db Db	AspAspLeuAspPheArgHisHisSerTyrLysAspMetArgGInLeuMetLysValVal	0 <
898 LeuThrPheMetGluGlnValHisArgGlyIleLysGlyValValThrAspGluGlnGly 917 :::	Db Qy	539 GlyCysSerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValValAlaThr 557	0 <
8 ABPLysPheProHisGluSerGluLeuProArgGluTrpGluAsnAsnLysGluAlaLeu       :::	Qy Db	521 ArgileTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeu 538 	0 4
1leAsnAspPheSerTyrLeuGlisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCys :::	dg Ab	501 ValAspLysAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIle 520	o. <
8 ABPTyrThrGlyGlyMetGlyIleValAsmGlyAlaLysTrpAsmProArgThrGlyThr    :::     :::     :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::   ::   ::   :::   :::   ::		481 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500	σ <
8 SerPheAlaSerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGln    :::	Oy dd	461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480	σ <
AspGluValSerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIle	dg Qy	441 ThrGlnTrpIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460 	σ <
ThrProThrGlnGlnGlnLeuLeuAlaAlaAlaAlaAlaAlaAlaArgGlyGluAspGlu ::: TCCCTGTGGAAGACCCAG	dg Vy	421 ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAspAspAlaArg 440 	σ <
	dg Qy	401 ArgAlaSerSerMetLeuArgH1sGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420       :::	σ <
	Qy da	83VallysCysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle 4	σ <
718 ValbroTyrArgValProAsnAsnAsnLeubroIlebroGluArgTyrLeuSerProAsp 737      ::       ::: ::          ::: ::	Qy Qy	382 382 487 AGCAAGAATCTTGAGAAAGCTGCCAGTGATGACCATGGTGTCCCTGTGGCTCATGAGGAT 546	σ <
LepheG.uaspheProAspLeuAspLevAstusTrgGIyALaGLuGLuAzgLySTrp	g Q	371 GluGluLeuGluGluGluTrpThrProThrGluLys	8 4
GlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAsp:::	Q dd	GluGluThrAspLysTrpAlaValGluLysGlyLysAspHisLysGluProArgLysGly 3 :::::	8 4
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TYPE: DNA

CONGLANISM: Homo Sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1069)..(1102)
COTHER INFORMATION: n is a,
US-11-266-748A-192182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Uninstan, Factick
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR TILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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SOFTWARE: Patentin version 3
SEQ ID NO 192182
LENGTH: 1437
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TyrThrGlyGlyMetGlyIleValAsnGlyAlaLysTrpAsnProArgThrGlyThrIle
                                                                                                                                       GluValSerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSer
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                                                                     PheAlaSerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAsp
                                                                                                                      GAGGTCTCCGAGGCCCAGGAGACTCCAGACCACGCCATCTTCCGGTGGCTTGCCATCTCC
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 Sequence 226230, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 226230
LENGTH: 1437
TYPER: DNA
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Best Local Similarity:
Query Match:
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ORGANISM: Homo
FEATURE:
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GlyGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGlu
                                                                                                                                                                                                                                                        AsnAspPheSerTyrLeuH1sThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAsp
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                                                    ProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThrAlaSer
                                                                                                                        ThrPheMetGluGlnValHisArgGlyIleLysGlyValValThrAspGluGlnGlyIle
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                                   CCCATTGCCAACGCCACCATCTCTGTGAGTGGCATTAATCACGGCGTGAAGACAGCCAGT
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Conservative:
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APPLICANT: Carroll, Joseph M.

APPLICANT: Healy, Aileen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
FILE REFERENCE: MPIZOO1-28091RCP1OMNIM
CURRENT APPLICATION NUMBER: US/11/242,505A
CURRENT APPLICATION NUMBER: US 10/290,078
PRIOR APPLICATION NUMBER: US 10/290,078
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 0/347,949
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 10/320,351
PRIOR APPLICATION NUMBER: US 10/320,351
PRIOR APPLICATION NUMBER: 05/341,606
PRIOR FILING DATE: 2001-12-16
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                                                                      SOFTWARE: Fa
               TYPE: DNA
ORGANISM: Homo
                                                      LENGTH: 2452
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Alignment Scores

	Qy 520 eArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLe 538     :::                 :::      :::   Db 808 TCGCCTGCTCCAGACCTGGCTCCAGGGAGGCGCGCCTTGCCTCCGGGCAGAGATCCT 867	Qy 500 nValAspLysAspThrProValLeuSerGluLeuProGluProValValAlaArgPheI1 520	Qy 482 rGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAs 500	Qy 462 gAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsnAspSe 482	442 nTrpIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGlnGlyAr	422 YAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAspAspAlaArgThrGl	402 aSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGlnThrGl	Qy 382 sValLysCysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIleArgAl 402 	363 AspHisLysGluProArg-LysGlyGluGluGluGluGluTrpThrProThrGluLy :::::	344 LysGluAspSerSerProLysGluGluThrAspLysTrpAlaValGluLysGlyLys	324 GlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGluLeuLysLysProLys        ::::::::	304 ABpGlyTyrVallleProAsnTyrAspAspMetAspTyrTyrPheGlyProProProPro	284 G1 189 GC	Qy 271ProGluProProGluGluLysAlaProAlaProAlaPro 283	Qy 260	251 ArgArgGlnLysGlr     9 cgcccccgccgTAgc	/ Match: 27.7% Indels: 8 Gaps: 0-642-946-3 (1-1158) x US-11-242-505A-22 (1-2452)	Pred. No.:  1.99e-78 Length: 2452 Score: 1735.50 Matches: 368 Percent Similarity: 59.4% Conservative: 117 Best Local Similarity: 45.0% Mismatches: 228
Qy 897 uLeuThrPheMetGluGlnValHisArgGlyIleLysGlyValValThrAspGluGl 916	** SASDLY SETERIOR SOLUTION CONTROL SOLU	1774 CATGAATGACTTCAGCTACCCTACACACCGACTTTGAGGTCACTGTGGAGCTGTCCTG	Oy 857 xIleAsnAspPheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCy 877	817 eserbhealaseralahishedintredintredintrediyrargelyelyeysysimalagi.	797 uAspGluValSerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIl	Oy 777 gThrProThrGlnGlnLeuLeuAlaAlaAlaAlaAlaAlaAlaArgGlyGluAspGl 797	Qy 757   LeuGlyAlaAsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaAr 777	Oy 737 pAlaThrValSerThrGliValArgAlaILeILEALATTpMetGlULyBAShProPheva 757	717 pValProTyrArgValProAsnAsnLeuProIleProGluArgTyrLeuSerProAs	Qy 697 pilePheGluAspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTr 717	Qy 677 aGlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAs 697	Qy 657 IG1nAspThrArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAl 677 : :::	Qy 637 uLeuMetGlnTyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuVa 657            ::         ::	17 uPheArgTyrThrAlaGly1LeH16GlyAsnGluValLeuGlyAsrgGlübeüLeüle 	1048 GAAGCTGTATGTGAAATGTCGGACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGA	577 988		

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CURRENT APPLICATION NUMBER: US/10/196,749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063120
PRIOR APPLICATION NUMBER: 60/063121
PRIOR APPLICATION NUMBER: 60/063121
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063540
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PRIOR APPLICATION NUMBER: 60/063541
PRIOR
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Godowski, Paul J.
Gurney, Austin L.
Pan, James
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                                                                                                  File Wrapper or PALM.
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SEQ ID NO 23
LENGTH: 2205
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Publication No. US20060099656A1
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Aileen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
TILE REFERENCE: MPICON 1001-288P1RCF10MNIM
CURRENT APPLICATION NUMBER: US11/242,505A
CURRENT FILING DATE: 2005-10-03
PRIOR APPLICATION NUMBER: US 10/290,078
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-12-16
PRIOR APPLICATION NUMBER: US 10/320,351
PRIOR APPLICATION NUMBER: 60/341,606
PRIOR FILING DATE: 2001-12-17
                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2205)
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SOFTWARE: FastSEQ for Windows Version
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OTHER INFORMATION: n is a, c, g, or t  US-11-266-748A-226229  Alignment Scores:	FILING DATE: 2005-03-14 APPLICATION NUMBER: US 60/700, FILING DATE: 2005-07-18 R OF SEQ ID NOS: 483996 ARE: PatentIn version 3.3 NO 226229 TH: 1184 : DNA NISM: Homo Sapiens URE: /KEY: misc feature /KEY: misc feature	FILE REFERENCE: 55915-0102 (319189)  CURRENT APPLICATION NUMBER: US/11/266,748A  CURRENT FILING DATE: 2005-11-03  PRIOR APPLICATION NUMBER: EP 04105479.2  PRIOR FILING DATE: 2004-11-03  PRIOR APPLICATION NUMBER: EP 04105482.6  PRIOR RILING DATE: 2004-11-03  PRIOR RILING DATE: 2004-11-03  PRIOR RILING DATE: 2004-11-03  PRIOR RILING DATE: 2004-11-03  PRIOR APPLICATION NUMBER: EP 04105485.9  PRIOR APPLICATION NUMBER: EP 04105485.9  PRIOR APPLICATION NUMBER: EP 04105486.2  PRIOR RILING DATE: 2004-11-03  PRIOR RILING DATE: 2004-11-03  PRIOR APPLICATION NUMBER: EP 04105484.2  PRIOR APPLICATION NUMBER: EP 04105484.2  PRIOR APPLICATION NUMBER: EP 04105484.2	Qy  999 nArgProlleProHislleAspProSerArgProMetThrProGlnGlnArgArgLeuGl 1019  Db  2151 GGTGCC
US-11-266-748A-167870 US-11-266-748A-167870 Sequence 167870, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION: APPLICANT: Harkin, Paul APPLICANT: Johnston, Patrick FILIE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189) CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT FILING DATE: 2005-11-03 PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR APPLICATION NUMBER: EP 04105482.6 PRIOR APPLICATION NUMBER: EP 04105483.4 PRIOR APPLICATION NUMBER: EP 04105483.4 PRIOR APPLICATION NUMBER: EP 04105483.4 PRIOR APPLICATION NUMBER: EP 04105483.9 PRIOR APPLICATION NUMBER: EP 04105483.9 PRIOR APPLICATION NUMBER: EP 04105485.9 PRIOR FILING DATE: 2004-11-03	Qy 1110 GluThrGlnLeuGluProGluPheGluThrClnLeuGluProGluPheGluGluGluGluI 1129		930 IleAsnHisGlyValLysThrAlaSerGlyGlyAspTyrTrpArgIleLeuAsnProGly

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; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILLING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILLING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 167870
; LENGTH: 950
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PATURE:
; NAME/KEY: misc feature
; LOCATION: (782)...(815)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-167870
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ATCCGGGAGATCATGGCCATGAACGGGAACCGGCCTATCCCACACATAGACCCATCGCGC
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                                                         YLeu-IleProProThrThrAlaGlyTrpGluGluSerGluThrGluThrTyrThrGluV
                                                                                                       lProProThrLeuProProAlaProAlaThrThrLeuSerThrThrIleGluProTrpGl 1069
                                                                                                                                                   ArgAlaGlnMetArgLeuArgArgLeuAsnAlaThrThrThrLeu-GlyProHisThrVa
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                                              GCCTCCCACGCTGCCCCTGCCCACCACCCTGAGCACTACCATAGAGCCCTGGGG
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Search completed: October 1, 2006, 00:15:22 Job time : 592 secs THIS PAGE BLANK (USPTO)

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Result
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-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-Q-/abse/ABSSWEB_spool/US10642946/runat_29092006_125310_12521/app_query.fasta_1
-Q-/abse/ABSSWEB_spool/US10642946/runat_29092006_125310_12521/app_query.fasta_1
-DB=EST -QFWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs806p
-USER-US10642946 @GCN 1 9528 @runat 29092006 125310 12521 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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## ALIGNMENTS

REFERENCE AUTHORS REFERENCE AUTHORS REFERENCE AUTHORS SOURCE ORGANISM LOCUS DEFINITION ACCESSION VERSION RESULT 1 AK159377 KEYWORDS JOURNAL PUBMED TITLE JOURNAL PUBMED TITLE Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) sequence. AK159377 AK159377

3825 bp mRNA linear HTC 21-SEP-2005
Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched
library, clone:1420018014 product:AE binding protein 1, full insert Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. Shibata, K., Mus musculus AK159377.1 GI:74196951 HTC; CAP trapper. 11042159 Mus musculus (house mouse) Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

JOURNAL PUBMED TITLE

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AUTHORS
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URLihttp://genome.gc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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RIKEN Genome Exploration Research Group
Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
prepare mouse tissues.
Tissues were provided by Takashi Ishikawa ( Department of & 2 Vokohama City University 3-9 Fukuura,Kanazawa-ku,Yokohama 236-0004 Japan ) whose assistance we gratefully acknowledge
                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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                                           ACCAAGAAGCCCAAGGAGAAGCCACCCAAGGCCAAGAAGCCTAAGGAGAAGCCACCC
                                                          ThrLysLysProLysGluGluProProLysAlaThrLysLysProLysGluLysProPro
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                                                                      PheHisGlyAsnValAspLysAspThrProValLeuSerGluLeuProGluProValVal
                                                                                                          GGCTTCAGCAATGACAGCCAGACCTGGGTGATGTACACCAATGGCTACGAGGAAATGACC
                                                                                                                                                               GTCATCACTCAGGGCCGTGACTCCAGCATCCATGACGACTTCGTGACTACCTTCTTTGTG
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Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory

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CDNA llbrary was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues

7. Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan ) whose assistance we gratefully acknowledge. Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                          URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/mol type="mRNA"
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Meth. Enzymol. 303, 19-44 (1999)
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AK159330.1 GI:74192986
HTC; CAP trapper.
Mus musculus (house mouse)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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Arakawa,T.,

Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K.,

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Suzuki, H.,

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                                                                                                                                                                                             The transcriptional landscape of the mammalian genome Science 309 (5740), 1559-1563 (2005)
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Prepare mouse tissues.

1 issues were provided by Takashi Ishikawa ( Department of Surgery Vision of City University 3-9 Fukuura, Kanazawa-ku, Yokohama 2 Kanazawa-ku, Yokoham
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                                                               PheLeuSerGluLeuGluProGlu-----ProArgGluAspAspValGluAlaProPro
                                                                                                                                                                          ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluGheLeuGluGly
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                                                                                      AspAsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArg
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Qy 1076 AlaGlYTrpGluGluSerGluThrTyrThrCluValValThrCluPheGlyThr	3111 CA 997 AS 997 AS 3171 AA 1017 AZ 1037 AZ 1037 AZ 1037 AZ 1037 AZ 1056 AL 3345 CC	Oy  897 LeLLeuTh-PheMetGluGLnValHsargGLyItelysGiyValValThrAspGluGLn Db 2871 CTGCTCACCTTCATGAGGGTGCACCGTGGATTAAGGGTGTGACAGATGACCAA  Oy  917 GlyIleProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThr Db 2931 GGCATCCCCATTGCCAATGCCACCATCTCTGTGAGTGGCATCAACCATGGTGTGACAGACA	2511 797 2571 817 2631 837 2691 857 2751

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                                                                                                                                                                                     FANTOM Consortium Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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3860 bp mRNA linear HTC 21-SEP-2009
Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched
library, clone:1420018N15 product:AE binding protein 1, full inser
                                                                                                                                                                                                                                                                                                      RIKEN Genome Exploration Research Group Phase II Team and the
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CONSRIM TITLE JOURNAL PUBMED REFERENCE

The transcriptional landscape of the Science 309 (5740), 1559-1563 (2005)

mammalian

(5740),

FANTOM Consortium

AUTHORS

Katayama,S., Nakamura,M.,

Tomaru, Y., Kasukawa, T., Waki, K., Nishida, H., Yap, C.C., Suzuki, M.,

Nakanishi,M., Kawai,J., Suz

Suzuki, H.,

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Nature 420 (6915), 563-573 (2002)
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PUBMED REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.

Tissues were provided by Takashi Ishikawa ( Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan ) whose assistance we gratefully acknowledge. Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.

Location/Qualifiers
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Fax:81-45-503-9216)
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                                                                                            PANTOM Consortium
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420 (6915), 563-573 (2002)
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RIKEN Genome Exploration Research Group Phase II Team
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Madda, N., Oyama, R., Ravasi, T., Lenhard, B., Wella, C., Kodzius, R., Ravasi, T., Lenhard, B., Wella, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Shimokawa, K., Bavis, V., Allen, J.E., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Landbesi-Impiombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Ambesi-Impiombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Chutterbuck, D.R., Chut, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Choudhary, V., Choo, B., Della Gatta, G., Groen, R.E., Grobort, T., Grarboldd, M., Garben, C.F., Fukushina, T., Furuno, M., Futaki, S., Gariboldd, M., Georgi-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Georgi-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Georgi-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Kutch, M., Kathara, S.P., Kruger, A., Kummerfeld, S.K., Kitamura, H., Kitamura, H., Kitamura, H., Kitamura, H., Kitamura, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Laraevu, D.F., Lazarevic, D., Lipovich, L., Liu, J., J., Liu, J., Lata, J., Marchionni, L., Majonoe, F., Miyake, S., Nakauchi, H., Nakauchi, H., Majonoe, F., Miyake, S., Nakauchi, H., Nakauchi, M., Nakauchi, H., Nakauchi, M., Nakauchi, H., Nakauchi, M., Nakau

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CRUA:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Emploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in Rike Genome Science Laboratory in Rike Genore Experimental Animal Research in Riken contributed to prepare mouse riseues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web site for further details. URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.
Tissues were provided by Takashi Ishikawa
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                                        /translation="WAPVRTASLLCGLLALLTLCPEGNPQTVLTDDEIEEFLEGFLSE
LETGSESPENDVEVQFLPEPTGRPKSKAGGKQRADVEVPPEKKNDKEKGKKDKGPK
ATKEPLEGSTRETKEYEKEPKATKK PKEKPKATKKPEKERPKATKK
PKEKPPKATKEPKEKPKATKR
PSAGKKFSTVAPLETLDRLLPSPSNPSAQELPQKRDTPFNAWQGGEETQVEAKQPR
PSPEEETEMPTLDYNDQIEKEDYEDFEYIR QKQPPFTPSRRLWPERPEKEENKKEKP
RKEVEPPLKPLLPDYNGDIEKEDYEDFEYIR QKQPPFTPSRRLWPERPEKEENKKEKE
RKEVEPPLKPLLPDYNGDIEKOKONHKAGPRKGEELEBEMAPVEKIKCPPIGMESHRIEDNQI
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                      RASSMLRHGLGAQRGRLNMQAGANEDDYYDGAWCAEDESQTQWIEVDTRRTTRFTGVI
                                                                                                                                                                                                                 /codon_start=1
/proteIn_id="BAE35513.1"
/db_xref="GI:74213393"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                note="unnamed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="FANTOM_DB:I420039P15"
/db_xref="taxon:1000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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MGI 1197012 GB|AK128980, evidence: BLASTN, 99%,
                                                                                                                                                                                                                                                                                                                                                                                                             type="osteoclast-like cell"
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| lib="RIKEN full-length enriched
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                      ProProAspTyrGlyAspGlyTyrValIleProAsnTyrAspAspMetAspTyrTyrPhe
                                                                                                                               ProAlaProAlaProGluGluArgIleGluProProValLysProLeuLeuProProLeu
                                                                                                                                                                                            ACACCCAGCAGGAGG
                                                                                                                                                                                                                      ProProSerArgArgArgArgProGluArgValTrpProGluProProGluGluLysAla
                                                                                                                                                                                                                                                                                                                  IleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgPro
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CAATACCTATGCCAGGAGTACCGCGATGGAACCCGAGAGTGCGCATACGCTATGCCAGAGAGTGCGCATGGAACCCCGAGAGTGCGCATGACCCTGATGGCTATGACACGCTATGACACCCTGATGGCTATGACACGCTATGACACGCTATGACACGCTATGACACGCTATGACACGCTATGACACACGCTATGACACGCTATGACACACGCTATGACACACAC	GlupheArgTyrThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeu	1902 GTCAATGAGGAGTGCCCCACAATCACTCGCACATACAGCCTGGGCAAGAGTTCACGAGGG 1961  597 LeuLysIleTyrAlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluPro 616	ThraspaspLeuAspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysVal 5	1722 GCCCGTTTCATCCGCATCTATCCACTCACTCGAATGGTAGCCTGGGACTGGGGCTGGAG 1781  537 ValleuGlyCysSerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValValAla 556	497 PheHisGlyAsnValAspLySAspThrProValLeUSerGluEcuProGluBroValVal 516	GlyPheSerAsnAspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThr 4	1482 GACGAGTCGCAGACCCAGTGGATCGAGGTCGAGGTCGAAGGACAACTCGGTTCACGGGC 1541 457 VallleThrGlnGlyArgAepSerSerIleHisAspAspPheValThrThrPhePheVal 476		AspAsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArg 	SMGAMMAKAANGGACCACAANGCAGGCCCACTAANGCAGGCCCACTAANGCAGGCCCACCCAAGGCCCAACCCAA	ATGAAGÄÄGCCCAAÄÄÄGGGAGGGTÄGTÄGCCCCAAGGÄGGACÄCÄGAGGACÄÄĞTGGACC ValGluLysGlyLysAspHisLysGluProArgLysGlyGluGluLeuGluGluGlu	CCTCCACCGCAGAAGCCTGATGTTGGACAAGAGGTGGATGAGGAA \ysProLysLysGluAspSerSerProLysGluGluThrAsp)	319 GlyProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGlu 338
Qy 1017 ArgLeuGlnGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArg 1036     :::	ABGGGAACCGTCCCATTCTCGCGAGTTGACCCCTCACGCACCCCCCCC	957 3042 977	Db 2922 GCATCCCCATTGCCACTCTCTGTGAGTGGCATCACCATGGTGAGACA 2981  Oy 937 AlaSerGlyGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHis 956	897 LeuLeuThrPheMetGluGlnValHisArgGlyIleLy8GlyValValThrAspGluGln	Db 2742 ACTTTCAATGACTTAGCTACCTGCACACAAACTGTCTGGAGCTCTCCGTATACCTGGGC 2801  877 CysaspLysPheProHisGluSerGluLeuProArgGluTrpGluAsnAsnLysGluAla 896	Qy 837 GlnAspTyrThrGlyGlyMetGlyIleValAsnGlyAlaLysTrpAsnProArgThrGly 856	Qy 817 IleSerPheAlaSerAlaHiBLeuThrLeuThrGluProTyrArgGlyGlyCygGlnAla 836	Db 2502 ĆĠĠĀĆĀĆĊŤĀGCĆĀĠĠĀĠĊĀĠĊŤĠŤŤĠĠĊĊGĀGĠĊĀCTGĠĊĀĠĊŤĠĊĊĠĠĠĀGĀĀĀĀ 2561  Qy 797 GluĀspGluValSerGluĀlaGlnGluŤħrProĀspĦisĀlaIlePheĀrgŤrpLeuĀla 816  :::	Qy 757 ValleuGlyAlaAsmLeuAsmGlyGlyGluArgLeuValSerTyrPrcTyrAsgMetAla 776	Qy 737 AspAlaThrValSerThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPhe 756	717 Tr    2322 TG	ନ୍ଲଞ୍ଚ	Qy 677 AlaGlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPhe 696

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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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3831 bp mRNA linear HTC 21-SEP-2005
Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched
library, clone:1420030M05 product:AE binding protein 1, full insert
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REFERENCE

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                                        Analysis of the mouse transcriptome based of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002)
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Tissues were provided by Takashi Ishikawa ( Depar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The transcriptional landscape of the mammalian genome science 309 (5740), 1559-1563 (2005)
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URL:http://fantom.gsc.riken.jp/.
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                                                                                                                                                                                                                                                                                                                                        clone="1420030M05"
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                                                                                                                                                                                                                                                                                                 _type="osteoclast-like cell"
                                                                                                                                                                                                                                                     lib="RIKEN full-length enriched mouse cDNA library"
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39 IleGlı       03 ATAGA	19 GluHi	99 GlyAla 83 GACAC	79 LeuGlu    :: 23 CTGGA	59 LysAla       63 AAGGC	ωφ	ωω	99 Lysası       86 AAGGAO	79 ProGly 26 CAGCGG	59 ProPro      78 CTTCCC	8	21 ProGly	1 MetAla        98 ATGGCT	46-3 (1-1	ores: .arity: .milari
uArgGluAs  :::      GAAGGAGGI	8GlnProG] :::      CCGGCCAG <i>I</i>	aProLeuse     ACCCTTCCC	uTrpProLe :    CGGTTAC1	aThrLysLy        :: CACTAAGAC	BLYBProL)          3AAGCCCAJ	YLYSGluL)         naaggagar	DLYSG1YPI          AAAGGCCC	/ThrAlaAl 3GCAGATG1	GluProTh	SerGluLe	GlyArgPr         GGGAACCC	Alavalar        ccagrace	158) x	0 5070.5 87.4% ETY: 82.7% 80.8%
apTyrGlua          TTACGAGG	luProGluG          \GCCAGAGG	erAsnAsnT      AAATGCCT	euProProF	RProPros	/sGluGluP     :::  \GGAGAAGC	/SProProL	COLYSVAlP	laGluValP          AGAAGTCC	TProArgV	uGluProG	oglnThrV          ACAGACGG	gGlyAlap          CACCGCAT	AK159774	### .5 O
.spPheGluTyrIleArg 	;luGluThrGluGlnPro           AGGAGACTGAGATGCCC	rpGlnAsnProGlyGlw        ogcaagGTCAAGGAGAA	roProSerProGlyPro    :::    :CTCCAACCCCAGCGCC	erglylybargProPro  -:        CAGGAAAGAAGTTCTCA	roProLygAlaThrLyg            cacccaaggccaccaag	ysalaThrLysLysPro            aggccaccaagaagccc	roLysGluSerLeuGlu      	roProGluLysThrLys            CTCCAGAAAAAAACAAA	ProProGluProThrProArgValArgLysAlaGlnAlaGlyGlyLys	luProArgGlu ;;          AGTCCCCGCCCCGGGAA	alLeuThrAspAspGlu              TGCTGACGGACGACGAG	roLeuLeuSerCysLeul       	(1-3831)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
IleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgPro 	GluHisGlnProGluProGluGluGluThrGluGlnProThrLeuAspTyrAsnAspGln ::: ::	GlyAlaProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHisValGluAlaGln	LeuGluTrpProLeuProProProProSerProGlyProGluGluLeuProGlnGluGly     ::     :::         ::: 	LygAlaThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThr 	ThrLysLysProLysGluGluProProLysAlaThrLysLysProLysGluLysProPro 	LysGlyLysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAl.	LysaspLysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLys	roglythralaalagluvalproproglulysthrlysasplysglylyslysglyly                    agcgggcagatgtagaagtccctccagaaaaaaaacaaagacaaagagaagaaaga	ProGlyLysAr	PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProPro                 	roGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly 	MetAlaAlaValArgGlyAlaProLeuLeuSerCy8LeuLeuAlaLeuLeuAlaLeuCy 		3831 962 55 109 17
0 258     962	n 238       902	n 218 : G 842	y 198 A 782	r 178   G 722	0 158   C 662	a 138    C 602	9 118     542	98  -   485	g 78 - 425	58       377	40	в 20   С 257		

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7 GlnAspTyrThrGlyGlyMetGlyIleValAsmGlyAlalysTrpAsnProArgThrCly               :::      CAGGACTACACCAGCGGCATGGGCATTGTCAACGGGGCCAAGTGGAATCCTCGCTCTGGG	B Q	477 GlyPheSerAsnAspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThr 496 
11eSerPheAlaSerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCygGlnAla 	D Q	457 ValileThrGlnGlyArgAspSerSerIleHisAspAspPheValThrThrPhePheVal 476 
GluAspGluValSerGluAlaGlnGluThrProAspH.sAlaI.ePheArgTrpLeuAla :::	D 5	437 AspAspAlaArgThrGlnTrpIleGluValAspThrArgArgThrThrArgPheThrGly 456
ArgThrProThrGInGluGInLeuLeuA,aAlaAlaMeEAlaA.LaAlaArgGlyGluAsp	A G	417 LeuhenMetGlnThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGlu 436 
ValleuG.yAlaAsmLeuAsmG.yG.yG.yAzgLeuVal.SerTyYzAspMetAla	) B &	397 AspAsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArg 416 
37 AspAlaThrValSerThrGluValArgAlaIIeIleAlaTryMetGluLysAsnProbhe	) B 9	377 TrpThrProThrGluLysVallysCysBroProIleGlyMetGluSerHisArgIleGlu 396
7 TryValProTyrArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerPro 	dg dy	358 ValGluLysGlyLysAspHisLysGluProArgLysGlyGluGluLeuGluGluGlu 376           200
ASPILEPHEGILASPPHEPTOASPLEUASNSETVAILEUTTPGLYALAGIUGILATGIYS	. Q	339 LeuLysLysBroLysGluAspSerSerProLysGluGluThrAspLysTrpAla 357 :::
AlaGlMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPhe	). B &	319 GlyProProProGlnLysGroAspAlaGluArgGlnThrAspGluGluLysGluGlu 338
ValGINASPTHYAYGI LEHISLEUVALPYOSETLEUASHPYOABGIYTYYGILVAIAIA 	B &	299 ProProAspTyrGlyAspGlyTyrVallleProAsnTyrAspAspMetAspTyrTyrPhe 318 
LeuneumetGiniyrLeucyBATGGIUYYTATGASDGIYABATGATGVAIATGSeTLEU                    :::	B 5	279 ProAlaProAlaProGluGluArgIleGluProProValLysProLeuLeuProProLeu 298
	ם ס	259 ProProSerArgArgArgArgProGluArgValTrpProGluProProGluGluLysAla 278                    :::           963 ACACCCAGCAGGAGGGAGGCTCTGGCCAGAGCGCCCTGAGGAGAGAGACT 1010

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wacahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format
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3854 bp mRNA linear HTC 21-SEP-2005
Mus musculus adult inner ear cDNA, RIKEN full-length enriched
library, clone:F930049P09 product:AE binding protein 1, full insert
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Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Huminiecki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katch, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kumerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Mateuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Wilder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavesi, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schopsch, C., Schonbach, C., Sckiguchi, K., Semple, C.A., Seno, S., Schneider, C., Schonbach, C., Sckiguchi, K., Sandelin, A., Seno, S., Sinclair, B., Sperling, S., Stupka, E., Sugiura, K., Sultana, R., Takenaka, Y., Taki, K., Tanmoja, K., Tan, S.L., Tang, S., Taylor, M.S., Techmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Suzuki, M., Aoki, J., Arakawa, T., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Tida, J., Imamura, K., Itoh, M., Kawaji, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Pangani, M., Waki, K., Watahiki, J., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose
                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iidda, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, Y.
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Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kanagawa, 230-0045, Japan (E-mai) URL:http://genome.gsc.riken.jp/, Fax:81-45-503-9216)
                                                                                                                                     URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                assistance we gratefully acknowledge. Please visit our web site for further
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PUBMED REFERENCE AUTHORS

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Percent Similarity:
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Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.
Hubisz,M.J., Fledel,-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans a
                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence
DQ035090
DQ035090.1 GI:66886299
                                                  This sequence them based on
                                                                             Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                                                                                                               Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
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                                                  was made by sequencing genomic exons and ordering alignment. Translation starts at the beginning of
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/db_xref="taxon:9606"
/chromosome="7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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                                                                             RIKEN Genome Exploration Research Group, Genome Science (Genome Network Core Team) and the FANTOM Consortium. Antisense Transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005)
                                                                                                                                                                                     Phase I and II Team.
Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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HTC; CAP trapper.
Mus musculus (house mouse)
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2836 bp mRNA linear HTC 02-SEP-2005
Mus musculus adult male lung cDNA, RIKEN full-length enriched
library, clone:1200011K15 product:AE binding protein 1, full insert
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                           332 ThrAspGluGluLysGluGluLeuLysLysProLysLysGluAspSerSerProLysGlu
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
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evidence: BLASTN, 99%, match=2799)
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/dev_stage="adult"
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/db_xref="FANTOM_DB:1200011K15"
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11  AK019509  3499 bp mRNA linear HTC 02-SEP-2005  ON Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632435Cll product:metallocarboxypeptidase 2, full insert sequence.	1146 ThrThrValGluThrTyrThrValAsn 1154 	1126 GluGluGluGluGluGluGluGluLysGluGluIleAlaThrGlyGlnAlaPheProPhe 1145 			1066 GluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGluSerGluThrGluThr 1085	1046 ProHisThrValProProThrLeuProProAlaProAlaThrThrLeuSerThrThrIle 1065	1026 ArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAlaThrThrThrLeuGly 1045	1006 AspProSerArgProMetThrProGlnGlnArgArgLeuGlnGlnArgArgLeuGlnHis 1025	NNNNN	2643 NININININININININININININININININININI	ThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPheIleLeuAlaArgSer	946 LeuabnProGlyGluTyrargValThralaHisalaGluGlyTyrThrProSeralaLys 965 2583 NANNANANANANANANANANANANANANANANANANAN	926 SerValSerGlyIleAsnHisGlyValLysThrAlaSerGlyGlyAspTyrTrpArgIle 945 	906 ArgGlyIleLysGlyValValThrAspGluGlnGlyIleProIleAlaAsnAlaThrIle 925 	886 LeuProArgGluTrpGluAsnAsnLysGluAlaLeuLeuThrPheMetGluGlnValHis 905	866 ThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPheProHisGluSerGlu 885	846 ValAsnGlyAlaLysTrpAsnProArgThrGlyThrIleAsnAspPheSerTyrLeuHis 865 	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium, Riken Genome Exploration Research Group Genome Science Group (Genome Network Project Core Group). The Transcriptional Landscape of the Mammalian Genome Science 309, 1559-1563 (2005)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)
                                                                                         Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC)
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RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Please visit our web site for further details.
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                           GCCCGTCTGGGGACCGCCTGCCCCTGCGCTGGCCGCTGGCACTTGTGGCGGTGGCC
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HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKY
PHESELPEEWENNRESLIVFMEQVHRGIKGIVRDLQGKGISNAVISVEGVNHDIRTAS
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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578 AsnGluGluCysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeu 597	ArgileTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeu	725 CATCAGTGGATCGAAGTGGATGCCCGGCCCTGACCAAGTTCACAGGGGTCATTACCCAA 784 461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480	VallysCysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle	317TyrPheGlyProProProProBnLysProAspAlaGluArg 330 251 CTCTGGCGGCGGGGCGTATTATGGGCATCCGAGGCCTGAGCCGGAGCAGGAGCTC 307 331 GlnThrAspGluGluLysGluGluLeuLysLysProLysGluAspSerSerProLys 350 350 TTCTCGCCTTCAATGCATGAAGACCTTAAGGTTGAGGAGCAGGAACAGCAGGAGCACC 367 351 GluGluThrAspLysTrpAlaValGluLysGlyLysAspHisLysGluProArgLysGly 370 351 GluGluThrAspLysTrpAlaValGluLysGlyLysAspHisLysGluProArgLysGly 370 368 CAGCAGGGCCACAGAACTCCCAAGAAGCCCTAAGCCCCAAGAAGGCTCCCAAGAAGGC 424 371 GluGluLeuGluGluGluTrpThrProThrGluLys
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918 CACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAAATGAAATGTGCCCAAT 977	Matches: 397 Conservative: 111 Mismatches: 186	Score: 2033.50 Percent Similarity: 64.4% Best Local Similarity: 50.3%
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738 GTTCTCAATGAGCTACCCGTCCCCATGGTGGCCCGCTACATCCGCATAAACCCCTCAGTCC 797	Litters Dp	source 1. 2237
507 ValLeuSerGluLeuProGluProValValAlaArgPheIleArgIleTyrProLeuThr 526	nt. Translation starts at the beginning of Qy	alignment
678 ACTGTTAAGAATGGATCTGGAGACATGATATTTGAGGGAAACAGTGAGAGAGGAGATCCCT 737	sequencing genomic exons and ordering	
487 MetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsnValAspLysAspThrPro 506	5) Celera Genomics, 45 West Gude Drive, Qy	
618 CTGAGTGACTGGGTGACATCCTATAAGGTCATGGTGAGCAATGACAGCCACACGTGGGTC 677	A., Tanenbaum,D.M., Civello,D., Adams,M.D. and Cargill,M.	
467 HisAspAspPheValThrThrPhePheValGlyPheSerAsnAspSerGlnThrTrpVal 486	Clark, A.G., Glanowski, S.,	2 (bases 1 t
558 GATGCTCGGCGCCTGACCAGATTCACTGGTGTCATCACTCAAGGGAAGGAA	, E170 (2005)	٠.
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427 AspTyrTyrAspGlyAlaTrpCysAlaGluAspAspAspAlaArgThrGlnTrpIleGluVal 446	NielBen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  Aubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,  White T. T. Grinsky T. T. Adams M. Band Carrill M. Charles M.	AUTHORS Nielsen,R., Bustaman Hubisz,M.J., Fledel- White T.J. Sninsky
438 CGCTATGGCCTGGGGGCACATCGAGGGGAGACTCAACATCCAGGCGGGCATTAATGAAAAT 497	uarchontoglires; Primates; Catarrhini;	
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387 ProlleGlyMetGluSerHisArgIleGluAspAsnGlnIleArgAlaSerSerMetLeu 406        :	95 Qy	VERSION DQ051196.1 GI:66904395 KEYWORDS GSS. SOURCE Homo sapiens (human)
318 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Ce. Db	DQ051196
ArgLysGlyGluGluLeuGluGluGluTrpThrProThrGluLysValLysCysPro	2237 bp DNA linear GSS 02-JUN-2005 e, VIRTUAL TRANSCRIPT, partial sequence,	DQ051196 DN Homo Bapiens HC
258 CCGCCTCCACCAGNINNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN		RESULT 12
367 Pro 367	AGCATACCTGCATGGCTTGGCTGACCCCAAAGGGGAGGCTGG 2579	Db 2537 AGCATACCTGCATGGCTT
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347 SerSerProLysGluGluThrAspLysTrpAlaValGluLysGlyLysAspHisLysGlu 366	GTAGTAACTCTGTAGCAGGCTTTCCCTGTTGTTTTGACTGTAATTCAAGAGACACTCAGG 2536 Qy	Db 2477 GTAGTAACTCTGTAGCAG
195 AGGCCGCCCAAGAGGCCCAAGCCCCAAGCCTCCCAAGAGGGAGAAG 245	SerThrThrIleGlu 1066	Qy 1058 AlaThrThrLeu
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GAGCCCGAGCTCGAGACCTTCTCTCCGCCGCCTGCCTGCGGGGGCCCGGGGAGGAGTGG	isArgLeuArgLeuArgAlaGlnMetArgLeuArgArg 1037	1018
287 IleGluProProValLysProLeuLeuProProLeuProProAspTyrGlyAspGlyTyr 306		Db 2351 GGGAAGCAGCCTGTCAGCCTA-

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                             ACCAAGAACTGTATGGCTATGACATGGGGGCCACAAGGTGTGACTTCACACTTAGC
                                                       AlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPheIleLeuAla 983
                                                                                                   ArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyrThrProSer
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Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp666J235) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp666J235 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp666J235 further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The German cDNA Consortium Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bahr, A., Lauber, J., Mewes, H.W. Fobo, G., Han, M. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens mRNA; cDNA AL833732
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                 QGRNSLMLSDWVTSYKVNVSNDSHTWVTVKNGSGDMIFEGNSEKEIPVLNELPVPMVA
RYIRLNPQSWFDNGSICMRNEILGCPLPDPNNYYHRRNEMTTTDDLDFKHNYKEMRQ
LMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGAHGNEVL
GRELLLLLLVQFVCQSYLARNARIVHLVEETRIHVLPSINPDGYEKAYEGGSELGGWSL
GRWTHDGIDINNFPDLNTLLMEAEDRQNVPRKVPNHYIAIPEMFLSENATVAAETRA
VIAWMEKIPFVLGGNLQGGELVVAYPYDLYNSPWKTQBHFFTEDHVERWLAYSYAST
HRLMTDARRVCHTEDFQKEBGTVNGASWHTVAGSINDFSYLHTNCFERLSIYVGCDKY
PHESQLPEEWENNRESIIVFMEQVHRGIKGLVRDSHCKGIPNAIISVEGINHDIRTAN
DGDYRRLLNPGEYVVTAKABGFTASTKNCNVGYDMGATRCDFTLSKTNMARIREIMEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="stomach"
/clone lib="666 (synonym:
DH10B; sites Not! + Sal!"
FGKQPVSLPARRLKLRGRKRRQRG"
                                                                                                                                                                                                                                                                                          /product="hypothetical
/protein_id="CAH56260.1
/db_xref="GI:52545817"
                                                                                                                                                                                                                                                                                                                                                                                /gene="DKFZp666J235"
/codon_start=1
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/mol_type="mRNA"
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/clone="DKFZp666J235"
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/db_xref="RZPD:DKFZp666J235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="DKFZp666J235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="carboxypeptidase-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dev_stage="adult"
                                                                                                                                                                                                                                                                         translation="RLNIQAGINENDFYDGAWCAGRNDLQQWIEVDARRLTRFTGVIT"
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Alignment Scores:
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Query Match:
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                                                                                                    GTCGGTGAGCCCGAGTTCCACTACATCGCGGGGGCCCACGGCAATGAGGTGCTGGGCCGG
                                                                                                                                                                                                                                                    CACGATGGAATTGACATCAACAACAACTTTCCTGA
                                     GluGluGlyPheAspIlePheGluAspPheProAspLeuAsnSerValLeuTrpGlyAla
                                                                            TyrGluValAlaAlaGlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThr
                                                                                                                                                                                        LeuGlyGluProGluPheArgTyrThrAlaGlyIleHisGlyAsnGluValLeuGlyArg
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Pan troglodytes HC19233 gene,
genomic survey sequence.
DQ051197
DQ051197.1 GI:66904396
                                                                        MetArgLeuArgArgLeuAsnAlaThrThrThrLeuGlyProHisThrValProProThr
                                                                                                              ProGlnGlnArgArgLeuGlnGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGln
                                                                                                                                                  ATCATGGAGAAGTTTGGGAAGCAGCCCGTC----
                                                                                                                                                                                      GACATCCGAACAGCCAACGATGGGGGATTACTGGCGCCTCCTGAACCCCTGGAGAGTATGTG
                                                                                                                                                                                                                                                                         GlyValLysThrAlaSerGlyGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArg
                                                                                                                                                                                                                                                                                                            ThrAspGluGlnGlyIleProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHis
                                                                                                                                                                                                                                                                                                                                      ACCGTCGCTGGAAGTCTGAACGATTTCAGCTACCTTCATACAAACTGCTTCGAACTGTCC
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                                                                                                                                                                  IleMetAlaMetAsnGlyAsnArgProIleProHisIleAspProSerArgProMetThr
                                                                                                                                                                                                                                                                                                   AGAGATTCACATGGAAAAGGAATCCCCAAACGCCATTATCTCCGTAGAAGGCATTAACCAT
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                             bp DNA linear
VIRTUAL TRANSCRIPT,
                            GSS 02-JUN-2005 partial sequence,
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RESULT 15
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 2169)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
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Direct Submission
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Inferring nonneutral evolution from human-chimp-mouse ortho
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Search completed: October 1, 2006, 04:45:29
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-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-Q-labss/ABSSWEB ppool/US10642946/runat_29092006_125306_12469/app_query.fasta_1
-DB=N Geneseq -QFMT-fastap -SUFFIX=p2n.rng -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -STAKT=1 -END=-1 -MATRIX+blosum62 -TRANS-human140.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000 -HOST=abss03p
-USER-US10642946_@CGN 1 1.1177_@runat_2909206_125306_12459 -NOPU=6 -ICPU=3
-NORMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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## ALIGNMENTS

ABZ34770 standard; cDNA; 3935

ВP

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Garcia T, Roman Roman S, Baron R, (Connolly T, Jackson A, Bushnell SE,
                                                                                                                                                                 Osteopathic; osteogenesis modulator; gene therapy; osteogenesis; osteoporosis; bone disease; downregulator; human; enzyme; ss.
                                                                                                                                                                                                  Coding sequence SEQ ID 128, upregulated in osteogenesis
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                                 (AVET ) AVENTIS PHARMA SA
                                                       05-APR-2001; 2001US-0281400P
                                                                              05-APR-2002; 2002WO-IB002211.
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Human; breast
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cancer; cytostatic; gene therapy; gene;
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21-JUN-2002; 2002WO-US019669

21-JUN-2001; 2001US-0299887P.
27-JUN-2001; 2001US-0301572P.
18-JUL-2001; 2001US-0306501P.
25-SEP-2001; 2001US-0325002P.
05-MAR-2002; 2002US-0362585P.
14-MAY-2002; 2002US-0380391P.

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(MILL-) MILLENIUM PHARM INC

Lillie J, Mertens M, Bast RC, H Gannavarapu M, Glatt K, Hoersh S, Kamatkar S; , Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers R Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;

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P-PSDB; ABR47386.
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CAGGCATTCCCCTTCACAACAGTAGAGACCTACACAGTGAACTTTGGGGACTTC
                                                              CTGGAACCCGAGTTTGAGGAAGAGGAGGAGGAGGAGAAAGAGGAGGAGATAGCCACTGGC
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DNA; 3935 ВP

Hepatic fibrosis; marker; chronic hepatitis; liver hepatic carcinoma; human; ds. Human hepatic-fibrosis disease marker SEQ ID 115.

cirrhosis;

11-MAR-2002; 2002JP-00065013

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatic fibrosis disease markers comprising polynucleotides or antibodies, useful for improved diagnosis, screening and developing to treat hepatitis, to control cirrhosis and carcinoma.
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 WPI; 2005-273381/28
                                                          (CHIB-) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHARM CO
(NIGA ) NGK INSULATORS LTD.
                                                                                                           25-SEP-2003; 2003US-0505614P
                                                                                                                                 24-SEP-2004;
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to microarrays for assessing the prognosis of neuroblastoma, which contains 25-45 good prognosis probes selected from CC among 96 polynucleotides which are hybridizable with a gene transcriptional product that shows accelerated expression in patients CC having good prognosis of neuroblastoma, which comprise the nucleotide sequences of ADZ26035-ADZ26130, their partial consecutive sequences or CC complementary chains, and 25-45 bad prognosis probes selected from among 104 polynucleotides which are hybridizable with a gene transcriptional CC prognosis of neuroblastoma, which comprise the nucleotide sequences of ADZ26131-ADZ26234, their partial consecutive sequences of CC chains. Also described is a method for assessing neuroblastoma prognosis comprising: (a) labeling a gene transcriptional product obtained from the tumor cells of patients with neuroblastoma; (b) contacting the labeled CC material with the microarray, and (c) measuring label signals from the CC hybridized gene transcriptional product. The patient is judged to show good prognosis when significant label signals are obtained from those hybridized with 25 good prognosis probes, but however when significant clabel signals are obtained from those probes, such patient is judged to have poor prognosis. The method and microarrays are for assessing neuroblastoma prognosis, and therefore are useful in diagnosis, therapy selection and management of patients are contacting the patient as gene transcriptional product which shows accelerated expression in gatients having good prognosis of neuroblastoma accelerated expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-642-946-3 (1-1158) x ADZ26196 (1-3935)
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                                         AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn
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GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158
                                                                                                                                   PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120
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Human tumour-associated antigenic target (TAT) cDNA sequence

human; tumour-associated antigenic target; cancer; cell proliferative disorder; gene; TAT; cytostatic; gene therapy;

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The present invention describes an isolated tumour-associated antigenic (RAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% certified: (1) an expression vector comprising the above uncleic acid; (2) a host cell comprising the above expression vector comprising the above comprising: (a) an amino acid sequence encoded by the full-length coding region of the above expression vector; (3) (c) a process for producing a polypeptide; (4) an isolated polypeptide (c) length coding region of the above encoded by the full-cell comprising the above polypeptide; (b) an amino acid sequence encoded by the full-cell coding region of the above nucleotide sequences; or (c) a sequence comprising the above polypeptide; (f) a chimeric polypeptide; (f) an isolated antibody; (f) an anino acid sequence encoded by the full-cell comprising the above polypeptide; (f) a process for producing the antibody; (f) an anino acid sequence; or (c) a sequence comprising the above polypeptide; (f) a process for producing the antibody; (f) an anino acid sequence encoded by the full-cell comprising the above polypeptide; (f) a process for producing the antibody; (f) an anino acid sequence; or (c) a sequence comprising the above polypeptide; (f) a process for producing the antibody; (f) an antibody; (f) a nethod of comprising a container and the composition of matter comprising the above (chimeric) polypeptide; (f) a chimeric polypeptide; (f) a matibody; (f) an antibody and antibody; (f) a method of container; (f) method of cell that expresses the above protein, where the growth of the above protein; (f) a method of determining the protein cell state and the protein of antibody; (f) a method of antibody; (f) a method of attermining the protein of a medical and the present of a sequence represents a medical proliferative
                                                                                                                               Percent Similarity:
                                                                                                                                                                                              Alignment Scores:
                  US-10-642-946-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
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                                                                                 Local Similarity:
                                                                                                                                                                                                                                                                                      human TAT cDNA
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1081 SerGluthrGluthrfyrfhrediwyal Valifhrediyfhrediyfhrediwyalgluprociu 1100 		721 ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740
Leuse Thrithe 1 eGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGlu	da	701 AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTrpValProTyr 720 
1041 ThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrThr 1060	dg	681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu 700 
ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla 	dg dg	661 ArgileHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly 680 
ProlleProHisileAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGln	Ωy	641 TyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660 
981 IleLeuAlakrgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000 	Ωy Db	621 ThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuLeuLeuMetGln 640 
ThrProSerAlaLysThrCysAenValAspTyrAspIleGlyAlaThrGlnCysAenPhe	Db Db	601 AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 620 
941 AspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyr 960 	0y	581 CysProThrlleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr 600 
AlaAsmAlaThrIleSerValSerGlyIleAsmHisGlyValLySThrAlaSerGlyGly	dg Qy	561 AspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValValAsnGluGlu 580 
MetGluGlnValHisArgGlyIleLysGlyValValThrAspGluGlnGlyIleProIle	ОУ	541 SerValAlaBroValTyrSerTyrTlaGlnAsnGluValValAlaThrAspAspLeu 560 
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3-2	Db .	501 ValAspLysAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIle 520 
41 G19G19MetG19T1EValasmG19A1aLysTrpAsmProArgThrG19ThrI1EASmAsp	40 Ag	481 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500 
SetalalsLeuintLeuintGluProlytaRgGlyGlyGlyClyClnAlaGlnAspTyrInt B	, B &	461 GlyArgAspSerSerIleHisaspAspPheValThrThrPhePheValGlyPheSerAsn 480 
SerGluAlaGluGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla	o do Oy	441 ThrGlnTrpIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460
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ABILEUASIGIYGIYGIYGIYAFYEOTYFASIMEALAAFGTHFFFOTHF	, d &	401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420 
SeringuvalargalalielleAlairpmecGluly86sprophevalleuglyAla	P &	381 GluLysValLysCysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle 400 
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manmals. The invention also relates to nucleic acid and polypeptide
sequences at least 80% identical to the TAT nucleic acids and
polypeptides; expression vectors and host cells comprising a TAT nucleic
acid; an antibody specific for a TAT polypeptide; apeptide or organic
molecule which binds to a TAT polypeptide; fusion proteins comprising a
TAT polypeptide; and methods and compositions for the treatment or
diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
antibodies, antagonists, binding molecules and compositions are useful
for diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
increased TAT expression, particularly cancers such as breast cancer,
colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
cancer, pancreatic cancer, cervical cancer, liver cancer bedder
cancer, melanoma and leukaemia. TAT nucleic acids may further be
used as hybridisation probes, in chromosome and gene mapping, in
chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour-associated antigenic target; TAT; human; overexpression; cutumour; diagnosis; cell proliferative disorder; breat cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                     The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour-associated antigenic target (TAT) cDNA DNA324930, SEQ ID NO:2248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 2248; 7273pp; English.
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                                                                                                                                                                                                                              ArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgProProPro
                                                                                                                                                                                                                                                                                           CAGCCTGAGCCGGAGGAGGAGCCGAGCAACCCACACTGGA
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AGCCTGGTGCAGGAC	rgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAsp	1 ThrAlaGlyIleH1sGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuLeuMetGln 640	etGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 6 	Lysse        AGAG	561 AspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValValAsnGluGlu 580 	541 SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValValAlaThrAspAspLeu 560 	1 ArgileTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 5	STATE	1 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 5	1 GlyargaspSerSerIleHisaspAspPheValThrThrPhePheValGlyPheSerAsn 48	pileGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln 4 	1 ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAspAspAlaArg 44	ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420	BValLysCysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle 4 	GYLY8ASPHISLY8GluProArgLy8GlyGluGluLeuGluGluGluTrpThrProThr 380	41 LysProLysLysGluAspSerSerProLysGluGluThrAspLysTrpAlaValGluLys 360 	1 ProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGluLeuLys 34	301 ABPTYrG1YASPG1YTYrVallleProAsnTyrAspAspMetAspTyrTyrPheG1YPro 320 
δ δ	. Q	B 8	, B &	B &	Qy dd	Db Q	gg Qg	g Q	B 6	φ <b>φ</b>	B &	B Q	Db Qy	, Q	9d Qy	dg VQ	dd Vy	Db Oy
ATCCCACAC ArgLeuGlr	1 ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGln	981 IleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000 	961 ThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe 980 	941 AspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyr 960 	21 AlaasuAlaThrIleSerValSerGlyIleAsuHisGlyValLysThrAlaSerGlyGly 	901 MetGluGlnValHisArgGlyIleLysGlyValValThrAspGluGlnGlyTleProIle 920 	ProHisGluSerGluLeuProArgGluTrpGluAsnAsnLysGluAlaLeuLeuThrPhe	861 PheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880	841 GlyGlyMetGlyIleValAsnGlyAlaLysTrpAsnProArgThrGlyThrIleAsnAsp 860	821 SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840 	801 SerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla 820 	781 GlnGluGlnLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluVal 800 	761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrFroTyrAspMetAlaArgThrProThr 780 	741 SerThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPheValLeuGlyAla 760	721 ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740 	701 AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTrpValProTyr 720 	681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu 700 	661 ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly 680 

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The present invention describes a method for diagnosing and treating a cancer, e.g. breast, lung, colon, or kidney cancer. The method comprises detecting and blocking the over expression of a gene of a protein found in breast, lung, colon, or kidney tissue. Also described is an antibody or binding portion of an antibody that specifically binds a protein found in breast tissue, lung tissue, colon tissue, or kidney tissue. The methods, antibodies, polynucleotides and polypeptides from the present invention are useful for detecting, diagnosing, preventing and treating cancer, e.g. breast, lung, colon, or kidney cancer. The present sequence
                                                                                                                                                                                                                                                                              Diagnosing and treating a cancer, e.g. breast, lung, colon, or kidney cancer, comprises detecting and blocking the over expression of a gene a protein found in breast, lung, colon, or kidney tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; tumour; breast cancer; lung cancer; colon cancer; kidney cancer;
antibody; cytostatic; gene therapy; human; colon tumour tissue;
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888888¥& represents a nucleotide sequence given in the present invention, which is over expressed in human colon tumour tissue. N.B. All 385 sequences referenced in this patent are detailed in the US provisional application SN 60/447,900, filed 02/13/2003. In this application only one sequence, representing the longest sequence of each of the 65 clones is listed in Appendix A (and given as SEQ ID NO:1 to 65 in the Sequence Listing). Sequence 4125 967 A; 1321 Ç 1227 <u>Ω</u> 610 .<del>.</del> 0 ď 0 Other;

4125 1156 2 0 0

US-10-642-946-3 (1-1158) x ADR44022 666 909 101 546 366 306 966 906 201 181 786 161 726 141 121 486 426 261 221 81 61 41 21 μ ATGGCGGCCGTGCGCGCGCGCCCTGCTCCTGGCGTTGCTGGCCCTGTGC MetAlaAlaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys GlnProGluProGluGluGluThrGluGlnProThrLeuAspTyrAsnAspGlnIleGlu LysProLysGluGluProProLysAlaThrLysLysProLysGluLysProProPsAla LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys LysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysLysGly ThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLysLysAsp GAGCCCACCCCGCGGTCCGAAAAGCCCCAGGCGGGGGCAAGCCCAGGGAAGCCGGCCAGGG GluProThrProArgValArgLysAlaGlnAlaGlyGlyLysProGlyLysArgProGly PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProProPro ArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgProProPro| TrpProLeuProProProProSerProGlyProGluGluLeuProGlnGluGlyGlyAla AAAGGCCCCAAGGTGCCCAAGGAGTCCTTGGAGGGGGTCCCCCAGGCCGCCCAAGAAGGGG **ACGGCCGCAGAAGTGCCTCCGGAAAAGACCAAAGACAAAGGGAAGAAAGGCAAGAAAGAC** TTCCTGTCAGAGCTAGAACCTGAGCCCCGGGAGGACGACGTGGAGGCCCCGCCGCCTCCC SerArgArgArgArgProGluArgValTrpProGluProProGluGluLysAlaProAla CAGCCTGAGCCGGAGGAGGAGCCGAGCAACCCACACTGGACTACAATGACCAGATCGAG CCCCTCTCAAATAACTGGCAGAATCCAGGAGAGGAGGACCCATGTGGAGGCACGGGAGCAC ProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHisValGluAlaGlnGluHis AAGCCCAAGGAGAAGCCACCCAAGGCCACCAAGAAGCCCCAAAGAGAAGCCCACCCCAAGGCC AAGGAGAAGCCACCCAAGGCCAACAAGAAGCCCAAGGAAGCCCACCTAAGGCCACCAAG 4.47e-290 6264.00 100.0% 99.8% 99.9% (1-4125)Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1085 80 485 425 40 365 1025 240 905 200 845 180 785 160 725 140 665 120 605 545 60 965

981 IleLeuAlaArgSerAshTrpLysArgIleArgGCIUILeMetAlaMetAshGlyAshArg 1000 	- da	621 ThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGln 640 	B 8
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The invention relates to a combination comprising cDNAs or their complements that are differentially expressed in respiratory disorder. The combination is useful for preparing a composition for diagnosing o treating respiratory disorders e.g. lung cancer, chronic obstructive pulmonary disease, emphysema or asthma. The present sequence represent
                                                                                                                            New combination comprising cDNAs that are differentially expressed in respiratory disorders, useful for diagnosing or treating respiratory disorders e.g., lung cancer, chronic obstructive pulmonary disease, emphysema or asthma.
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601 AlametGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 620	561 AspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValValAsnGluGlu 580	521 ArgileTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540	481 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500	441 ThrGlnTrpileGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460	401 ArgalaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyAxgLeuAsnMetGln 420		1 LysProLysLysGluAspSerSerProLysGluGluThrAspLysTrpAlaValGluLys 360	301 AspTyrGlyAspGlyTyrVall1eProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320
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  This sequence represents a full-length nucleotide sequence that codes human E2A binding protein (E2A-BP, see AAW36816). It was isolated from human aortic RNA following 3 rounds of 5'RACE procedures. E2A-BP is expressed in vascular smooth muscle cells; mRNA is preferentially expressed in the aorta. E2A-BP interacts with E2A proteins in vivo, bit to both E12 and E47 and inhibits binding of E47 homodimer to an E-box
                                                                                                                                                                          DNA encoding human and mouse E2A binding proteins - useful for inhibiting or stimulating growth of vascular smooth muscle cells, e.g. for wound healing or treatment of rheumatoid arthritis or retinopathic diabetes.
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probe (see AAT97606). Mouse (see AAT97611) and rat (see AAT97612-13) E2A-BP sequences have also been isolated. E2A-BP nucleic acids may be used in gene therapy and antisense methods for treating vascular diseases such as arteriosclerosis, to produce transgenic or knock-out animals, as well as in methods of producing E2A-BP polypeptides that can be used therapeutically to promote vascular smooth muscle cell growth e.g. for wound healing, or to screen for modulator compounds useful e.g. for the treatment of arteriosclerosis and angiogenesis. The E2A-BP gene promoter can be used in gene therapy methods to direct vascular smooth muscle cell specific expression of the E2A-BP gene, antisense sequences or
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Qy 967 CysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPheIleLeuAlaArgSerAsn
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                                                                                                                                                                                                                                           kw protein modification; protein maintenance molecule; PMMM;
whosphatase; protein stabilisation; protein degradation; kinase;
whosphatase; protease inhibitor; isomerase; transferase;
whosphatase; protease; protease inhibitor; isomerase; transferase;
whosphatase; protease; protease inhibitor; isomerase; transferase;
whosphatase; protease; antiallergic; antiinflammatory;
whosphatase; antiparkinsonian; nootropic; anticonvulsant;
whosphatase; antiparkinsonian; nootropic; antiinflammator; isomerase; antiarthritic;
whosphatase; hepatotropic; dermatological; antidiabetic; nephrotropic;
whosphatase; inflammatoric; osteopachic; antiarthritic;
whosphatase; hemostatic; antibacterial; virucide; protozoacide;
whosphatase; gene therapy; cell proliferative disorder; arteriosclerosis;
whosphatitis; polycythaemia vera; psoriasis; primary thromobocytopaenia;
whosphatitis; polycythaemia vera; psoriasis; primary thromobocytopaenia;
whosphatitis; polycythaemia psoriasis; primary thromobocytopaenia;
whosphatitis; polycythaemia; mental retardation;
whosphatitis; polycythaemia; partialis; partialis; partialis; allergies;
whosphatitis; osteoporosis; antiamatory disorder; allergies;
whosphatitis; osteoporosis; pancreatitis; Sjogren's syndrome;
whistophatitis; osteoporosis; pancreatitis; Sjogren's syndrome;
whistophatitis; osteoporosis; pancreatitis; Sjogren's syndrome;
whistophatitis; osteoporosis; pancreatitis; Sjogren's syndrome;
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                                                                                                                                                                                                                           microbial infection; human;
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MetAlaAlaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys

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CC protein modification and maintenance molecules (PMMM). The cellular CC processes regulating modification and maintenance of protein modecules CC coordinate their function, conformation, stabilisation and degradation. CC Each of these processes is mediated by key enzymes or proteins such as CC kinases, phosphatases, proteases, protease inhibitors, isomerases, CC kransferases and molecular chaperones. Compounds which modulate the CC proteins of the invention may have anti-HIV, antiallergic, antiinflammatory, antiansemic, antiparkinsonian, nootropic, antityroid, cycostatic, hepatotropic, dermatological, antidiabetic, CC antityroid, cycostatic, hepatotropic, antiapreterio, immunosuppressive, cc antityroid, cycostatic, hepatotropic, antiapreterio, cycostatic, unopathic, chyopathic, antiparastic, antihelmintic, antiparathic, osteopathic, CC ophthalmological, antirheumatic, haemostatic, antibacterial, virucide, protezoacide or fungicide activities. The DNA sequence which encode the protezoacide or fungicide activities. The bunds of protein modification and maintenance molecules (PMMMs), the DNA sequences which encode them and their modulating compounds are useful for cidingnosing, treating or preventing disorders associated with aberrant cc primary thromobocytopaenia or cancer), developmental disorders (for example anteriosclerosis, hepatitis, polycythaemia vera, psoriasis, proteins of their modulating compounds are useful for cc example alzheimer's disease, Parkinson's disease or epilepsy').

CC autoimmune/inflammatory disorders (for example AlDS, allergies, asthma, autoimmune/inflammatory 
                                                                             Percent Similarity:
Best Local Similarity:
US-10-642-946-3 (1-1158) x ADE79067
                                                                                                                            Score:
                                                              Query Match:
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25-FEB-2002;
21-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human protein modification and maintenance molecules and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to novel isolated human proteins, which are human protein modification and maintenance molecules (PMMM). The cellular
                                                                                                                                                                                                              Sequence 4025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sclerosis or cancer.
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DB; ADE79009.
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Ison CH, Marquis
Becha SD;
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Kable AE;
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361 GlyLy8AspHisLy8GluProArgLy8GlyGluGluLeuGluGluGluTrpThrProThr 380 	341 LysProLysLysGluAspSerSerProLysGluGluThrAspLysTrpAlaValGluLys 360 	321 ProProProGlnLysProAspAlaGluArgGlnThrAspGluGluLysGluGluLeuLys 340 	301 AspTyrGlyAspGlyTyrVallleProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320 	281 ProAlaProGluGluArgIleGluProProValLysProLeuLeuProProLeuProPro 300 	261 SerArgArgArgArgProGluArgValTrpProGluProProGluGluLygAlaProAla 280 	241 ArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgProProPro 260 	1 GlnProGluProGluGluGluThrGluGlnProThrLeuAspTyrAsnAspGln] :::	201 ProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHisValGluAlaGlnGluHis 220 	181 TrpProLeuProProProProSerProGlyProGluGluLeuProGlnGluGlyGlyAla 200 	161 ThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThrLeuGlu 180 	141 LysProLysGluGluProProLysAlaThrLysLysProLysGluLysProProLysAla 160 	121 LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys 140 	101 LysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysLysGly 120 	81 ThralaalaGluValProProGluLy8ThrLy8AspLy8GlyLy8Ly8GlyLy8Ly8Asp 100 	3lnAlaGlyGlyLy8ProGlyLy8Arg                AGGCGGGGGCAAGCCAGGGAAGCG	41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProProPro 60 	21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly 40 
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706 nSerValLeuTrpGlyAlaGluGluArgLysTrpValProTyrArgValProAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnA	19 CTCACTGAACCCTGATGGCTACGAGGTGGCAGCGCAGAGTTGGGAACTG	46 FARGASDGIVASHPYOARGVALAKGSETLENVALGINASDIKKARGILEHISLENVALPY 64 FARGASDGIVASHPYOARGVALAKGSETLENVALPY 64 FARGASDGIVASHPYOARGVALAKGSETLENVALPY 64 FARGASDGIVASHTARGVALFIKARGVALTAGILEHILIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	26 YASTGILVALLEUGIYAETGILLEULEULEULEULEULEUGINTYYLEUCYBAETGILTY 6	06 pasmrrodlyGluHisGluLeuGlyGluProGluPheArgTyrThrAlaclyIleHisGl 6	86 gThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyrAlaMetGluIleSerAs 	19 CI	46 rSe     59 CAC	99 CT	06 oValleuSerGluLeuProGluProValValAlaArgPheIleArgIleTyrProLeuTh 	496	19 AGGCTCTTGGCTCTGCTCCCATTGTCTGGGCGAGGGGTGGGGTCTCAGAGGGGCTGGCAG	485	1 GlyargAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 4	A I	421 ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAspAspAlaArg 440 	401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420	ទ=-១

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KW protein modification; protein maintenance; protein function;
W protein conformation; protein stabilisation; protein degradation; kinase;
W phosphatase; protease inhibitor; isomerase; transferase;
KW molecular chaperone; anti-HIV; antiallergic; antiinflammatory;
KW antianaemic; antiparkinsonian; nootropic; anticonvulsant;
KW antiarteriosclerotic; antiasthmatic; immunosuppressive; antiathyroid;
KW antigout; thyromimetic; antisathmatic; immunosuppressive; antiatrhritic;
KW antiparasitic; antihelmintic; antiparasitic; uropathic; antiatrhritic;
KW antiparasitic; haemostatic; antibacterial; virucide; protozoacide;
KW fungicide; gene therapy; cell proliferative disorder; arteriosclerosis;
KW fungicide; gene therapy; cell proliferative disorder; arteriosclerosis;
KW cancer; developmental disorder; anaemia; mental retardation;
KW cancer; developmental disorder; anaemia; mental retardation;
KW meurological disorder; Alzheimer's disease; Parkinson's disease;
KW epilepsy; autoimmune disorder; inflammatory disorder; AIDS; allergies;
KW glomerulonephritis; Goodpasture's syndrome; multiple sclerosis;
KW arthritis; osteoporosis; pancreatitis; Sjogren's syndrome;
microbial infection; human; gene; ds.
                                                                                                                      Hafalia AJA, Li JX, Gorvad AE, Chawla NK, Sprague WW, Lee S Chang H, Elliott VS, Ramkumar J, Khare R, Emerling BM, Kabl Tang YT, Yue H, Gietzen KJ, Lee S, Swarnakar A, Baughn MR; Wilson AD, Jin P, Chien D, Hawkins PR, Jiang X, Jackson AA; Bhatla U, Burrill JD, Blake JJ, Ho A, Zheng W, Ison CH, Ma Tran UK, Lal PG, Warren BA, Xu Y, Honchell CD, Becha SD;
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25-FEB-2002; 2002US-0359903P
21-MAR-2002; 2002US-0366837P
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Kable AE;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to novel isolated human proteins, which are human concesses regulating modification and maintenance molecules (PMMM). The cellular processes regulating modification and maintenance of protein molecules coordinate their function, conformation, stabilisation and degradation. CE Each of these processes is mediated by key enzymes or proteins such as continuous proteins or proteins such as continuous proteins or proteins such as continuous proteins of the invention may have anti-HIV, antiallergic, antiinflammatory, antianaemic, antiparkinsonian, nootropic, antiinflammatory, antianaemic, antiparkinsonian, nootropic, contiinflammatory, antianaemic, antiparkinsonian, nootropic, antiinflammatory, antianaemic, antipartial immunosuppressive, contiinflammatory, antianaemic, antipartial immunosuppressive, contiinflammatory, antianaemic, antipartial, immunosuppressive, contiinflammatory, antianaemic, antipartial, virucide, cophthalmological, antirheumatic, haemostatic, antiparatic, virucide, cophthalmological, antirheumatic, haemostatic, antiparaticle, virucide, cophthalmological, antirheumatic, haemostatic, virucide, cophthalmological, antirheumatic, haemostatic, virucide, cophthalmological, antirheumatic, haemostatic, the DNA sequence which encode the protein modification and maintenance molecules (PMMMs), the DNA sequences which encode the protein of PMMM, particularly cell proliferative disorders (for cample anteriosclerosis, hepatitis, polycythaemia vera, psoriasis, cophthalmological, antirheumatic, haemostatitis, polycythaemia vera, psoriasis, cophthalmological, antirheumatic, haemostatic, antiparative disorders (for example Alzheimer's disease, Parkinson's disease or epilepsy, allergies, asthma, cophthalmological
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                      GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn
                                                                                         ThrGlnTrpIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln
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	nrGluValArgAlaIle 	ProAspLeuAsnServ	heGlyAsnTrpAlaI            TTGGGAACTGGGCG	GCCGAGAGTACCGC isLeuValProSe1	lyIleHisGlyA            GATCCATGGCA  ysArgGluTyrA	ulleSerAspAs            GATCTCAGACAA	hrileTh	rghishi	ProvalTyrSe	leTyrProLeuThrTrpA 	)LysAspThrProVall             aaGGaCaCCCCGTGC	:rGlnThrTrpValMetTyrT              :cAGACATGGGTGATGTACA
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ABQ54610
ID ABQ54610 standard; cDNA; 3523 BP.
XX
AC ABQ54610;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HNTAK22 cDNA, Human ovarian antigen HNTAK22 cDNA, SEQ ID NO:490.

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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP41228) and to CDNAs encoding them (ABQ54131-ABQ56305), and also CC encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen CC polymucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, conformation of ovarian control ovarian cancer and breast-related disorders. Such conditions include ovarian cancer and breast-related CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC polycystic ovary syndrome, ovarian cystes, and dysmenorrhoea), endocrine CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic conditions (e.g., mastitls, oophoritis and commune disorders (e.g., congenital and acquired toxic conditions), immune disorders (e.g., congenital and acquired toxic conditions), immune disorders (e.g., congenital and acquired toxic conceptions), inflammatory conditions (e.g., mastitls, oophoritis and conceptions), inflammatory conditions (e.g., mastitls, oophoritis and conceptions), congenital and acquired toxic conditions (e.g., mastitls, ophoritis and conceptions), congenital and acquired conditions (e.g., respiratory disorders, neurological disorders, gastrointestinal disorders, candural control compounds which conditions (e.g., mastitls, systemic lupus erythematosus), conditions (e.g., mastitls, and toxic conditions), congenital and acquired polymucleotides may system disorders. Ovarian antigen polypeptides and conditions (e.g., mastrointestinal disorders, candural conditions), congenital and acquired polymucleotides may be used as food additives or to prepare antibodies constitutions (e.g., candural conditions), and the conditions (e.g., candural conditions), and the conditions (e.g., candural conditions), and the conditions (e.g., candural conditions), and the condition
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     Sequence 3523
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2.1e-264 5725.00 99.8% 99.6%

Length:
Matches:
Conservative:
Mismatches:

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	erMet	allysCysPro            CAAGTGTCCC	ti sLysGluP)             ACAAAGAGCC	8G1 uAs               GGAGGI	CCAGAAGCC	rGlyaspGlyTyrValI1            rGGTGATGGTTACGTGAT	ProGluGluAr            CGGAGGAGAC	ArgArgPı          AGGAGGCC	luaspTyrGluaspPheGluTyr            aggacTaTgaggaCTTTGagtac	ProGluGluGluThr             CCGGAGGAGGAGACC	SerAsnAsnTı 	ProProPi	ProProSe	GluGluPr    :::   GAGAAGCC	ProProLy	LygValPr          AGGTGCC	) × ABQ5	91.3%
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0000	isGlyLeuGlyAl 	ProlleGlyMetGluSe 	roArgLysGlyGluGluLe 	erSerProLysGluGluTh              GCAGCCCCAAGGAGGAGAC	laGluArgGlnThr             TGAGCGCCAGACG	eProAsnTyrAspAspMetAspTyrTyrPheGlyPr 	uProProValLysProL             CCTCCTGTGAAGCCTC	rgArgArgArgProGluArgValTrpp 	TYTILEA	GluGlnE         GAGCAAC	nTrpGlnasnProGlyGluGluTh             CTGGCAGAATCCAGGAGAGGAGAC	ProGlyP          CTGGCC	~ <del>-</del> =	AlaThrLys           GCCACCAAG	rLysLysP          CAAGAAGC	SerI	-3523)	Indels Gaps:
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2000000	aGlnArgGly <i>F</i>           	<u>입</u> _품	euGluGluG]            GGAGGAGG!	hrAspLysTrpAi             ccgacaagTggg	oGluGluI          cgaagaga	oMetAspi          CATGGACT	oLeuLeuProProI               CTGCTGCCCCGG	oProGluc          CCTGAGO	nLysGlni        GAAGCAA			uLeuPro         3CTACCC	LeuAlaPros            CTGGCTCCC	OLYSG1ul	GRULYSProp	rProArg		00
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SerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla 8	781 GlnGlnLeuLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaSpGluAspGluAspGluVal 800 	761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780 	741 SerThrGluValArgAlaIleIleAlaTrpMetGluLygAsnProPheValLeuGlyAla 760 	721 ArgValProAsnAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740 	2 1 Ω—≯	681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu 700 	661 ArgIleHisLeuValProSerLeuAsnDroAspGlyTyrGluValAlaAlaGlnMetGly 680 	641 TyrLeuCyBArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660 	621 ThralaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuLeuMetGln 640 	601 AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 620 	581 CysProThr1leThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr 600 	61 82	541 SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValValAlaThrAspAspLeu 560 	521 ArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540	01 ValAspLysAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIle 5	481 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500 	461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480 	441 ThrGlnTrpIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460 
RESULT 13 AAT97611		3062 CTGGAACCCGAGTTTGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	101 FAMEGI   INTUMARATE   INTUM	2942	1061 Geuserinrilaeilueroirpidykeullerrobrothintaklaglyipiduolu 	1041 INTINITINITINITINITINITINITINITINITINIT	1021 AT 9AT 9 BENJAMI BALGAT 9 BENJAMI 9 BENJA	1001 PTOLLEPTOHBILEABPETOSETÄRGPTOMETINETTOGLIGITMATGAEGLEGGEGETGERAGE	981 ITELEUMIAKEGSEKABRITEDYSKATGITEN SEGULITEREKATAREKASIGSYKASIASEGERAKEGEGAKEGEGAKAGAKEGEGERAKEGEGERAKEGEGERAKEGEGERAKEGEGERAKEGEGERAKEG	961 ThrProSerAlaLysthrCysAshvalAsbiyFasbileGyAlaLhrGuncysAshrhc	941 ASDIYTIEDAGGILEUGUNSHEROOLYGUUTAGGALIILALGALGALGGIUSLYYY 	921 AIAASHATATITI LESETVALSETCAJI LEASHATAGOT VALLAJSHILAJSHICA JOST VALLAJSHILAJSHILAJSHICAJOT VALLAJSHILAJ	2402 ATGGAGCAGCTACCGCGGCATTAAGGGGGTGGTGACGAGCAAGCA	COLUMN   C	2282 T	841 GLYGLYMECGLYLLEWALABUGLYALDIYBLI PABBIFLOAT JINLILEAGUADA GERMANA JINLILEAGUADA GERMANA JINLILEAGUADA GERMANA GERM	821 SEFALAHISLEUTITLEGITITGITUFLOTYRIYEYYYYYYYGIRALAGITINSDIYYTTI 	2102 TCCGAGGCCCAGGAGACTCCAGACCACGCCATCTTCCGGTGGCCTTGCCATCTTCGCC

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                                                                                       US-10-642-946-3 (1-1158) x AAT97611
                                                                                                                                                                                                                                                                        This sequence represents a full-length nucleotide sequence that codes for compose E2A binding protein (E2A-BP), see AAWA5817). It was isolated using CS FARCE with primers designed from mouse AEBP CDNA. E2A-BP is expressed in the vascular smooth muscle cells; mRNA is preferentially expressed in the CS aorta. E2A-BP interacts with E2A proteins in vivo, binds to both E12 and E47 and inhibits binding of E47 homodimer to an E-box probe (see CS AAT97668). Human (see AAT97699-10) and rat (see AAT97612-13) E2A-BP sequences have also been isolated. E2A-BP nucleic acids may be used in gene therapy and antisense methods for treating vascular diseases such as arteriosclerosis, to produce transpenic or knock-out animals, as well as in methods of producing E2A-BP polypeptides that can be used therapeutically to promote vascular smooth muscle cell growth e.g. for the creating or to screen for modulator compounds useful e.g. for the treatment of arteriosclerosis and anglogenesis. The E2A-BP gene promoter can be used in gene therapy methods to direct vascular smooth muscle cell especific expression of the E2A-BP gene, antisense sequences or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding human and mouse E2A binding proteins - useful for inhibiting or stimulating growth of vascular smooth muscle cells, e.g. for wound healing or treatment of rheumatoid arthritis or retinopathic diabetes.
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                                                                                                                                                                                                                                     Sequence 3633
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   ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly
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978 CysAsnPheIleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsn	u 637	18 PheArgTy
2890 GAGGGCTACACCTCAAGTGCCAAGATCTGCAATGTGGACTACGATATTGGGGCCACTCAG	u 617     G 1869	598 Ly811eTyrAlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGl 
256 GluGlyTvrThrProSeralaIvsThrCygAgnValAspTvrAspTleGlyAlaThrGln	1 597 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	578 AsnGluGluCysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLes
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	1629	518 ArgPheIleArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluVal
	a 517   C 1569	498 HibGlyABRIValABpLyBABpThrProValLeuSerGluLeuProGluProValValAl.
April	e 497   C 1509	478 PheSerAsnAspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPh
	2 1449	458 IleThrGlnGlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGly
	1 457     C 1389	438 ABPAlaArgThrGlnTrpIleGluValAspThrArgArgThrThrArgPheThrGlyVa :::::::::
798 AgroluValSerGlualsoluGluThrProAgnHisalaTlePhoArgTrpLeuAlaIle	p 437     C 1329	418 AsnMetGlnThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAs;
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25-MAR-2003
23-SEP-1994
                                                                                                        The cDNA of mouse OSF-5 was isolated from a mouse osteoblastic cell line MC3T3-E1 cDNA library constructed by a combination of PCR and the subtraction cloning method, followed by cloning using the differential screening technique. OSF-5 is a bone-specific carboxypeptidase which acts as an adhesion molecule or growth factor; it takes part in osteogenesis at the site of bone induction. OSF-5 can be used to treat bone metabolic diseases, e.g. osteoporosis, Paget's disease, osteomalacia, hyperostosis or osteopetrosis. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 16-OCT-2003 to
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The invention relates to a gene expression profile comprising one or mor genes (AB234889-AB235692) and generated from a cell type. The cell type is a coronary artery endothelium, umbilical artery or vein endothelium, acrtic endothelium, dermal microvascular endothelium, pulmonary artery endothelium, myometrium microvascular endothelium, keratinocyte epithelium, bronchial epithelium, mammary epithelium, keratinocyte epithelium, renal cortical epithelium, renal proximal tubule epithelium, small cortical epithelium, umbilical artery smooth muscle, dermal fibroblast, pulmonary artery smooth muscle, dermal fibroblast, pulmonary artery smooth muscle, acrtic smooth muscle, mesangial cells, coronary artery smooth muscle, bronchial smooth muscle, uterine smooth muscle, lung fibroblast, bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
                                                                                                                                                                                                                                                        New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer
                                                                                                                                                                                                                          Disclosure; Page 487-489; 850pp; English
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GAGCCTCCTCCATGCTGCGCCACGGCCTGGGGGGCACAGCGCGGCTCAACATGCAGA

646

Db 2807 AGGCATTCCCCTTCACAACAGTAGAGACCTACAGTGAACTTTGGGGACTTC 2859
Search completed: September 30, 2006, 23:57:34
Job time : 1662 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

DEFINITION ACCESSION VERSION KEYWORDS RESULT 2 AX515275/c LOCUS REFERENCE AUTHORS TITLE RESULT 1
AR688470
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM 밁 Ś ORIGIN FEATURES Query Match Best Local Similarity Matches 28; Conserv ORGANISM JOURNAL source 54 AGCTGCTGCCTCACCTGCTTTTCCAAAACCCCACCCTGTAA 1 (bases 1 to 50)

Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N. Methods and compositions for diagnosing or me and chronic inflammatory diseases
Patent: US 695827-A 7899 14-JUN-2005;
Expression Diagnostics, Inc.; So. San Francis
Location/Qualifiers Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sequence 1473 from Patent AX515275 AX515275.1 GI:23562180 AR688470 Sequence 7899 from patent AR688470 AX515275 Unknown. Unknown. AR688470.1 Unclassified. AGCTGCTGCTTCTCTTTCAGTTGCAAATGCAAACCTGTTA 8.6%; ilarity 70.0%; Conservative /organism="unknown" /mol\_type="genomic DNA" GI:74470240 0; Score 20.8; DB 2; Pred. No. 3.7e+05; 0; Mismatches 12; 50 50 41 bp DNA WO02052044. bp DNA 6905827. San Francisco, 12; Length 93 Indels linear monitoring auto immune linear CA 50; PAT 05-OCT-2002 PAT 12-SEP-2005 0 Gaps 0,

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Sequence 3970 from Patent
AX517772
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                                                                                                 Homo sapiens (human)
                                                                                                                                                   Sequence 3127 from Patent Ax612102
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura,Y., Sekine,A., Iida,A. and Saito,S. Detection of genetic polymorphisms Patent: WO 02052044-A 3970 04-JUL-2002;
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                       AX612102.1 GI:28407531
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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          Patent: WO 02072882-A 3127 19-SEP-2002;
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WO02052044.
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Sequence 3128 from Patent WO02072882.
AX612103
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Sequence 3125 from Patent
AX612100
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Patent: WO 02072882-A 3128 19-SEP-2002;
OGHAM GmbH (DE)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                       OGHAM GmbH (DE)
                                                                                                                                                                        fominidae;
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Pred. No. 8.5e+05;
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Pred. No. 8.5e+05;
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PAT 12-SEP-2005

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AR017890
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                                                                     41 GCTCCACCTCCCAGCTGCTGCTCACCTGCTTTTCCAAACC 82
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AR017890
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Inouye,S. and Inouye,M.
Hybrid molecules
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Coronary chip
Patent: WO 02072882-A 3126 19-SEP-2002;
OGHAM GmbH (DE)
                                                                                                                                                                                                                                                              Unknown
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                                                 GGTAAAACCTCCCACCTGCGTGCGTTGGCACACC 43
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNJ
/db_xref="taxon:9606"
                                                                                                                                                     /organism="unknown"
/mol_type="unassigned DNA"
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Pred. No. 8.6e+05;
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Pred. No. 8.6e+05;
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AR096904/c
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1 (bases 1 to 50)

1 (bases 1 to 50)

Wohlgemuth, 7, Fry, K., Woodward, R. and Ly, N. Wethods and compositions for diagnosing or moniand chronic inflammatory diseases

Patent: US 6905827-A 1159 14-JUN-2005;

Expression Diagnostics, Inc.; So. San Francisci Location/Qualifiers
                                                                                                                                                                                                                          211 TGTATCAGATACCCAACTAAAACTGGATTCAC
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Sequence
AR096904
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Sequence
AR016521
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AR681730
Vaccines for treatment of lymphoma and leukemia Patent: US 5972334-A 35 26-OCT-1999; Location/Qualifiers
                                   1 (bases 1 to 39)
Denney, D.W. Jr.
                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 39)
Denney.D.W. Jr.
Gene amplification methods
Patent: US 5776746-A 35 07-JUL-1998;
                                                          Unclassified
                                                                       Unknown.
                                                                                   Unknown.
                                                                                                          AR096904.1
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Similarity 66.7%;
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                                                                                                                                                                                                                                                                                                                    organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
/mol_type="genomic
                                                                                                          GI:10009428
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Pred. No. 1.1e+06;
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Pred. No. 8.6e+05;
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AR031665
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BD136099/c
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GENITOPE CORP

OS Unidentified

PN JP 2002509426-A/29

PD 26-MAR-2002

PP 25-APR-1997 JP 199751

PR 01-MAY-1996 US 08,

DAN W DENNEY JR 08,

CC C12N15/86,C12N15/63,C

CC Strandedness: Single

CC Topology: Linear;

CC Vaccines for treatmen
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Vaccines for treatment of
BD136099
BD136099.1 GI:23231044
JP 2002509426-A/29.
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                                                                                                         AR031665
Sequence 25
AR031665
AR031665.1
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Houtz,R.L.
Cloning and developmental expression of pea
ribulose-1,5-bisphosphate carboxylase/oxygenase
epsilon N-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                        33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccines for treatment of lymphoma and leukemia Patent: JP 2002509426-A 29 26-MAR-2002;
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1 (bases 1 to 39)
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                                                                                                                                                                                                      TGAAACAGATACGAACCTAAACTTGGATCCAC
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                                               (bases 1 to 42)
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25-APR-1997 JP 1997539097
01-MAY-1996 US 08/644664,06-DEC-1996 US 08/761277 PI
9 DENNEY JR
C12N15/86,C12N15/63,C12N15/00,C12P19/24,A61K39/395,C07H21/04
Strandedness: Single;
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Vaccines for treatment of lymphoma
Location/Qualifiers
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                                                                                                                                25
                                                                                                                                                                                                                                                                                                            /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                         /organism='Unidentified'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
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Garner, H.R., Wren, J.D., Minna, J.D. ar Polymorphic repeats in human genes Patent: US 6472154-A 43 29-OCT-2002;

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ALIGNMENTS

FEATURES Source	COMMENT	TITLE JOURNAL	AUTHORS	PUBMED	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	VERSION	ACCESSION	DEFINITION	RESULT 1 ATH520369
plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).  Location/Qualifiers 1. 50 //organism="Arabidopsis thaliana" //mol_type="genomic DNA" //cultivar="Wassillewskija"	PCR was performed on DNA from transformants of Arabidopsis thaliana	Direct Submission Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue	Balzerque.S.	12446565 2 (hases 1 to 50)	of pre-insertion sites EMBO Rep. 3 (12), 1152-1157 (2002)	Lepiniec, L., Caboche, M. and Lecharny, A. T-DNA integration into the Arabidopsis genome depends on sequences	Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,	1	<pre>gukaryota; viridiplantae; Streptopnyta; Embryopnyta; Tracneopnyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids: eurosids II; Brassicales: Brassicaceae; Arabidonsis.</pre>	Arabidopsis thaliana	Arabidopsis thaliana (thale cress)	AJ520369.1 GI:26788605	027A07, genomic survey sequence. AJ520369	is thaliana T-DNA flanking sequence, left borde	ATH520160 50 hp DNA 11mear GSS 08-FEB-2006

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                                                                                                         DU532846
YHB292 BayGenomics Gene Trap
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T. Expressed genes in Ciona intestinalis Unpublished (2000)
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Ciona intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV960508 Nori Satoh unpublished cDNA library, cleavage stage embryo Ciona intestinalis cDNA clone cicllzn17 5', mRNA sequence.
                                                           DU532846.1 GI:77358565
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                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nori Satoh
Department of Zoology
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1 (bases 1 to 45)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mus musculus
                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 satoh@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="027A07"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="T-DNA flanking sequence
left border"
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole animal"
/dev_stage="cleaving embryo"
/clone_lib="Nori Satoh unpublished cDNA library, cleavage
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                                                                                                                                                                                                                                                                                                                                                                                                          clone="cicl12n17"
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Pred. No. 8.5e+05;
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Pred. No. 7
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                                                                                                         pGT0Lxf Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymenidae, Tetra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@Daygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KBY=YHB292
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Unpublished (2001)
Contact: BayGenomics
                                                                                                                                                                                                                                                                                                                                                                                          Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L. EST from Tetrahymea thermophila, strain CU428.1, growing cells Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM392535 42 bp mRNA linear EST 17-50071-2-10-A02.f.1 Chilcoat/Turkewitz cDNA (small fraction)
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BayGenomics.
                                                                                                                                                                                                                                                                    Tel: 773 702 4374 Fax: 773 702 3172
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                                                                                                                                                                                                                                              Email: apturkew@midway.uchicago
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            /organism="Tetrahymena thermophila"
/mol type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (small fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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/mol_type="mRNA"
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/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/note="Vector: pGT0Lxf"
                                                                                                                                                                                                     ocation/Qualifiers
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strain="129 ola"
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                                                                                                                                                             49 bp DNA linear 02F0151-13C2-B12 UniformMu MuTAIL Library Zea maye 02F0151-13C2-B12, genomic survey semience CZ550Aoo
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EST from Tetrahymena thermophila, strain CU428.1, growing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
1 (bases 1 to 49)
Latshaw, S., Tan, B-.C., Settles, A.M. and McCarty, D.R.
Sequence tagged transposon insertions from the Unifo
                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Clade; Panicoideae; Andropogoneae; Zea.
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetr
                                                                                                                          CZ550492.1 GI:66476962
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
Contact: Turkewitz AP
                                                                                             Zea maye
                                                                                                           Zea таув
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: apturkew@midway.uchicago
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BM393595.1 GI:18193648
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                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="mRNA"
|strain="CU428.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                             0,
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                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 2; 1
Pred. No. 1.1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 2;
Pred. No. 1.1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thermophila"
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   the UniformMu maize
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(large fraction)
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                                                                                                                                                                                    GSS 24-MAY-2005
genomic clone
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                                                              Tracheophyta;
aceae; PACCAD
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BH801643
LOCUS
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                                                                                                                                                                                                                                                                   COMMENT
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                             source
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JOURNAL
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                     Very probable ligation site of ends cut
Reverse complemented post-ligation seque
Plate: 1008118 row: 21
                                                                                                                                                                                                                                                           Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                             Stanford University
855 California Ave, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                           Maize genomic sequences 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH801643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
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Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
                                                                                                                                          Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH801643.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence flanking probable Mu insertion site in UniformMu line:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: drm@ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:4577"
/clone="02F0151-13C2-B12"
/clone="02F0151-13C2-B12"
/clone="02F0151-13C2-B12"
/clone="bullet "UniformMu MuTAIL Library"
/clone="bullet "UniformMu MuTAIL Flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo assymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."
/organism="Zea mays"
/mol_type="genomic_DNA"
/cultivar="mixed background
/db xref="taxon:457"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="UniformMu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
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pred. No. 1.1e+06;
0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                               found using
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                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               engineered
                                                  W23/A188/B73"
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                                                                                                                                                                                                                by single
ence from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACCAD
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28 CACCTGGCTGGGAGCTCCACCTCCCCAGCTGCCTGCCTCACC 68
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ORIGIN

Matches Query Match Best Local S

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Query Match
Best Local S
Matches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF297420
45 bp mRNA linear EST 14-30DGS--08-E12.b1 Rice leaf plasmid cDNA library I (30DGS) (sativa (japonica cultivar-group) cDNA clone 30DGS--08-E12,
  27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                 Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics and Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF297420.1 GI:33666453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="DH10B"
/clone lib="1008 - RescueMu Grid I"
/clone lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from /note="Organ: leaf; Vector: RescueMu (engineered from /note="Organ: leaf; Vector: RescueMu (engineered from /note 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmdb.iastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from last punches, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
  Conservative
                                                                                                                          /tisule_type="leaf"
/dev stage="30 days after germination"
/dev stage="30 days after germination"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/ob_xref="taxon:39947"
//db_xref="taxon:39947"
                                                                                                                                                                                                                                                                  clone="30DGS--08-E12"
                    7.7%;
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Pred. No. 1.3e+06;
0; Mismatches 12;
                    Score 18.6; DB 5;
Pred. No. 1.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                        bhnahm@bio.myongji.ac.kr
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GreenGene Biotech Inc.; Division
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                                         Length
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(30DGS) Oryza
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AUTHORS
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CR249499/c
LOCUS
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                         FEATURES
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                            TITLE
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RESULT 8 CF297420

DEFINITION

ACCESSION KEYWORDS VERSION

ORGANISM

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JOURNAL COMMENT

TITLE AUTHORS

REFERENCE

FEATURES

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Query Match
Best Local Similarity
                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG892412 46 bp DNA linear GSS 03-0150720-08D1-CO3 UniformMu MuTAIL Library Zea mays genomic 01S0720-08D1-CO3, genomic survey sequence.
CG892412
CG892412.1 GI:38646609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 50)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Rogers, J. and Bradley, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               v
                                                                                                                                                                                                                                                                                                                                                                                                       1 TTCTCCAGCACAGCACTGGATTTTGGTCACCTGGCTGGGAG 41
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                           Contact: Donald R. McCarry
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 46)
Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSD
                                                                                                        Sequence flanking probable Mu insertion site 01S0720-08, Primer set: D Class: transposon insertion site.
                                                                                                                                                                                                                                                                                                      Unpublished (2003)
                                                                                                                                                                                                                                                                                                                            population
                                                                                                                                                                            Email: drm@ufl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN350a08"
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="MHPN"
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Nishijima, I., Y
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yenomic clone
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AU105790
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KEYWORDS
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                                                                             Query Match
Best Local S
Matches 28
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PUBMED
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.

1 (bases 1 to 50)
Suzuki Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Suzuki Y., Taira, H., Tsunoda, T., Morishita, S., Okubo, K., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scampping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
6
                                                                                                                                                                                                                                                                                                                                           Email: ysuauki@hgc.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Virology
Institute of Medical Science, 1
4-6-1, Shirokanedai, Minatoku,
Tel: 81-3-5449-5343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU105790
AU105790.1 GI:13555311
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU105790 Sugano Homo sapiens HRC09728, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 63.6
28; Conservative
                       ACCTCTCACGTGGAGCTGAACAGAACGACCTGTTAAGCCCACCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCCTCCATTTCGTCGAATCACCTCTCTCTTGTCACAAACCAAA 3
NACTOGCGCTGCGGGATGAACCGAACGCCGGGTTAAGGCGCCCCG 49
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     81-3-5449-5416
                                                                                                                                                                              /organism="Homo Bapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="HRC09728"
/clone_lib="Sugano Homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="UniformMu MuTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
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/clone="0180720-08D1-C03"
                                                                                                                                                                                                                                                                                                          ocation/Qualifiers,
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                                                                         Score 18.4; DB 1;
Pred. No. 1.7e+06;
0; Mismatches 16;
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Pred. No. 1.7e+06;
0; Mismatches 16;
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, Tokyo 108-8639, Japan
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                                                                                                                 Length 50;
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KEYWORDS
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AI719194/c
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l (bases 1 to 44)
Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
Hominidae; Homo.

1 (bases 1 to 46)

1 (bases 1 to 46)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Hillier,L., Allen,M., Bowles,L., Lennon,G., Marra,M., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. washU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                        AI719194 46 bp mRNA linear EST 10-JUN-1999 at06h08.x1 Barstead aorta HPLRB6 Homo sapiens CDNA clone IMAGE:2354367 3' similar to TR:004154 Q04154 SALIVARY PROLINE-RICH PROTEIN RP15 PRECURSOR. ;contains MER22.b2 TAR1 repetitive element
                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                           Homo sapiens
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AI719194.1
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Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=P063E09' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
'Inhouse Sequence Identifier: 24822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German Genetrap Consortium (GGTC)
Email: info@genetrap.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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/cell_line="ES cells [C57BL/6J x 12986/SvEvTac] F1"
/clone_lib="GY09C05"
/note="Vector: rF1pROSAbetageo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="p063E09"
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Pred. No. 1.9e
0; Mismatches
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clone P063E09,
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                                                                                         Jost, S.,
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CF661282
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                                                                                                                                                                                                                                                       1 (bases 1 to 49)
Gracey,A.Y., Fraser,E.J., Li,W., Fang,Y., Taylor,R.R., Rogers,J., Brass,A. and Cossins,A.R.
Coping with cold: An integrative, multitissue analysis of the transcriptome of a poikilothermic vertebrate
Proc. Natl. Acad. Sci. U.S.A. 101 (48), 16970-16975 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CcLM09a34i20f1 Carp muscle
34i20 5', mRNA sequence.
CF661282
CF661282.2 GI:50743501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.1lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40Up from Gibco
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Wilson RK
                                                              School of Biological Sciences, The Biosciences Building, Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
                                                                                                                                    On Oct 7, 2003 this sequence version replaced gi:37558440 Contact: Andrew R. Cossins Laboratory for Environmental Gene Regulation University of Liverpool
                                                                                                                                                                                                                                                                                                                                                                                                 Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyprinus carpio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
                    Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyprinus carpio (common carp)
Vector has been trimmed from this EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 66.7
26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCGGATCGAAC 3' and 5' GTTGGATCGG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/lab_host="DH10B (phage resistant)"
/clone_lib="Barstead aorta HPLRB6"
/note="Organ: aorta; Vector: pT7T3D-PacI; Site_1: EcoRI;
Site_2: NotI; 1st strand cDNA was primed with a Not I -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
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e library
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RESULT 15
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Bakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)

11375929
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AU102840 Sugano Homo sapiens
CAS09777, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                            Email: ysuzuki@hgc.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200
                                                                                                                                                                                                                                                                                                                                                                Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                          Tel: 81-3-5449-5343
Fax: 81-3-5449-5416
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU102840.1 GI:13552361
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/tissue_type="Muscle"
/dev_stage="Adult"
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challenged animals"
                                                                         /organism="Homo sapiens"
/mol type="mRNA"
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/mol_type="mRNA"
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Post-processing: Minimum Match
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3: geneseqn200
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geneseqn2003ds:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Adu25275 Retroelem Adu22742 Human tra	Aav33949 Gibbon in	Adu25276 Retroelem Adu22743 Human tra	Abz48256 Human org	Abz46086 Human org	Abz79597 Quinoprot		Adu22741 Human tra	Adu25263 Retroelem	Adu25274 Retroelem	Adu22045 Human tra	Adu24578 Retroelem	Adu22766 Human tra	Adu25299 Retroelem	Adu22514 Human tra	Adu25047 Retroelem	Description	

The invention relates to a method of assigning an expression pattern of transposable elements to the level of developmental potential of a cell

Disclosure; SEQ ID NO 518; 50pp; English

Assigning an expression pattern of transposable elements to the level of developmental potential of a cell comprises determining expression of one or more families of transposable elements, and assigning the expression pattern.

WPI; 2004-804756/79.

Mcdonald JF;

29-APR-2003; 2003US-0466801P.

(UYGE-) UNIV GEORGIA RES FOUND INC.

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## ALIGNMENTS

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RESULT 1
ADU25047
Expression pattern; transposable element; developmental potential; stem cell; cellular differentiation induction factor; methylation pattern; chromatin status pattern; endogenous retrovirus; ERV; short interspersed nuclear element; SINE;
                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                  29-APR-2004; 2004WO-US013667
                                                                                                                                                                                    11-NOV-2004.
                                                                                                                                                                                                                                                                                                 Retroelement consensus sequence identifier oligonucleotide #517.
                                                                                                                                                                                                                                                                                                                   27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                        ADU25047 standard; DNA; 50 BP
                                                                                                                                                                                                      WO2004097005-A2
                                                                                                                                                                                                                                                                                                                                      ADU25047;
                                                                                                                                                                                                                                          long interspersed nuclear element; LINE; retroelement; ss
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RESULT 2
ADU22514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC The method comprises determining the expression of one or more families of transposable elements, and assigning the expression pattern obtained CC to the level of developmental potential of a cell. Also disclosed are a CC method of identifying a cellular differentiation induction factor, a CC method of identifying a factor that increases the developmental potential of a stem cell, a cell, a method of assigning a methylation pattern of transposable celements to the level of developmental potential of a cell, and a method of assigning a methylation pattern of transposable clements to the level of developmental potential of a cell, and a method of assigning a transposable celements to the level of developmental potential of a cell, and a method of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem cell, or a differentiated cell. The expression pattern is determined by microarray analysis. One or more of the families of transposable elements cell, or DNA element families. One or more of the families of compositing of the transposable elements (SINES) and a family of long interspersed nuclear elements (SINES) and a family of long interspersed nuclear elements cell assaying for the mRNA transcribed from the genes or proteins translated from an mRNA transcribed from the genes or proteins translated from an mRNA transcribed from the genes or proteins translated cell monitored by enzymatic means, microarray analysis, or methylation-genes in monitored by enzymatic means, microarray analysis, or methylation-genes in pattern of transposable elements to the level of developmental contential of a cell. This sequence represents an oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human transposable element representative sequence, SEQ ID 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 50 BP; 10 A; 12 C; 12 G; 15 T; 0 U; 1 Other;
Determining expression, methylation or chromatin status pattern of
                                                                                                                                                                                                                                                                                                                            29-APR-2004; 2004WO-US013522
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004096021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADU22514 standard;
                                                                    WPI; 2004-804580/79
                                                                                                                                                                                                                                                               29-APR-2003; 2003US-0466798P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      snort
                                                                                                                                                                                              (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dentifier of a retroelement consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interspersed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .ong interspersed nuclear element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIGAGITCACGIGAGAGCIGGITGITIGAAAGAGCCIGGCCCCCCTCIC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTAGTTCACGCGAGATCTGGTTGTTTAAAAGAGTNTGGCACCTCCCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transposable element; DNA methylation; chromatin; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nuclear element; HERV; human endogenous retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.8%;
79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32.6;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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29-APR-2003; 2003US-0466801P. 29-APR-2004; 2004WO-US013667.

(UYGE-) UNIV

GEORGIA RES FOUND INC

2004-804756/79

Assigning an expression pattern of transposable elements to the level on developmental potential of a cell comprises determining expression of or more families of transposable elements, and assigning the expression

pattern.

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cc sample comprises determining expression, methylation or chromatin status of one or more families of transposable elements. Also included are a cc method of assigning an expression pattern of transposable elements to a ctype of cancerous cell in a sample, a method of diagnosing cancer, a cc method of determining the effectiveness of an anti-cancer therapeutic in cc a subject, a method of assigning a methylation pattern of one or more families of transposable elements to a type of cancerous cell in a sample can determining an expression, methylation or chromatin status pattern of transposable elements to a type of cancerous cell in a sample. The method is useful in cc determining an expression, methylation or chromatin status pattern of one or more families of transposable elements (e.g. LINE, long interspersed cc endogenous retrovirus) in a sample for diagnosing cancer or determining the effectiveness of an anti-cancer therapeutic. The presentations of the transposable element, used in a microarray to study the expression, methylation or chromatin status pattern of the transposable element, used in a microarray to study the expression, methylation or chromatin status cc pattern of the transposable elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        families of transposable elements in a sample e.g. for diagnosing cancer, comprises determining the expression, methylation or chromatin status of the elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to determining expression, methylation or status pattern of one or more families of transposable elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO 518; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromatin
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                                         Matches
                                                 Query Match
Best Local (
            61 GTGAGTTCACGTGAGAGCCTGGTTGTTTGAAAAGAGCCTGGCCCCCTCTC
                                         38;
                                                   Similarity
GTTAGTTCACGCGAGATCTGGTTGTTTAAAAGAGTNTGGCACCTCCCC
                                         Conservative
                                                  13.8%;
79.2%;
                                         0
                                                   Score 32.6;
Pred. No. 1.
                                          Mismatches
                                                              BB
                                         10;
                                                              Length
                                         Indels
                                         0
                                         Gaps
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0

Sequence

50 BP; 10 A; 12 C;

12 G; 15 T; 0 U; 1 Other;

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methylation pattern; chromatin status pattern; endogenous retrovirus; ERV; short interspersed nuclear element; SINE;
                                                                                                                                                                                                                                Expression pattern; transposable element; developmental potential; stem cell; cellular differentiation induction factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADU25299 standard;
                                                                                                                                                                                                                                                                                                             Retroelement consensus sequence identifier oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                       27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                        ADU25299;
11-NOV-2004
                                                 WO2004097005-A2
                                                                                                                                                         interspersed nuclear element; LINE;
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
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                                                                                                                                                            retroelement; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC The invention relates to a method of assigning an expression pattern of CC transposable elements to the level of developmental potential of a cell. CC of transposable elements, and assigning the expression of one or more families CC of transposable elements, and assigning the expression pattern obtained CC method of determining the developmental potential of a stem cell, a CC method of identifying a cellular differentiation induction factor, a CC method of identifying a factor that increases the developmental potential of a stem cell, a method of assigning a methylation pattern of transposable CC elements to the level of developmental potential of a cell, and a method CC of assigning a chromatin status pattern of transposable elements to the level of developmental potential of a cell. In assigning an expression CC pattern of transposable elements to the level of developmental potential of a cell, and a method CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem CC cell, or a differentiated cell. The expression pattern is determined by CC microarray analysis. One or more of the families of transposable elements (CC language) and a family of long interspersed nuclear cell cendents (SINES) and a family of long interspersed nuclear elements (SINES) and a family of long interspersed nuclear elements (CC cendents (SINES) and a family of short interspersed nuclear elements (SINES) and a family of seven the genes or proteins translated CC from an mRNA transcribed from the genes or proteins translated CC from an mRNA transcribed from the genes or proteins translated CC from an mRNA transcribed from the genes or proteins translated CC from an mRNA transcribed from the genes or proteins translated CC from an mRNA transcribed from the genes or proteins translated CC from an mRNA transcribed from the genes or proteins translated CC from 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from an mRNA transcribed from the genes. The expression of two or more families of transposable elements is determined and used to form the pattern of expression. The methylation of the transposable element gene is monitored by enzymatic means, microarray analysis, or methylation-specific PCR. The methylation pattern is determined by microarray analysis. The methods of the invention are useful for assigning an expression pattern of transposable elements to the level of development potential of a cell. This sequence represents an oligonucleotide
                                                                                                                                                                                                                                                                                                                                      Human; 88; transposable element; DNA methylation; LINE; long interspersed nuclear element; SINE;
                                                                                                                                                                                                                                                                                                                                                                                                            Human transposable element representative sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50 BP; 5 A; 15 C; 10 G; 20 T; 0 U; 0 Other;
                                                                                                                                                             11-NOV-2004
                                                                                                                                                                                                        WO2004096021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADU22766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADU22766 standard; DNA; 50
                                                              29-APR-2003; 2003US-0466798P
                                                                                                            29-APR-2004; 2004WO-US013522
                                                                                                                                                                                                                                                                                                                        Bhort
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                   (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 CCTGCTCCCCCTTCTCCTGCCATGATTTTAAGATTCCAGGGACTT 186
                                                                                                                                                                                                                                                                                                                   interspersed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a retroelement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                        nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                   element; HERV; human endogenous retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; I
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                 chromatin; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                 P
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Sequence 50 BP; 5 A; 15 C; 10

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20 T; 0 U; 0 Other;

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method of assigning an expression pattern of transposable elements to a crown of transposable elements to a comment of transposable elements to a comment of transposable elements to a comment of transposable elements of an anti-cancer therapeutic in a subject, a method of assigning a methylation pattern of one or more comment of transposable elements to a type of cancerous cell in a sample and a method of assigning a chromatin status pattern of transposable elements to a type of cancerous cell in a sample. The method is useful in determining an expression, methylation or chromatin status pattern of one or more families of transposable elements (e.g. LINE, long interspersed nuclear element, SINE, short interspersed nuclear element, or the elements of the effectiveness of an anti-cancer thrasposable element, or the effectiveness of an anti-cancer thrasposable element, or the present sequence is a representative sequence for a human transposable element, used in a committee of the transposable elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to determining expression, methylation or chromating status pattern of one or more families of transposable elements in a sample comprises determining expression, methylation or chromating status of one or more families of transposable elements. Also included are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining expression, methylation or chromatin status pattern of families of transposable elements in a sample e.g. for diagnosing cancer comprises determining the expression, methylation or chromatin status of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 770; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-804580/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcdonald JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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RESULT 5
ADU24578
ADU24578
ADU24578
AC ADU2
AC ADU2
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AC Retx
AX Expr
KW Expr
KW Exten
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression pattern; transposable element; developmental potential; stem cell; cellular differentiation induction factor; methylation pattern; chromatin status pattern; endogenous retrovirus; ERV; short interspersed nuclear element; SINE; long interspersed nuclear element; LINE; retroelement; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retroelement consensus sequence identifier oligonucleotide #48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADU24578 standard; DNA; 50
                                                                                                                                                                                                                                         29-APR-2003; 2003US-0466801P
                                                                                                                                                                                                                                                                                                                        29-APR-2004; 2004WO-US013667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004097005-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 CCTGCTCCCCCTTCTCTCCCATGATTTTAAGATTCCAGGGACTT 186
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                                                                                                                                                              VIND
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                                                                                                                                                              GEORGIA RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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WPI; 2004-804756/79

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CT The method comprises determining the expression of one or more families of transposable elements, and assigning the expression pattern obtained to the level of developmental potential of a cell. Also disclosed are a care a method of determining the developmental potential of a stem cell, a care a ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                           Human; 88; transposable element; DNA methylation; chromatin; cancer;
LINE; long interspersed nuclear element; SINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assigning an expression pattern of transposable elements to the level of developmental potential of a cell comprises determining expression of one or more families of transposable elements, and assigning the expression
                                                                                                                                  Homo sapiens.
                                                                                                                                                                                        LINE; long interspersed nuclear element; short interspersed nuclear element; HERV;
                                                                                                                                                                                                                                                                                          Human transposable element representative sequence,
                                                                                                                                                                                                                                                                                                                                         27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                      ADU22045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transposable elements
29-APR-2004; 2004WO-US013522.
                                              11-NOV-2004
                                                                                        WO2004096021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                ADU22045 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identifier of a retroelement consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               otential of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAGTGCCATCCCCTTGGTGATGAGTGAGTTCACGTGAGAGCTGG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGTGCTGTCCTCGTGATAGTGAGTGAGTTCTCGTGAGATCTGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 6 A; 11 C; 16 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 48; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a cell. This sequence represents an oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to a method of assigning an expression pattern to the level of developmental potential of a co
                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 50
                                                                                                                                                                                                      human endogenous retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potential of a cell
                                                                                                                                                                                                                                                                                             SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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The invention relates to determining expression, methylation or chromatin CC status pattern of one or more families of transposable elements in a CC sample comprises determining expression, methylation or chromatin status of one or more families of transposable elements. Also included are a CC type of cancerous cell in a sample, a method of diagnosing cancer, a CC method of determining the effectiveness of an anti-cancer therapeutic in a subject, a method of assigning a methylation pattern of one or more CC families of transposable elements to a type of cancerous cell in a sample canded and a method of assigning a chromatin status pattern of the sample CC and a method of assigning a chromatin status pattern of transposable elements to a type of cancerous cell in a sample. The method is useful in CC determining an expression, methylation or chromatin status pattern of one or more families of transposable elements (e.g. LINE, long interspersed CC unclear element, SINE, short interspersed nuclear element, or HERV, human CC endogenous retrovirus) in a sample for diagnosing cancer or determining cancerous sequence is a representative sequence for a human transposable element, used in a microarray to study the expression, methylation or chromatin status
Sequence
                                                pattern of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 48; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining expression, methylation or chromatin status pattern of families of transposable elements in a sample e.g. for diagnosing cancer, comprises determining the expression, methylation or chromatin status of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-804580/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-2003; 2003US-0466798P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYGE-) UNIV GEORGIA RES FOUND INC
50 BP; 6 A; 11 C; 16 G; 17 T; 0 U; 0 Other;
                                                the transposable elements.
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밁
                                   Matches
                                          Query Match
Best Local
                                          Local Similarity
                 37
                                   35;
σ
          TTAGTGCCATCCCCTTGGTGATGAGTGAGTTCACGTGAGAGCTGG
TTGGTGCTGTCGTGATAGTGAGTGAGTTCTCGTGAGATCTGG
                                   Conservative
                                          12.3%;
                                   0
                                           Score 29; DB
Pred. No. 23;
                                   Mismatches
                                                     DB
                                   10;
                                                   Length 50;
                                   Indels
50
                 81
                                   0
                                  Gaps
                                   0
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ADU25274
ADU25274
ID ADU25274
ID ADU2
XX ADU2
XX ADU2
XX Expr
XX Iong

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methylation pattern; chromatin status pattern; ERV; short interspersed nuclear element; SINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression pattern; transposable element; developmental potential; stem cell; cellular differentiation induction factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004097005-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retroelement consensus sequence identifier oligonucleotide #744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         long interspersed nuclear element; LINE; retroelement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromatin status pattern; endogenous
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29-APR-2003; 2003US-0466801P 29-APR-2004; 2004WO-US013667

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RESULT 8
ADU25263
SXEXEXEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of transposable elements, and assigning the expression pattern obtained to the level of developmental potential of a cell. Also disclosed are a method of determining the developmental potential of a stem cell, a method of identifying a cellular differentiation induction factor, a method of identifying a factor that increases the developmental potential of a cell, a method of assigning a methylation pattern of transposable elements to the level of developmental potential of a cell, and a method of assigning a methylation pattern of transposable clements of assigning and a method of assigning a chromatin status pattern of transposable elements to the level of developmental potential of a cell, and a method of assigning a chromatin status pattern of transposable elements to the level of developmental potential of a cell, or a differentiated cell. The expression pattern is determined by microarray analysis. One or more of the families of transposable elements families of retroelement families, or DNA element families. One or more of the families of retroelements is selected from the group consisting of elements (SINES) and a family of long interspersed nuclear elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assaying for the mRNA transcribed from the genes or proteins translated from an mRNA transcribed from the genes. The expression of two or more families of transposable elements is determined and used to form the pattern of expression. The methylation of the transposable element geneis monitored by enzymatic means, microarray analysis, or methylation-
                                                         Expression pattern; transposable element; developmental potential; stem cell; cellular differentiation induction factor; methylation pattern; chromatin status pattern; endogenous retrovir ERV; short interspersed nuclear element; SINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific PCR. The methylation pattern is determined by microarray analysis. The methods of the invention are useful for assigning an expression pattern of transposable elements to the level of developmental potential of a cell. This sequence represents an oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assigning an expression pattern of transposable elements to the level of developmental potential of a cell comprises determining expression of or more families of transposable elements, and assigning the expression
Synthetic
                                                                                                                                                                                                     27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50 BP; 10 A; 11 C; 12 G; 17 T; 0 U; 0 Other;
                                                                                                                                                        Retroelement consensus sequence identifier oligonucleotide #733.
                                                                                                                                                                                                                                                                                    ADU25263 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transposable elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pattern
                                    long interspersed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identifier of a retroelement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYGE-) UNIV GEORGIA RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to a method of assigning an expression parapposable elements to the level of developmental potential a method comprises determining the expression of one or more
                                                                                                                                                                                                                                                                                                                                                                                                                149 CTTCTCCTTCTGCCATGATTTTAAGATTC 177
                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         CTTCCCCTTCCGCCATGATTGTAAGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO
                                                                                                                                                                                                     (first entry)
                                      nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.6%;
                                                     chromatin status pattern; endogenous retrovirus; sed nuclear element; SINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOUND INC
                                    element; LINE; retroelement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22.6;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .9e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 9
ADU22741
ID ADU2
XX
AC ADU2
XX
AC ADU2
XX
AC ADU2
XX
XX
XX

ADU22741 standard; DNA; 50

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27-JAN-2005 ADU22741;

(first entry)

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Gaps

0

genes

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S
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Best Local :
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of assigning a chromatin status pattern of transposable elements to the level of developmental potential of a cell. In assigning an expression pattern of transposable elements to the level of developmental potential of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem cell, or a differentiated cell. The expression pattern is determined by microarray analysis. One or more of the families of transposable elements are retroelement families, or DNA element families. One or more of the families of retroelements is selected from the group consisting of
                                                                                                                                                                                                                                                                          is monitored by enzymatic means, microarray analysis, or methylation-
specific PCR. The methylation pattern is determined by microarray
analysis. The methods of the invention are useful for assigning an
expression pattern of transposable elements to the level of developmental
potential of a cell. This sequence represents an oligonucleotide
identifier of a retroelement consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endogenous retroviruses (ERVs), a family of short interspersed nuclear elements (SINES) and a family of long interspersed nuclear elements (LINES). The expression of the transposable elements is measured by assaying for the mRNA transcribed from the genes or proteins translated from an mRNA transcribed from the genes. The expression of two or more families of transposable elements is determined and used to form the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of transposable elements, and assigning the expression pattern obtained to the level of developmental potential of a cell. Also disclosed are a method of determining the developmental potential of a stem cell, a method of identifying a cellular differentiation induction factor, a method of identifying a factor that increases the developmental potential of a cell, a method of assigning a methylation pattern of transposable elements to the level of developmental potential of a cell, and a method of second control of the level of developmental potential of a cell, and a method of second control of the level of developmental potential of a cell, and a method of second control of the level of developmental potential of a cell, and a method of second control of the level of developmental potential of a cell, and a method of second control of the level of developmental potential of a cell, and a method of second control of the level of developmental potential of a cell, and a method of second control of the level of developmental potential of a cell, and a method of second control of the level of developmental potential of a cell, and a method of second control of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of a cell of the level of developmental potential of the level of th
                                                                                                                                                                                                            Sequence 50 BP; 14 A; 13 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assigning an expression pattern of transposable elements to the level o developmental potential of a cell comprises determining expression of or more families of transposable elements, and assigning the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of assigning an expression transposable elements to the level of developmental potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pattern.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The method comprises determining the expression of one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 734; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-804756/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-APR-2004; 2004WO-US013667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pattern of expression. The methylation of the transposable element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-2003; 2003US-0466801P
   197 AAATGCTAACGCCATGCTTCTTGTTCTGTCTGCAAAACT
                                                                       28;
                                                                                                        Similarity
                                                                       Conservative
                                                                                                    9.6%;
                                                                    1;
                                                                                                                                                                                                            10 G;
                                                                                                    Score
Pred.
                                                                       Mismatches
                                                                                                                                                                                                         12 T; 0 U; 1 Other;
                                                                                                    22.6; DB 1
No. 2.9e+03
                                                                                                                                        DB 13;
                                                                    10;
235
                                                                                                                                     Length
                                                                    Indels
                                                                                                                                            50,
                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pattern of
l of a cell
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cell.

one

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RESULT 10
ADU22730
ID ADU22
XX
AC ADU22
XX
DT 27-JA
XX
DE Humar
XW Humar
KW LINE;
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                                                                                                                                                                                                                                                                                    Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to determining expression, methylation or chromatin CC status pattern of one or more families of transposable elements in a CC sample comprises determining expression, methylation or chromatin status of one or more families of transposable elements. Also included are a CC method of assigning an expression pattern of transposable elements to a CC method of determining the effectiveness of an anti-cancer therapeutic in CC method of determining the effectiveness of an anti-cancer therapeutic in CC dements to a method of assigning a methylation pattern of one or more CC families of transposable elements to a type of cancerous cell in a sample CC and a method of assigning a chromatin status pattern of transposable elements to a type of cancerous cell in a sample. The method is useful in CC determining an expression, methylation or chromatin status pattern of one or more families of transposable elements (e.g. LINE, long interspersed CC nuclear element, SINE, short interspersed nuclear element, or HERV, human CC endogenous retrovirus) in a sample for diagnosing cancer or determining the effectiveness of an anti-cancer therapeutic. The present sequence is a representative sequence for a human transposable element, used in a microarray to study the expression, methylation or chromatin status
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining expression, methylation or chromatin status pattern of families of transposable elements in a sample e.g. for diagnosing can comprises determining the expression, methylation or chromatin status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human transposable element representative sequence, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-804580/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcdonald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-2004; 2004WO-US013522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004096021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
 Human; ss;
LINE; long
                                                      Human transposable element representative sequence, SEQ ID 734.
                                                                                                                                                                                                                                                                                                                                                                                                                                    microarray
pattern of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 745; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-APR-2003; 2003US-0466798P
                                                                                         27-JAN-2005
                                                                                                                             ADU22730
                                                                                                                                                                ADU22730 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; transposable element; DNA methylation; chromatin; cancer; long interspersed nuclear element; SINE; interspersed nuclear element; HERV; human endogenous retroviru
                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                        CTTCCCCTTCCGCCATGATTGTAAGTTTC 50
                                                                                                                                                                                                                                                                                        CTTCTCCTTCTGCCATGATTTTAAGATTC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                      the
 transposable element; DNA methylation; chromatin; cancer; interspersed nuclear element; SINE;
                                                                                                                                                                                                                                                                                                                                                                                                   BP; 10
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    transposable elements.
                                                                                                                                                                                                                                                                                                                                                                                                   A; 11 C; 12 G;
                                                                                                                                                                                                                                                                                                                                             9.6%;
                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                              Score 22.6;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   17 T;
                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                .9e+03;
                                                                                                                                                                                                                                                                                                                                                               DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human endogenous retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                     0 Other;
                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 11
ABZ79597/c
ID ABZ795
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                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to determining expression, methylation or chromatin CC status pattern of one or more families of transposable elements in a CC sample comprises determining expression, methylation or chromatin status of one or more families of transposable elements. Also included are a CC method of assigning an expression pattern of transposable elements to a CC method of determining the effectiveness of an anti-cancer therapeutic in CC method of determining the effectiveness of an anti-cancer therapeutic in CC determining the elements to a type of cancerous cell in a sample of an ambject, a method of assigning a methylation pattern of transposable elements to a type of cancerous cell in a sample of and a method of assigning a chromatin status pattern of transposable of transposable elements (e.g. LINE, long interspersed cor more families of transposable elements (e.g. LINE, long interspersed cor more families of transposable elements (e.g. LINE, long interspersed cor endogenous retrovirus) in a sample for diagnosing cancer or determining cancerous retrovirus) in a sample for diagnosing cancer or determining cancerous sequence is a representative sequence for a human transposable element, used in a microarray to study the expression, methylation or chromatin status
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining expression, methylation or chromatin status pattern of families of transposable elements in a sample e.g. for diagnosing can comprises determining the expression, methylation or chromatin status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  short interspersed nuclear element; HERV; human endogenous retrovirus;
                                                               Quinoprotein dehydrogenase; 12.10; enzyme; malignant tumour; haemopathy; Human Immunodeficiency virus; HIV; immunological disease; inflammation;
                                                                                                                                                                                     ABZ79597;
                                                                                                                                                                                                                     ABZ79597 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 734; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-804580/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcdonald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-2004; 2004WO-US013522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                Quinoprotein dehydrogenase 12.10 related probe #SEQ
                                                                                                                                                    27-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYGE-) UNIV GEORGIA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                          197
                                                                                                                                                                                                                                                                                                        щ
                                                                                                                                                                                                                                                                                                                               AAATGCTAACGCCATGCTTCTTGTTCTGTCTGCAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                          AGATGCTCGCACCATGCTTTTTGTCCAGCCAGCAGAAYT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the transposable elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                           B₽;
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003US-0466798P
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                     DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                         71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            13 C;
                                                                                                                                                                                                                                                                                                                                                                                                           9.6%;
                                                                                                                                                                                                                                                                                                                                                                         ۲,
                                                                                                                                                                                                                                                                                                                                                                        Score 22.6; DI
Pred. No. 2.9e-
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            10 G; 12 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                             .9e+03
                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                    IJ
                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                             50;
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer,
                                                                                                                                                                                                                                                                                                                                                                           0
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Unidentified

probe; ss.

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RESULT 12
ABZ46086
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention discloses a polypeptide for a quinoprotein dehydrogenase 12.10, the polypucheotide for coding the polypeptide, and a method for producing this polypeptide using DNA recombination technology. Also disclosed is a method for curing several diseases, such as malignant tumour, haemopathy, Human Immunodeficiency virus (HIV) infection, immunological disease and various inflammations. The invention also discloses the antagonist for resisting this polypeptide, and its therapeutic action. The current sequence represents a quinoprotein dehydrogenes 13 for other products are presents a quinoprotein dehydrogenes.
                                                                                                                                                                                                                                                         Human; drug metabolising enzyme; gene; drug metabolism; chromosome polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP;
                        27-DEC-2000; 2000JP-00399443
02-MAY-2001; 2001JP-00135256
27-AUG-2001; 2001JP-00256862
                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 41
                                                                                                                                  WO200252044-A2
                                                                                                                                                                                          variation
                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                          26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                      ABZ46086
                                                                                                                                                                                                                                                                                                                                                                                                                ABZ46086 standard; DNA; 41 BP
(RIKE ) RIKEN
                                                                             27-DEC-2001; 2001WO-JP011592
                                                                                                           04-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dehydrogenase 12.10 related probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-APR-2001; 2001CN-00105895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-2001; 2001CN-00105895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide-quinoprotein dehydrogenase-12.10 and polynucleotide for oding this polypeptide.
                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                              organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTACACCGGCTTCCCCTTTGCCTTCTGCCA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGACACCTGCTCCCCCTTCTCCTTCTGCCA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                              anion
                                                                                                                                                                          Location/Qualifiers replace(21,A) /*tag= a
                                                                                                                                                        /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 7 C; 18 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (disclosure); 30pp; Chinese.
                                                                                                                                                                                                                                                                                                                             transporter OATP2 gene polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22.4;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
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و
                                                                                                                                                                                                                                                         polymorphism; SNP; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 41;
                                                                                                                                                                                                                                                                                                                             site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                   12;
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RESULT 13
ABZ48256
ID ABZ48

standard;

DNA;

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N

141 TGCTCCCCCTTCTCCTGCCATGATTTTAAGATTCC 178

TGCTCTTCCTTCATCTTCCGCCATGATTGTGAGGCCCCC

Matches Query Match

28;

Local

Similarity

9.3%;

Score 22; DB Pred. No. 4.3e 0; Mismatches

DB 6; .3e+03; 10;

Length 41; Indels

o ;•

Gaps

0

SXEXEXEXEXEX SXFX

26-JUN-2003 ABZ48256; ABZ48256

(first

entry)

Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site; drug evaluation; drug screening; genot genetic profiling; therapeutic customisation; adverse reclinical trial; drug approval; single nucleotide polymor

ug evaluation; drug screening; genotyping; herapeutic customisation; adverse reaction; approval; single nucleotide polymorphism;

chromosome 12;

SNP;

ab

Human organic anion transporter OATP2 gene polymorphic site,

Homo sapiens

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CC one polymorphism is such drug metabolising enzyme-encoding genes. The CP polymorphism have identified in a nucleic acid sample using probes or CP primers specific for a sequence selected from ABZ43217-ABZ50887 using a CC variety of detection assays, including hybridisation assays, nucleic acid convariety of detection assays, including hybridisation assays, nucleic acid convariety of detection assays, including hybridisation assays, nucleic acid convariety of detection assays, nucleic acid convariety of detection assays, nucleic acid convariety of surface acid convariety of activations and particularly that relating to single nucleotide convariety of activations and human diseases, conditions, and responses to converge that cause or exacerbate certain diseases, conditions, and responses to that cause or exacerbate certain diseases, conditions, and responses to that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations come are peating sequences. The detection and analysis of polymorphisms converge therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. CC methods of the invention are also useful in the drug discovery and the convergence of their genetic profiles individual be selected for capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more capacitate patient populations. The methods, data and compositions of the inventions of the profile of the patients of the patient of the patients of the patient of the patients of the patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying individuals having a polymorphism, useful for determining effectiveness or side effect of a drug or treatment protocol, comprise detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.
Sequence 41 BP; 4 A; 16 C; 7 G; 14 T; 0
                                                                                          the invention may therefore lead to a an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention related methods and compositions for identifying individuals who have at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Page 112; 2785pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-583571/62.
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                                                         a patient needs to take before finding an effective therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sekine A,
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U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates
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Key

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CC evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphism (SNPB), may be used in studying the relationship between CC polymorphisms (SNPB), may be used in studying the relationship between CC that cause or exacerbate certain diseases, conditions, and responses to that cause or exacerbate certain diseases. SNPB are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations of in genes encoding drug metabolising enzymes allows the customisation of CC drug therapeutic effect for a particular patients. This would not only take the genetic profile of individual patients. CC This would not only take the genetic profile of individual patients. CC reduce the likelihood of adverse reactions, thereby increasing safety. CC reduce the likelihood of adverse reactions, thereby increasing safety. CC reduce the likelihood of adverse reactions, thereby increasing safety. CC clinical trials only if their genetic profiles indicate that they are CC capable of responding to a particular drug ording to a particular drug of drug class, and previously cfailed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a na increase in the range of cc possible drug targets and decreases in the number of adverse drug class, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy xxx
                                                                                                                                                      Matches
                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphism may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-DEC-2000; 2000JP-00399443
02-MAY-2001; 2001JP-00135256
27-AUG-2001; 2001JP-00256862
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                                                                                                                                                                                                                                                                                                             Sequence 41 BP; 4 A; 16 C; 7 G; 14
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                                                                             141
N
                                                                                                                                                                                           Similarity
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                                                                         TGCTCCCCCTTCTCCTTCTGCCATGATTTTAAGATTCC 178
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                                                                                                                                                                                       9.38;
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                                                                                                                                                  Score 22; DB
Pred. No. 4.3e
0; Mismatches
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4.3e+03;
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Sequence 50 BP; 13 A; 15 C; 9 G;

13 T; 0 U; 0 Other;

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RESULT 14
ADU25276
ID 25276
AC ADU25
XX Expre
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                                                                                                               co of a cell, a method of assigning a methylation pattern of transposable cell elements to the level of developmental potential of a cell, and a method of assigning a chromatin status pattern of transposable elements to the cell evel of developmental potential of a cell. In assigning an expression cell evel of developmental potential of a cell. In assigning an expression cell, the cell is a fully pluripotent stem cell, a pluripotent stem cell, or a differentiated cell. The expression pattern is determined by cell or a cell in a ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transposable elements to the level of developmental potential of a cell. The method comprises determining the expression of one or more families of transposable elements, and assigning the expression pattern obtained to the level of developmental potential of a cell. Also disclosed are a method of identifying a cellular differentiation induction factor, a method of identifying a factor that increases the developmental potential potential potential potential potential potential potential potential cellular differentiation induction factor, a method of identifying a factor that increases the developmental potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of assigning an expression pattern of transposable elements to the level of developmental potential of a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assigning an expression pattern of transposable elements to the level developmental potential of a cell comprises determining expression of or more families of transposable elements, and assigning the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methylation pattern; chromatin status pattern; endogenous retrovirus; ERV; short interspersed nuclear element; SINE; retroelement; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression pattern; transposable element; developmental potential; stem cell; cellular differentiation induction factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADU25276 standard; DNA; 50 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-2005
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RESULT 15
ADU22743
     The invention relates to determining expression, methylation or chromatin CC status pattern of one or more families of transposable elements in a CC sample comprises determining expression, methylation or chromatin status CC of one or more families of transposable elements. Also included are a CC method of assigning an expression pattern of transposable elements to a CC type of cancerous cell in a sample, a method of diagnosing cancer, a CC method of determining the effectiveness of an anti-cancer therapeutic in CC a subject, a method of assigning a methylation pattern of one or more CC families of transposable elements to a type of cancerous cell in a sample CC and a method of assigning a chromatin status pattern of transposable elements to a type of cancerous cell in a sample. The method is useful in CC determining an expression, methylation or chromatin status pattern of one CC or more families of transposable elements (e.g. LINE, long interspersed nuclear element, SINE, short interspersed nuclear element, or HERV, human CC the effectiveness of an anti-cancer therapeutic. The present sequence is a representative sequence for a human transposable element, used in a CC microarray to study the expression, methylation or chromatin status CC pattern of the transposable elements.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining expression, methylation or chromatin status pattern of families of transposable elements in a sample e.g. for diagnosing cancer, comprises determining the expression, methylation or chromatin status of the elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ss; transposable element; DNA methylation; chromatin; cancer; LINE; long interspersed nuclear element; SINE; short interspersed nuclear element; HERV; human endogenous retrovirus microarray.
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 747; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-804580/79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human transposable element representative sequence, SEQ ID
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B₽;
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 13 A; 15 C; 9 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    element; HERV; human endogenous retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 13;
Pred. No. 4.6e+03;
0; Mismatches 5
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Query Match 9.3%; Best Local Similarity 83.3%; Matches 25; Conservative

0

Score 22; DB 13; L Pred. No. 4.6e+03; 0; Mismatches 5;

DB 13; Length 50;

Indels

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Gaps

0

Search completed: October Job time: 325.377 secs ۲ 2006, 00:26:41

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Result
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Maximum DB seq
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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      1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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      120
6 US-11-175-859-68666

6 US-10-819-260-4357

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1 US-11-060-756-81500

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1 US-10-035-833A-2870

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Sequence 2870, Ap
Sequence 5039, Ap
Sequence 1072814,
Sequence 96670, A
Sequence 151, App
                                                                                                                                                                                                                                                                                           Description
                                                                            Sequence 86372, A
Sequence 58606, A
Sequence 51557, A
Sequence 437, App
Sequence 1034, Ap
Sequence 1140145,
Sequence 55008, A
Sequence 81500, A
Sequence 81501, A
Sequence 81511, A
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US-10-131-827-584	0-668-767-25	-11-175-85	-11-175-	-11-121-	US-11-121-849-597791	US-10-310-914A-1073215	-10-310-	US-11-175-859-28848	US-11-175-859-19544	5-859	US-11-121-849-630324	US-11-121-849-628945	060-756	-060-756-8149	-11-060-756-8148	-11-175-	US-10-891-260-7439	US-10-310-914A-116013	US-10-310-914A-596177	US-11-175-859-94140	'n	-11-175-859-	-11-060-756-8150	-11-060-756-	US-11-060-756-81487	US-11-175-859-54038	US-10-680-067-9
584,	25, App	Sequence 101653,	æ	o o	0	æ	o o	e 28848,	Sequence 19544, A	e 2594,	e 6303	e 62894	e 81505,	Sequence 81497, A	e 81488,	9616	e 7439,	Sequence 116013,	e 5961	,	e 91368,	Sequence 60129, A	e 81501,	e 81498,	e 81487,	e 54038	Sequence 9, Appli

### ALIGNMENTS

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RESULT 2
US-11-15-859-68606
JS-11-175-859-68606
JSequence 68606, Application US/11175859
Publication No. US20060024715A1
GENERAL IMPORMATION:
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; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-86372
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Sequence 86372, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.2 SEQ ID NO 86372
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INTENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
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                                                                                                                                                                                                                                                                                            5 TGGGTCATGGGGGCAGATCCCTCATGAATGGTTTAGTGCCATCCCC 50
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APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Pol
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
SEQ ID NO 51557
LENGTH: 50
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; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-68606
                                                                         CURRENT APPLICATION NUMBER: US/10/891,260
CURRENT FILING DATE: 2004-07-13
PRIOR APPLICATION NUMBER: 10/681,773
PRIOR FILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 10244
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 437
LENGTH: 33
TYPE: DNA
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; ORGANISM: homo sapien
US-11-175-859-51557
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US-11-175-859-51557/c
                                       ; ORGANISM: homo sapien
US-10-891-260-437
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Publication No. US20060024715A1
GENERAL INFORMATION:
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Best Local Similarity
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Best Local (
  Query Match
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PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                               TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms FILE REFERENCE: 3522.3
                                                                                                                                                                                                                                                                                                     APPLICANT: Affymetrix, Inc. APPLICANT: Matsuzaki, Hajime APPLICANT: Mei, Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 11.4%;
Local Similarity 77.5%;
nes 31; Conservative
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  9.8%;
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  Score 23.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26.8; |
Pred. No. 73;
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  DB 10;
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Length 33;
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RESULT 7 US-10-310-914A-1140145/c

Sequence 1140145, Application US/10310914A Publication No. US20060003322A1

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APPLICANT: Affymetrix, Inc.
APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
APPLICANT: Mei, Rui
APPLICANT: Mei, Rui
APPLICANT: Mei, Rui
AFILE OF INVENTION: Methods of Analysis of Human Polymorphisms
FILE REFERENCE: 3522.3
CURRENT APPLICATION NUMBER: US/10/891,260
CURRENT FILING DATE: 2004-07-13
PRIOR APPLICATION NUMBER: 10/681,773
PRIOR APPLICATION NUMBER: 10/681,773
PRIOR FILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 10244
SOFTWARE: Patentin version 3.2
SEQ ID NO 1034
LENGTH: 33
TYPE: DNA
ORGANISM: homo sapien
US-10-891-260-1034
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT FLILING DATE: 205-07-05
CURRENT FLILING DATE: 205-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
SEQ ID NO 57653
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 57653, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                         Matches
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Best Local :
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Best Local Similarity
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                                                                                                                                                                  LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
                                   105 TCTCATTCTCCTGCTCCCACTCTTGCATGAGACACCTGCT 144
48
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                                                                                           Similarity
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llarity 80.6%;
Conservative
                                                                                           9.5%;
72.5%;
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                                                                                           Score 22.4; DB 16
Pred. No. 2.6e+03;
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Pred. No. 1.9e+03;
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                                                                                                             DB 16;
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                                                                                                             Length 50;
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RESULT 9
US-11-060-756-81484/c
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US-11-175-859-55008/c
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TYPE: DNA
ORGANISM: homo sapien
US-11-175-859-55008
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                             APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM10.1083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEC ID NOS: 303.84
SOFTWARE: Patentin version 3.2
SEQ ID NO 81484
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TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT PAPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1140145
LENGTH: 28
TYPE: RNA
ORGANISM: Human
ORGANISM: Human
                                                                                                                                                                                                                                                              Sequence 81484, Application US/11060756 Publication No. US20050221354A1 GENERAL INFORMATION:
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APPLICANT: Bentwich,
APPLICANT: Shiler,
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CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Affymetrix, Inc. APPLICANT: Liu, Guoying et
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TITLE OF INVENTION: Method of Analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 3690.1
                     TYPE: DNA
ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 9.4%;
Local Similarity 66.7%;
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Pred. No. 2.5e+03;
0; Mismatches 3;
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                                                                                                                                                      APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031895-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81511
LENGTH: 25
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Best Local S
Matches 23
                                                      Query Match
Best Local Similarity
Matches 23; Conserv
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SEQ ID NO 81500
LENGTH: 25
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Best Local Similarity
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CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wyeth
APPLICANT: Mounts, william Martin
TITLE OF INVENTION: Nucleic Acid Arrays for
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM10.083 (031896-04200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                   154 CCTTCTGCCATGATTTTAAGATTCC 178
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                                                               9.2%; ilarity 92.0%; Conservative
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92.0%;
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92.0%; Pred. No. 3.2e+03;
tive 0; Mismatches 2
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                                                                             Score 21.8; DB 13
Pred. No. 3.2e+03;
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Pred. No. 3.2e+03;
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RESULT 12 US-11-175-859-75179 ; Sequence 75179, Application US/11175859 ; Publication No. US20060024715A1

GENERAL INFORMATION:

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APPLICANT: Nakamura, Yuho
APPLICANT: Sekine, Akihiro
APPLICANT: Sidko, Aritoshi
APPLICANT: Iida, Aritoshi
APPLICANT: Iida, Aritoshi
APPLICANT: Saito, Osamu
TITLE OF INVENTION: Detection of Genetic Polymorphisms
FILE REFERENCE: FORS-66904
CURRENT APPLICATION NUMBER: US/10/035,833A
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 7669
SOFTWARE: Patentin version 3.2
SEQ ID NO 2870
LENGTH: 41
TYPE: DNA
ORGANISM: Homo sapiens
US-10-035-833A-2870
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; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION SID 10 16251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75179
; LENGTH: 50
; TYPE: DAN ADMO Sapien
US-11-175-859-75179
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US-10-035-833A-2870
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Best Local Similarity 74.3%;
                  SEQ ID NO 5039
                                APPLICANT: Nakamura, Yuho
APPLICANT: Sekine, Akihiro
APPLICANT: Sida, Aritoshi
APPLICANT: Sida, Aritoshi
APPLICANT: Sida, Aritoshi
APPLICANT: Saito, Osamu
TITLE OF INVENTION: Detection of Genetic Polymorphisms
FILE REFERENCE: FORS-06904
CURRENT APPLICATION UMBER: US/10/035,833A
CURRENT APPLICATION UMBER: US/10/035,833A
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 7669
SOFTWARE: Patentin version 3.2
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 9.2%;
Local Similarity 71.1%;
les 27; Conservative
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Pred. No. 4.3e+03;
1; Mismatches 8;
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Pred. No. 4.7e+03;
1; Mismatches 10;
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Sequence 1072814, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of I
TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 1072814

LENGTH: 23
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Search completed: October Job time: 773.184 secs
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US-10-310-914A-1072814/c
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Best Local Similarity
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l Similarity 95.7%;
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                                                                                                                           Score 21.4; DB 11
Pred. No. 4.3e+03;
0; Mismatches 1
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Pred. No. 4.7e+03;
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Maximum DB seg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_NA_New:*

| / EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| / EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
| / EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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Maximum Match 100%
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US-10-554-759-518
US-10-554-711-770
US-10-554-711-734
US-10-554-711-734
US-10-554-711-745
US-10-554-711-747
US-10-554-711-747
US-10-554-711-747
US-10-554-711-747
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US-10-554-711-746
US-10-554-711-746
US-11-370-584-7113015
US-11-370-584-2714
US-11-370-584-2714
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518, App
770, App
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745, App
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747, App
746, App
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749, App
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49	46	36 .			25			. 47		31										25	25
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-11-348-099-9	-251-208-849	218-976-42	-348-413-94849	-348-413-91932	-348-413-38123	-217-529-18423	-370-584-3412	370-584-1959	-349-724-229	-255-139A-6688	-10-513-490-218	255-139A-6737	078-073-85	-078-073-84	078-073-83	078-073-82	-078-073-81	-404-272-3	-370-584-137	-348-413-779975	217-529-168000
•	9		8498	9324	1233	4234	12	59	9	889	80	737							7	9975	8000
Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
9, Appli	849, App	42, Appl	948498,	919324,	381233,	184234,	3412, Ap	1959, Ap	229, App	6688, Ap	218, App	6737, Ap	85, Appl	84, Appl	83, Appl	82, Appl	81, Appl	<ol> <li>Appli</li> </ol>	137, App	779975,	168000,

### ALIGNMENTS

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RESULT 2
US-10-554-759-518
J Sequence 518, Application US/10554759
Publication No. US20060177825A1
GENERAL IMPORMATION:
APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LCCATION: 37
OTHER INFORMATION: n=G, A,
US-10-554-711-518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/466,798
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 778
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 518
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 518, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local
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APPLICANT: McDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of Cancer
FILE REFERENCE: 21099.0075
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:/noteOTHER INFORMATION: Synthetic Construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                       Local Similarity 79.2
les 38; Conservative
                                                                                                                                                                                                                                    61 GTGAGTTCACGTGAGAGCCTGGTTTGTTTTGAAAGAGCCTGGCCCCCCCTCTC 108
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US-10-554-759-770
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PRIOR FILING DATE: 2005-10-28
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 518
LENGTH: 50
TYPES: **CONTINUE OF THE PROPERTY OF THE PROPERT
                                                                                                        Sequence 770, Application US/10554759 Publication No. US20060177825A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of Cancer
FILE REFERENCE: 21099.007591
CURRENT APPLICATION NUMBER: US/10/554,711
CURRENT FILING DATE: 2005-10-28
RRIOR APPLICATION NUMBER: 60/466,798
PRIOR FILING DATE: 2005-04-29
NUMBER OF SEQ ID NOS: 778
SOFTWARE: FastSEQ for Windows Version 4.0
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                                     APPLICANT: University of Georgia Research Foundation APPLICANT: McDonald, John F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION: n=G, A,
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       OF INVENTION: Global
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o. US20060115806A1
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   Analysis of
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Pred. No. 0.27;
0; Mismatches 10;
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Pred. No. 0.43;
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Transposable Elements
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FILE REFERENCE: 21099.0077P1

CURRENT APPLICATION NUMBER: US/10/554,759

CURRENT FILING DATE: 2005-10-28

PRIOR APPLICATION NUMBER: 60/466,801

PRIOR FILING DATE: 2003-04-29

NUMBER OF SEQ ID NOS: 770

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 770

LENGTH: 50
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US-10-554-759-48
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US-10-554-711-48
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          Sequence 48, Application US/10554759

Publication No. US20060177825A1

GENERAL INFORMATION:

APPLICANT: University of Georgia Research Foundation

APPLICANT: McDonald, John F.

TITLE OF INVENTION: Global Analysis of Transposable Elements

TITLE OF INVENTION: as Molecular Markers of the Developments

TITLE OF INVENTION: Cells
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CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,798
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 778
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 50
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Best Local Similarity
Matches 35; Conserv
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FILE REFERENCE: 21099.0077P1
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:/noteOTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Description of Artificial Sequence:/note OTHER INFORMATION: Synthetic Construct
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                                                                                                                                                                                                                                                                                       37 TTAGTGCCATCCCCTTGGTGATGAGTGAGTTCACGTGAGAGCTGG
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Pred. No.
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Pred. No. 0.43;
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                                  Developmental
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CURRENT APPLICATION NUMBER: US/10/554,759

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APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of Cancer
FILE REFERENCE: 21099.0075P1
CURRENT APPLICATION NUMBER: US/10/554,711
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,798
PRIOR APPLICATION NUMBER: 60/466,798
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 778
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 734
LENGTH: 50
Sequence 745, Application US/10554711

Publication No. US20060115806A1

GENERAL INFORMATION:

APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.

TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of Cancer
FILE REFERENCE: 21099.007591

CURRENT APPLICATION NUMBER: US/10/554,711

CURRENT FILING DATE: 2005-10-28

PRIOR APPLICATION NUMBER: 60/466,798

PRIOR APPLICATION NUMBER: 60/466,798

PRIOR FILING DATE: 2003-04-29

NUMBER OF SEG ID NOS: 778

SOFTWARE: FASESEQ for Windows Version 4.0
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OTHER INFORMATION: Description of Artificial Sequence:/note; OTHER INFORMATION: Synthetic Construct
US-10-554-711-734
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OTHER INFORMATION: Synthetic
US-10-554-759-48
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Best Local Similarity
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LENGTH: 50
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PRIOR APPLICATION NUMBER: 60/466,801
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FABUSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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71.8%;
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Pred. No. 6.2e+02;
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Pred. No. 4.4;
0; Mismatches
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TITLE OF INVENTION: as Molecular Markers of the Developmenta
TITLE OF INVENTION: Cells
FILE REFERENCE: 21099.0077P1
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: US/10/554,759
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,801
PRIOR APPLICATION NUMBER: 60/466,801
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 734
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LENGTH: 50
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 745
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                                                              CURRENT APPLICATION NUMBER: US/10/554,759
CURRENT FILLING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,801
PRIOR FILING DATE: 2003-04-29
PRIOR FILING DATE: 2003-04-29
                                                                                                                                                                  APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of the Development
TITLE OF INVENTION: Cells
                                                                                                                                                       FILE REFERENCE: 21099.0077P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: University of Georgia Research Foundation APPLICANT: McDonald, John F.
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OTHER INFORMATION: Description of Artificial Sequence:/note
OTHER INFORMATION: Synthetic Construct
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Pred. No. 6.2e+02;
1; Mismatches 10
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Pred. No. 6.2e+02
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APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of Cancer
FILE REFERENCE: 21099.0075P1
CURRENT APPLICATION NUMBER: US/10/554,711
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,798
PRIOR APPLICATION NUMBER: 50/466,798
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 778
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 747
LENCTH: 50
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                                                                                  APPLICANT: University of Georgia Research Foundation
APPLICANT: WcDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
TITLE OF INVENTION: Cells
FILE REFERENCE: 21099.0077P1
CURRENT APPLICATION NUMBER: US/10/554,759
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,801
PRIOR APPLICATION NUMBER: 60/466,801
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 770
SOPTWARE: FastSEQ for Windows Version 4.0
SOPTWARE: 50
TYPE: DNA
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Best Local Similarity
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Best Local (
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                                                               ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence:/noteOTHER INFORMATION: Synthetic Construct
                                              FEATURE:
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Similarity 83.3%;
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Pred. No. 9.9e+02;
0; Mismatches 5;
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Pred. No. 6.2e+02;
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TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of Cancer
FILE REFERENCE: 21099.007591
CURRENT APPLICATION NUMBER: US/10/554,711
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,798
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 778
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 746
LENGTH: 50
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                                                                                                NUMBER OF SEQ ID NOS: 770
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 746
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                  Sequence 746, Application US/10554759
Publication No. US20060177825A1
GENERAL INFORMATION:
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Publication No. US20060115806A1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                          FILE REFERENCE: 21099.0077P1
CURRENT APPLICATION NUMBER: US/10/554,759
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,801
PRIOR FILING DATE: 2003-04-29
                                                                                                                                                                                                                                                                      APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
TITLE OF INVENTION: Cells
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/note = OTHER INFORMATION: Synthetic Construct
                                                            ORGANISM: Artificial Sequence
                                                                                  TYPE: DNA
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Pred. No. 1.2e-
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APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.

TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of Cancer
FILE REFERENCE: 21099.0075p1
CURRENT APPLICATION NUMBER: US/10/554,711
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,798
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 778
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 640
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/note =
FOUNDER INFORMATION: Synthetic Construct
Search completed: October 1, 2006, 01:14:07 Job time: 123.925 secs
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; NAME/KEY: misc_feature
; LOCATION: 8 COTHER INFORMATION: n=G, A, T, or C
US-10-554-759-746
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US-10-554-711-640
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                                                                                 163 ATGATTTTAAGATTCCAGGGACTTCACAAGAAGC 196
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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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gb_est6:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length DB	BG	ID	Description
۲	21.2	9.0	45	13	CL529018	CL529018
ი 2	19.8	8.4	44	11	AZ862104	AZ862104
c 3	19.6	8.3	44	11	BH804777	BH804777
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ហ	19.2	8.1	49	10	DT933089	DT933089
ი 6	19.2	8.1	50	10	DV774160	DV774160
c 7	19	8.1	37	11	AZ836826	AZ836826
	19	8.1	41	14	BX128197	BX128197
ი 9	18.8	8.0	44	11	AZ968544	AZ968544
10	18.8	8.0	46	14	BX650405	BX650405
c 11	18.8	8.0	50	11	AZ765968	AZ765968
12	18.8	8.0	50	13	CZ194703	CZ194703
c 13	18.6	7.9	43	11	AZ862121	AZ862121
c 14	18.6	7.9	47	11	AZ331496	AZ331496
15	18.6	7.9	50	œ	CX001254	CX001254
16	18.4	7.8	46	۲	AI941313	AI941313
17	18.4	7.8	48	_	AI749566	AI749566
c 18	18.2	7.7	40	ᆫ	AA257023	AA257023
c 19	18.2	7.7	49	4	CA966474	C2966474

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AZ479185 1M029911 AZ328467 1M0052E18 AZ793917 2M0047L24	AV674036 AV674036 CF322787 HDN02-B AV965544 AV965544 AJ920737 AJ920737 AZ387638 1M0147814 AT561118 FG26611 ×		AZ789792 ZM0037J19 CF334268 JMT03-H BF507210 3659P-23 AI334100 qp97c03.x AZ324079 1M0045C24 AU104247 AU104247	BE882523 601507265 AZ504116 1M0344K08 A1521631 to65h01.x AZ407440 1M0178H15 BE299660 600944319 D458809 HUMGGS0327

## ALIGNMENTS

	FEATURES SOUTCE	JOURNAL COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 CL529018 LOCUS DEFINITION
/Organism= Homo Saplens"  /mol_type="genomic DNA"  /db_xref="taxon:9606"  /clone="HIV55C09.fwd"  /clone="HIV55C09.fwd"  /clone="Hib="HIV-vector integration sites in human IMR90  primary lung fibroblasts"  /note="Human primary lung fibroblasts (IMR90) were  infected with an HIV-based vector. DNA was isolated and  cleaved with restriction enzymes; linkers were ligated  onto the cleaved DNA and DNAs were amplified using one  primer that bound to the linker DNA and one that bound to  the HIV cDNA. Junctions between integrated HIV proviruses	Tel: 858 : Fax: 858 : Email: bus Class: PCF	hed Fre titu	5) eit: er,	Survey sequence. CL529018 CL529018.1 GI:47422229 CSS. Homo sapiens (human) Homo sapiens (human) Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	CL529018  45 bp DNA linear GSS 17-MAY-2004 HIV55C09.fwd HIV-vector integration sites in human IMR90 primary lung fibroblasts Homo sapiens genomic clone HIV55C09.fwd, genomic

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ORIGIN
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AZ862104/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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Tel: 801 585 5606
Fax: 801 585 7177
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ862104.1 GI:13059089
GSS.
Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0169 row: D column: 04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2M0169D04R Mouse 10kb plasmid clone UUGC2M0169D04 R, genomia
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primer: CACACAGGAAACAGCTATGACC
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            10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: pw042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UUGC2M0169D04"
                                                                                                                                                                                                                                                                                                                                                                                           'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:10090"
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Pred. No. 2.
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                   44
                                                   20 GATCCCTCATGAATGGTTTAGTGCCATCCCCTTGGTGATGAG 61
                     GATCCTGAATTAATGGGCTGGTGCCTTGCCTAGTGTGATGGG 3
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137 CACCTGCTCCCCCTTCTCTGCCATGATTTTAAGAT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize genomic sequences 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 1008098 row: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: walbot@stanford.edu
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8.3%;
nilarity 66.7%;
Conservative
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                                                                                                                                                           /clone lib="1008 - RescueMu Grid I"
/clone lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu (spineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BgIII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmdb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BgIII, and ligated to form circular plasmids. DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                   ampicillin.
                                                                                                                             cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:4577"
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Score 19.6; DB 11
Pred. No. 7.5e+05;
0; Mismatches 14
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Pred. No. 6.5e+05;
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RESULT 5
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Matches 23
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                                                                                                                                                                                                                                                                                   ω
                                                                                                                                            DT933089 49 DP MKWA 1111CG1. 20. 10. BH006A10 Leptosphaeria starvation library Leptosphaeria maculans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Trace considered overall poor quality
Insert Length: 864 Std Error: 0.00
Seq primer: -40n3 fwd. ET from Amersham
High quality sequence stop: 1.
Leptosphaeria maculans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Leptosphaeriaceae; Leptosphaeria; Leptosphaeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI022023 31 bp mRNA linear EST 28-
ow72a02.x1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens
clone IMAGE:1652330 3' similar to TR:Q69340 Q69340 ORF1, OR
ORF3. ;contains TAR1.t3 TAR1 repetitive element ;, mRNA seq
                                                                                                     DT933089.1 GI:75966345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                              Leptosphaeria maculans (blackleg
                                                                                                                                          CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
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1 (bases 1 to 31)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stages"20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_libs"Soares_fetal_liver_spleen_INFLS_S1"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver_spleen INFLS_library. 1st strand_cDNA was primed
with a Pac I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:1652330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
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79.3%;
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Pred. No. 7.
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                                                            fungus)
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Best Local (
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                                                                                                                                                                                                                                                                                                                                800 Rose St., Lexington, KY 40536-0298, USA
Tel: 859 323 1083
Fax: 859 323 1070
                                                                                                                                                                                                                                                                                                                                                                                        Department of Physiology University of Kentucky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene expression and specificity in the mature zone of the lobster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 50)
Stepanyan,R., Day,K., Urban,J., Hardin,D.L., Shetty,R.S.,
Derby,C.D., Ache,B.W. and McClintock,T.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DV774160 50 bp mRNA linea:
McClintock24_C06.ab1 Homarus EST library project
CDNA_clone McClintock24_C06.ab1, mRNA sequence.
DV774160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TTTTAAAANTCTGGGTTCTTNACATGAATAAAT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Cozijnsen A.J. Blackleg Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardiner, D.M., Cozijnso
Leptosphaeria maculans
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: McClintock TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nephropoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homarus americanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: + 61 3 8344 5056
Fax: + 61 3 9347 5406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The School of Botany,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homarus americanus (American lobster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: a.cozijnsen@unimelb.edu.au.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The University of Melbourne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                              mcclint@uky.edu.
/clone_lib="Homarus EST library project"
/note="Organ: Olfactory organ; lateral ramus of first
/notenae; Vector: pBluescript; Site_1: NotI; Site_2: SalI,
send sequences from a subtracted CDNA library. The
frequency of common sequences in this library was reduced
by screening filter lifts of colonies with complex probes'
                                                                                                                                                                                             /organism="Homarus americanus"
/mol type="maka"
/db xref="reaxon:6706"
/clone="McClintock24_C06.ab1"
                                                                                                                  /dev_stage="adult"
/lab_host="Dh5alpha"
                                                                                                                                                           /sex="male and female"
/tissue runn=""
                                                                                                                                                                                                                                                                                         Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Leptosphaeria maculans"
/mol_type="mRNA"
/strain="IBCN18 (M1)"
/db xref="taxon:5022"
/sex="MAT1-2"
                                                                                                                                                         tissue_type="#mature zone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Mycelium"
/clone_lib="Leptosphaeria starvation library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Pred. No. 1e+0
0; Mismatches
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JOURNAL COMMENT
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AUTHORS
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AZ836826/c
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Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0131 row: A column: 20
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ836826
AZ836826.1 GI:13006734
GSS.
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37 bp DNA linear GSS 20-FEB-200
2M0131A20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0131A20 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murodea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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        was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNP42 (gi | 4732.14 | gb | AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGCIM lik
/note="Vector: PWD42nv; Purified genomic
musculus C57BL/6J (male) was obtained fr
chemically-competent E.
                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0131A20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
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coli XL10-Gold (Stratagene) cells
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AUTHORS
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BX128197/c
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AUTHORS
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 44)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Nouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                     AZ968544 44 bp DNA linear GSS 2
2M0240J20R Mouse 10kb plasmid UUGC2M library Mus musculus
clone UUGC2M0240J20 R, genomic survey sequence.
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BX128197
                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX128197.1 GI:27959151
                                                                                                                                                                                                                                                                               AZ968544.1
                                                                                                                                                                                                                                                                                                   AZ968544
                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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nilarity 81.5%;
Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="Testis"
                                                                                                                                                                                                                                                                                 GI:13839771
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and selected for ampicillin resistance."
Score 19; DB 11; ~
Pred. No. 1.1e+06;
Migmatches 5;
  Indels
  0;
  Gaps
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0;

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enque humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 26118. part of the Daniokey BAC Library created by R. Plasterk an Keygene. Further details: Submitted (13-MAR-2003) The Sanger Institute, Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; http://www.sanger.ac.uk/Projects/D\_rerio/ note="vector pIndigoBAC-536" Huckle, E. and Durham, J.L. Score 19; DB 14; Pred. No. 1.1e+06; DKEY-26118, genomic survey sequence. .1e+06; 5; DNA Length 41; Wellcome Trust Genome . E-mail enquiries: Plasterk and N.V. GSS 13-MAR-2003 0 0

GSS 27-APR-2001

genomic

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REFERENCE
AUTHORS
TITLE
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VERSION
                                                                                                                                                                                                                                                                                                                                              RESULT 10
BX650405
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Best Local S
Matches 26
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                             Arabidopsis thaliana T-DNA genomic survey sequence. BX650405 BX650405.1 GI:37606793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0240 row: J column: 20
Seq primer: CACACAGGAAACAGCTATGACC
                                    Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                 Arabidopsis thaliana (thale cress) Arabidopsis thaliana
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
Bioinformatics 19 (11), 1441-1442 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308,
308,
USA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD2 (gi|473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. coli strain XL10-Gold, T1-resistant, F/clone_lib="Mouse 10kb plasmid UUGC2M library" /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC2M0240J20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                               DNA
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AUTHORS
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ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Euchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5942400. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                 50 bp DNA linear GSS 16-FEB-2011M0563N12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0563N12 F, genomic survey sequence.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 GCTATCCTTCTCGTTCTGCCATCTTTGCCATATGCTA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High-throughput generation of sequence mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strizhov, N.,
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                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                             (bases 1 to 50)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-DNA derived sequences were removed."
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                 GI:12882543
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Pred. No. 1.3e+06;
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whole genome scaffolding with paired end reads from 10kb

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REFERENCE
AUTHORS
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CZ194703
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 TGAGAGCTGGTTGTTTGAAAGAGCCTGGCCCCCCCCTCTCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                Rex2, genomic survey sequence. CZ194703 CZ194703.1 GI:58833147
                                                                                                                                                                                                                                                                                                       PST6723-NR MICB1 Mus musculus ge
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Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0563 row: N column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                               GSS.
    Contact: Hicks GG
                           Unpublished
                                            www.EScells.ca
                                                                        Hicks,G.G
                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAGGCCTGGTAGTGTATGAGCCATGCCCCATGTGA 11
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                                                                                        (bases 1 to 50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732.114 [gb]AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: pW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC1M0563N12"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.8; DB 11 Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                 bp DNA linear GSS 15-AUG-2005 genomic clone PST6723-NR similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.00
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VERSION
KEYWORDS
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                                                                FEATURES
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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
UNeoSV1 gene trap. Tag generated by plasmid rescue. Additional
uneoSV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
'http://140.193.242.7/esdb/PSTReport.php?PST=PST6723-NR'
Class: Gene Trap.
                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0169 row: H column: 01
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 43)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 bp DNA linear GSS 21
2M0169H01R Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC2M0169H01 R, genomic survey secuence
AZ862121
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                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B.
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                                                                                    High quality sequence stop: 43.
                                                                                                                                                                                                                                                                                                University of Utah Genome Center University of Utah
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ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
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ilarity 76.7%;
Conservative
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                                                                                                        plasmid ends
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/mol type="genomic DNA"
/strain="129 sv"
/db xref="taxon:10090"
/clone="psT6723-NR"
                                                                                                                                                                                                                                                                                 Biomedical
/mol_type="genomic DNA"
                        organism="Mus musculus"
                                                                Location/Qualifiers
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/cell_line="D3H ((1 subclone)"
/clone_lib="MVICB1"
/note="Vector: U3NeoSV1"
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                                                                                                                                                                                                                                                                                                                                             Weiss
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Pred. No. 1.3e
0; Mismatches
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/strain="C57BL/6J"

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Best Local Similarity
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                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: P column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ331496 47 bp DNA linear GSS 29
IM0059P21F Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0059P21 F, genomic survey sequence.
AZ331496
AZ331496.1 GI:10394261
GSS.
                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1. (bases 1 to 47)
                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
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gh quality sequence stop: 47.
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWDA2 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/organism="Mus musculus"
                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, /clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
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Pred. No. 1.5e+06;
0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rocus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 GTGAGAGCTGGTTGTTTGAAAGAGCCTGGCCCC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 GTGGGATGTGGTGGTTTGAATAAGAATGCCCCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canida
                                                                                                                                                                                                                                                                                                                                                                                                                                         ESTs from Canis familiaris left
Unpublished (2004)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                     Tel: 516 367 8884 Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 50)
Balija, V.S., Nascimento, L.U. and McCombie, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CX001254 50 bp mRNA linear EST 03-DE iv40a04.bl Left Cardiac Ventricle (DOGEST7) Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CX001254.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CX001254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.9%;
ilarity 72.7%;
Conservative
                                                                                                                                                                                                                                                                     mccombie@cshl.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072,1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
/tissue_type="Cardiac muscle"
/dev stage="3 month old normal canine"
/lab_host="XLI0 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1:
ECORI; Site_2: XhoI; Library constructed using pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymelectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                      organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="UUGC1M0059P21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:56272670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lib="Mouse 10kb plasmid
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Pred. No. 1.5e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac ventricle
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XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

ORIGIN

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Minimum |
Maximum |
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No.
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    and is
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  16.8
16.8
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19.2
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| EMC_Colerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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242
1 ttctccagcacagcactgga......
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Maximum Match 100%
Listing first 45 summaries
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    2006, 00:58:57;
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                                   US-10-554-711-527
US-10-554-711-343
US-10-554-711-343
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(without alignments)
3514.157 Million cell updates/sec
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16, App1
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2387, Ap
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49117, Ap
1835, Ap
1835, Ap
9537, Ap
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6.7	6. 8	6.8	6.8	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9
25	48	43	25	47	25	25	25	.25	25	25	25	25	25	25	25	25	25	25	25	25
8	7	7	9	7	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
US-11-217-529-153307	US-11-368-338-30	US-11-043-842-584	US-11-348-413-852337	US-11-370-584-275	US-11-348-413-952629	US-11-348-413-952628	US-11-348-413-952627	US-11-348-413-923507	US-11-348-413-923506	US-11-348-413-923505	US-11-348-413-683036	US-11-348-413-624722	US-11-348-413-624683	US-11-348-413-624682	US-11-348-413-624681	US-11-348-413-100416	US-11-348-413-50182	US-11-348-413-36615	US-11-348-413-36614	US-11-348-413-36613
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
153307,	30, App	584, Ap	852337,	275, App	952629,	952628,	952627,	923507,	923506,	923505,	683036,	624722,	624683,	624682,	624681,	100416,	50182, A	36615, A	36614, A	36613,

#### ALIGNMENTS

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RESULT 2
US-10-554-759-527
(Sequence 527, Application US/10554759
; Sequence 527, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John F.
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; TITLE OF INVENTION: Cells
; TITLE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-554-711-527
; Sequence 527, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 778
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 527
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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APPLICANT: McDonald, John P.
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of Cancer
FILE REFERENCE: 21099.0075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:/noteOTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                      133
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    9.1%;
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Pred. No. 9.16
1; Mismatches
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; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 527
; LENCTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
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US-10-554-711-343
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US-11-155-444-16/c
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                                                                                                                       Sequence 343, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
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SEQ ID NO 16
LENGTH: 50
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Publication No. US20060104971A1
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PRIOR FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: 60/435,154
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/435,185
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 23
                 APPLICANT: University of Georgia Research Foundation APPLICANT: McDonald, John F. TITLE OF INVENTION: Global Analysis of Transposable Elements TITLE OF INVENTION: as Molecular Markers of Cancer FILE REFERENCE: 21099.0075P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GARBER, ELLEN
APPLICANT: BAILLY, VERONIQUE
APPLICANT: BROWNING, JEFFREY L.
TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
CURRENT APPLICATION NUMBER: US/10/554,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/155,444
CURRENT FILING DATE: 2005-06-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: primer
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28; Conservative
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                                                                                                                                                                Application US/10554711
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 8;
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PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 778
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 778
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 723
                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                           Publication No.
                                                                                                                                                                                                                                               Sequence 343,
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             APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
TITLE OF INVENTION: as Molecular Markers of the Developments
TITLE OF INVENTION: Cells
FILE REFERENCE: 21099.0077P1
CURRENT APPLICATION NUMBER: US/10/554,759
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,801
PRIOR FILING DATE: 2003-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: University of Georgia Research Foundation APPLICANT: McDonald, John F. TITLE OF INVENTION: Global Analysis of Transposable Elements TITLE OF INVENTION: as Molecular Markers of Cancer FILE REFERENCE: 21099.0075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/554,711
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,798
PRIOR FILING DATE: 2003-04-29
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Descriptio
OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:/noteOTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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o. US20060177825A1
ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Synthetic Construct
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NUMBER OF SEQ

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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
ITITLE OF INVENTION: Biallelic markers for use in constructing a h
TITLE OF INVENTION: density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/11/370,584
CURRENT FILING DATE: 2006-03-08
PRIOR APPLICATION NUMBER: US/10/349,143
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: US/09/298,850
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US-11-370-584-2387/c
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; OTHER INFORMATION: Synthetic Construct
US-10-554-759-723
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                                                                                                                                                                                                                                                                          Sequence 2387, Application US/11370584 Publication No. US20060177863A1 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/554,759
CURRENT FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,801
PRIOR FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 770
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 723
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OTHER INFORMATION: Synthetic Construct
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o. US20060177825A1
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GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in
TITLE OF INVENTION: density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/11/370,584
CURRENT FILING DATE: 2006-03-08
PRIOR APPLICATION NUMBER: US/10/349,143
PRIOR FILING DATE: 2003-01-21
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Matches
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Publication No. US20060177863A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2387
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.3 SEQ ID NO 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49117, Application US/11217529 Publication No. US20060099612A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: 1998-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 99-10720-63 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 20; Conserv
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nes 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 TGAACAGAACGACCTGTTAAGCCCACCGTGTCTGTTA 197
                                                                                                                                                                                                                                                                                                                                                                           97 GTAACTACATTTTGTGCCCACTAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 TTATCAGAAAGACCAYGTTAGCCCCCTGTTTCTTTAA
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                                                                                                                                                                                                                                                                                                                                        GAAGTTACATTTGGTGCCCACTAC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAKAO, YOSHIHIRO
NAKAMURA, NORIHISA
KODAMA, YUKIKO
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83.3%;
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Pred. No. 2.3e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.6; DB
Pred. No. 2e+04;
D; Mismatches
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                                                                                                                    constructing a high
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PRICE APPLICATION NUMBER: US 10/932,182
PRICE FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOSTWARE: PatentIn version 3.3
SEQ ID NO 22009
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-22009
                                                                                                                                                RESULT 12
US-11-217-529-99537
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                                                                                              Sequence 99537, Application US/11217529 Publication No. US20060099612A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 1835
LENGTH: 47
TYPE: DNA
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APPLICANT:
                               APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHII APPLICANT: NAKAMURA, NORII APPLICANT: KODAMA, YUKIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR PILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: 1998-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
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APPLICANT: NAKAMUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: S-38-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SUNTORY LIMITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: allele
LOCATION: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                Match 7.1%;
Local Similarity 86.4%;
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FILING DATE: 1999-10-20
APPLICATION NUMBER: US 09/298,850
FILING DATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                 180 AGCCCACCGTGTCTGTTAGGGT 201
                                                                                                                                                                                                                    25
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                                                                                                                                                                                                                    AGCCCACCGTCTCTGTTAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTAGACCAGAACTTAATTTTCRTCACTCTTCTTTGAGTTCTTCAT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGCACAGCACTGGATTTTGGTCACCTGGCTGGGAGCTCCACCT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAKAMURA, NORIHISA
KODAMA, YUKIKO
                               NAKAMURA, NORIHISA
KODAMA, YUKIKO
 ASHIKARI, TOSHIHIKO
               FUJIMURA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                               YOSHIHIRO
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                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                 Score 17.2;
Pred. No. 2
                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                   2.8e+04;
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US-11-348-413-461909

Sequence 461909, Application US/11348413 Publication No. US20060160121A1 GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: APPLICANT: APPLICANT:

Mounts, William N Murphy, Ellen Olmsted, Stephen RESULT 14

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; TYPE: DNA; ORGANISM: Homo sapiens US-10-511-937-263
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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 263, Application US/10511937 Publication No. US20060088836A1 GENERAL INFORMATION:
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
SEQ ID NO 263
LENGTH: 50
                                                                             Matches
                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR PILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOCST
                                    149 СТСАССТССАССТСААСАСАСАССТСТТААС 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 GTCTAGGCTGTATCAGATACCC 224
                                                                             23;
9 CCCAAGTGGAGCAGAACAGAGGGATTTGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prentice, James
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                                                                           Conservative
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                                                                                           7.0%;
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                                                                                             Score 17; DB 6;
Pred. No. 4.4e+04;
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                                                                             Mismatches
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                                                                                                                Length 50,
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                                                                             Gaps
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; NAME/KEY: misc_feature; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 13836; WANOIUPTD; Start 106; Stop 130; OTHER INFORMATION: 00000000011110
US-11-348-413-461910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature; LOCATION: (1)..(25); COTHER INFORMATION: SEQ ID NO: 13836; WANDIUPTD; Start 105; Stop 129; OTHER INFORMATION: 00000000011110
US-11-348-413-461909
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US-11-348-413-461910
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CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
PRIOR PRIOR DATE: 2004-10-05
PRIOR DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 461910
LENGTH: 25
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Matches
                                                                                                                                             Query Match 6.9%; Score 16.8; DB 9; Best Local Similarity 90.0%; Pred. No. 3.8e+04; Matches 18; Conservative 0; Mismatches 2;
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APPLICANT: Mount
APPLICANT: Murph
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Best Local Similarity 90.0%;
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APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
APPLICANT: Olmsted, Stephen
APPLICANT: Olmsted, Stephen
APPLICANT: Olmsted, Stephen
IIILE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial
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ACTATAACTACATTTTGTGC 23
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Pred. No. 3.8e+04;
0; Mismatches 2
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Search completed: October 1, 2006, 01:14:07 Job time : 128.075 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

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# SUMMARIES

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7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	8.1	8.1	8.1	8.3	8.4	8.4	8.6	8.6	9.1	9.1	Query Match I
50	50	50	42	42	42	42	39	50	42	31	48	41	41	50	50	50	50	Length DB
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ADU22340	ADU24873	ADU25252	AAX16811	AAX16801	AAV16941	AAV16931	AAT97180	ABZ01168	AAQ74160	AAA51766	ABK97936	ABZ44689	ABZ47186	ADQ12194	ABZ07908	ADU22523	ADU25056	ID
Adu22340 Human tra	Adu24873 Retroelem	Adu25252 Retroelem	Aax16811 Pea Rubis	Aax16801 Pea Rubis	Aav16941 Antisense	Aav16931 Sense PCR	Aat97180 T cell re		Aaq74160 Mouse hea	Aaa51766 31-mer CY	Abk97936 DNA encod	Abz44689 Human ATP	Abz47186 Human ATP	Adq12194 Primer of	Abz07908 Human leu	Adu22523 Human tra	Adu25056 Retroelem	Description

The invention relates to a method of assigning an expression pattern of transposable elements to the level of developmental potential of a cell.

Disclosure; SEQ ID NO 527; 50pp; English

Assigning an expression pattern of transposable elements to the level of developmental potential of a cell comprises determining expression of one or more families of transposable elements, and assigning the expression pattern.

WPI; 2004-804756/79.

Mcdonald JF;

29-APR-2003; 2003US-0466801P.

(UYGE-) UNIV GEORGIA RES FOUND INC.

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<b>4</b> 5	44	43	42	41	40	39	38	37	36	S S	34	ω W	32	31	30	29	28	27	26	25	24	23	22	21	20	19
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7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.8	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9
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AAI71381	AAS10797	ABV72867	ABV72866	AAZ96036	ADZ48190	ABL40677	ADE80534	ABK82995	AAX17504	AAT64216	AAQ69754	AAC81686	AAV02469	AAV02490	AAS09540	AEB90482	ABL51688	AAD56821	ABZ06793	ABZ06403	AAL28699	ADH91213	ADH05426	ABK89785	ABX79718	ADU22719
Aai71381 Bovine MH	Aas10797 Bovine MH	Abv72867 Mouse bra	Abv72866 Mouse bra	Aaz96036 Polynucle	Adz48190 Cutaneous	Abl40677 Parkinson	Ade80534 Duplex ol	Abk82995 DNA bindi	Aax17504 Test sequ		Aaq69754 Herpes si	Aac81686 Chimeric	Aav02469 Primer MP	Aav02490 Bridge ol	Aas09540 Antibody	Aeb90482 1278 prob	Abl51688 Human GFR		Human	Abz06403 Human leu	Aal28699 Human SNP	Adh91213 1-beta-me	Adh05426 Gene poly	<ul> <li>Abk89785 Human zin</li> </ul>	Abx79718 EST polym	Adu22719 Human tra

### ALIGNMENTS

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RESULT 1
ADU25056
ID ADU25056
ID ADU25056
ID ADU25056
AC ADU2
XX ADU2
XX Expr
KW Expr
KW Expr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retroelement consensus sequence identifier oligonucleotide #526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JAN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-APR-2004; 2004WO-US013667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           long interspersed nuclear element; LINE; retroelement; ss.
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RESULT 2
ADU22523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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                                                                                                                                                                                                                                                                            29-APR-2004; 2004WO-US013522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, ss; transposable element; DNA methylation; chromatin; cancer; LINE; long interspersed nuclear element; SINE; short interspersed nuclear element; HERV; human endogenous retroviru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADU22523;
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WPI; 2004-804580/79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human transposable element representative sequence, SEQ ID 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JAN-2005
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                                                                                                                                       (UYGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identifier of a retroelement consensus sequence.
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                                                                                                                                       UNIV GEORGIA RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human endogenous retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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Determining expression, methylation or chromatin status pattern

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New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.

WPI; 2002-636525/68.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method of assigning an expression pattern of transposable elements to a crype of cancerous cell in a sample, a method of diagnosing cancer, a method of determining the effectiveness of an anti-cancer therapeutic in a subject, a method of assigning a methylation pattern of one or more cancilles of transposable elements to a type of cancerous cell in a sample cancers to a type of cancerous cell in a sample. The method is useful in determining an expression, methylation or chromatin status pattern of one or more families of transposable elements (e.g. LINE, long interspersed conclear element, SINE, short interspersed nuclear element, or HERV, human candogenous retrovirus) in a sample for diagnosing cancer or determining the effectiveness of an anti-cancer therapeutic. The present sequence is a representative sequence for a human transposable element, used in a microarray to study the expression, methylation or chromatin status cancer of the transposable elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                       T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte gene expression profiling probe
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of one or more families of transposable elements. Also included are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to determining expression, methylation or chromatistatus pattern of one or more families of transposable elements in a sample comprises determining expression, methylation or chromatin status
                                                                                                                     Wohlgemuth J,
                                                                                                                                                                                        20-OCT-2000;
08-JUN-2001;
                                                                                                                                                                                                                                                                                                                  WO200257414-A2
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABZ07908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ07908 standard; DNA; 50
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                                                                                                                                                                                                                                                                                25-JUL-2002
                                                                                                                                                         BIOC-) BIOCARDIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 TCTCTTTGGAGCACCTCTCACGTGGAGCTGAACAGAACGACCTGTTAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
31; Conserv
                                                                                                       Woodward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 BP; 13 A; 13 C; 12 G; 10 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGTTTGGGACACCAAGAGCCTGGAACTGCACRGCACCAKCTGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                        arthritis; osteoarthritis; cytomegalovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                          2000US-0241994P.
2001US-0296764P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                   d R, X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO 527; 68pp; English.
                                                                                                     Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.1%;
                                                                                                                     Matcuk G,
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Pred. No. 4e+01
1; Mismatches
                                                                                                     Altman P,
C, Johnson
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                                                                                                         'n
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                                                                                                                     Prentice J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
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in a
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Claim

1; Page

582; Opp; English.

comprises one or two isolated DNA molecules that detect expression, which gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ000010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infertice.

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54 AGCTGCTGCCTCACCTGCTTTTCCAAACCCCCACCCTGTAA

AGCTGCTGCTTCTCTTCAGTTGCAAATGCAAACCTGTTA

40 93 Query Match Best Local S Matches 28

28; Similarity

Conservative

0

Mismatches

12; 6

Indels

0

Gaps

0

8.6%;

Score 20.8; Pred. No. 1

le+04;

띪

Length

50;

Sequence 50 BP; 12 A; 11 C; 8 G; 19 T; 0 U; 0 Other;

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RESULT 4
ADQ12194/c
ID ADQ12194 standard;
Query Match
Best Local Similarity
                                                      The present invention relates to a multivalent antibody comprising at least one antigen recognition site specific for a lymphotoxin-beta receptor (LT-\&bgr_i-R) epitope. The antibody is useful for preparing a medicament for the treatment of cancer. The composition and method are used for diagnosing or treating cancer and for inhibiting tumour volume. The present sequence represents a primer of the invention.
                                                                                                                                                                      New multivalent antibody constructs beta receptor, useful for diagnosing
                                                                                                                                                                                                                                 Garber
                                 Sequence 50
                                                                                                                                                                                                                                                                              20-DEC-2002; 2002US-0435154P
                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-2004
                                                                                                                                       Example 5; SEQ ID NO 16;
                                                                                                                                                                                                                                                                                                   22-DEC-2003; 2003WO-US041393
                                                                                                                                                                                                                                                                                                                           15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                  WO2004058191-A2
                                                                                                                                                                                                                                                                                                                                                                                                lymphotoxin-beta receptor; LT-&bgr-R; Cytostatic; cancer; tumour; huCBE11; huBHA10; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer of the invention
                                                                                                                                                                                                                                                        (BIOG-) BIOGEN IDEC MA INC
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                                                                                                                                                                                                                                Bailly V,
                                 BP;
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                                  13
                                                                                                                                                                                                                                                                                                                                                                                               primer; ss.
                                 P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
8.6%;
70.0%;
                                 12 C;
                                                                                                                                                                                                                                Browning
                                                                                                                                                                                                                                                                                                                                                                                                                                  #6
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                                 19 G; 6
Score
Pred.
                                                                                                                                     English.
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20.8; DB 13;
No. 1e+04;
                                                                                                                                                                       specific for the human lymphotoxin-
g or treating cancer or for inhibiting
                                  ;
0
                                 U; 0 Other,
          Length
                                                                    volume
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RESULT 5
ABZ47186/c
ID ABZ471
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cc variety of detection assays, including hybridisation assays, nucleic acid carrays and PCR-based methods. The invention also encompasses methods of cevaluating and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide polymorphism (SNPs), may be used in studying the relationship between CC polymorphisms (SNPs), may be used in studying the relationship between CC drugs. SNPs are also useful as polymorphism markers for discovering genes to that cause or exacerbate certain diseases, conditions, and responses to that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of carug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                  encoding enzymes associated with drug metabolism. The invention relate to methods and compositions for identifying individuals who have at le one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes primers specific for a sequence selected from ABZ43217-ABZ50887 using primers specific for a sequence selected from ABZ43217-ABZ50887 using
                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying individuals having a polymorphism, useful for determining effectiveness or side effect of a drug or treatment protocol, comprise detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-2000; 2000JP-00399443
02-MAY-2001; 2001JP-00135256
27-AUG-2001; 2001JP-00256862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; drug metabolising enzyme; gene; drug metabolism; chromoso polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; (
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                             Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-583571/62.
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                                                                                                                                                                                                                                                                                                                                                                                                 Page 136; 2785pp; English
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                                              invention relates
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RESULT 6
ABZ44689/c
ID ABZ44689 standard; DNA; 41
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Best Local S
Matches 27
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encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at lease polymorphism in such drug metabolising annumeration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; drug metabolising enzyme; gene; drug metabolism; chromosome polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 41 BP; 9 A; 10 C; 20 G; 2 T; 0 U; 0 Other;
                                                                                                                             Identifying individuals having a polymorphism, useful for determining effectiveness or side effect of a drug or treatment protocol, comprise detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                               27-DEC-2000; 2000JP-00399443.
02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
                                                                                   Claim
                                                                                                               detecting at least nucleic acid.
                                                                                                                                                                                                                     Nakamura Y,
                                                                                                                                                                                                                                                                                                                                           27-DEC-2001; 2001WO-JP011592
                                                                                                                                                                                                                                                                                                                                                                                                     WO200252044-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTGCCCACCGGTCTGGCCGGTACCCCTCCCCGCCTG
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                                                                                                                                                                                                                       Sekine
                                                                                 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers replace(21,T) /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                 2785pp;
                                                                                                                           one polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                 English
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                                                                                                                                                                                                                       Saito
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No. 1.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site,
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                                                                                                                                             comprises
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therapy
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at least

WPI; 2002-547689/58 P-PSDB; ABG68863.

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RESULT 7
ABK97936/c
ID ABK979
XX
ABK979
XX
ABK979
XX
ABK979
XX
O7-OCT
XX
CYtOSE
KW Cancer
KW immuno
KW cancer
KW multip
XX
MO2002
XX
MO2002
XX
O6-JUN
XX
PD 06-JUN
XX
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PD 01-DEC
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XX
PF 30-NOV
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PF 31-DEC
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PF 158h E
XX
WPI; 2
DR WPI; 2
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Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 41 BP; 9 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple sclerosis; autoimmune disease; arthritis; ds; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive; antiarthritic; cytokine receptor; interferon; IFN; cancer; haematological malignancy; viral infection; hepatitis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; virucide; hepatotropic; antiinflammatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK97936 standard;
                                                                                                                                                                                                                                                               01-DEC-2000; 2000US-00727388
                                                                                                                                                                                                                                                                                                                            30-NOV-2001; 2001WO-CA001701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200244197-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                 罗
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                 FISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITTGGTCACCTGGCTGGGAGCTCCACCTCCCCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTGCCCACCGGTCTGGCCGGTACCCCTCCCCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFN-Con
                                                                                                                                                                                                 z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.4%;
71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRRP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 C; 20 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.4; DB Pred. No. 1.3e+C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
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RESULT 8
AAA51766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC This invention relates to a novel cytokine receptor binding peptide
CC construct comprising a cytokine receptor binding domain incorporated in a
CC suitable molecular scaffold so that the scaffold maintains the binding
CC domain in a configuration suitable for binding to the cytokine receptor.
CC The peptides of the invention may have cytostatic, virucide,
hepatotropic, antiinflammatory, neuroprotective, immunosuppressive and
CC construct is useful in the manufacture of a medicament as an interferon
CC (IFN) mimetic. A peptide that mimics the effect of IFN is useful in
CC medical therapies for cancer, haematological malignancies, viral
CC such as arthritis B or C), multiple sclerosis and autoimmune diseases
CC such as arthritis, to detect modulators of IFN action, in screening
CC such as arthritis, to detect modulators of IFN action, in screening
CC such as arthritis, to detect modulators of IFN action in screening
CC such as arthritis, to detect modulators of IFN action in screening
CC such as arthritis, to detect modulators of IFN action in screening
CC such as arthritis. The activity and/or interaction with another molecule
CC related disorders. A nucleic acid encoding the peptide of the invention
CC or is useful for the treatment and therapy of the mentioned medical
CC conditions. The peptide of the invention has less side effect than those
CC conditions. The peptide of the invention has less side effect than those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              22-DEC-1999;
                                                                                                                                                                                                                                                                                                                         06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                      WO200039332-A1
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism; Activator protein-3 motif; AP-3; basic transcription element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-mer CYP3A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA51766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA51766 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48
    metabolized
                                                                                              WPI; 2000-452418/39.
                                                                                                                                         Paulussen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine receptor binding peptide construct, in particular interferon receptor binding peptide construct for use as an interferon mimetic, comprises a cytokine receptor binding domain incorporated in a molecular scaffold.
                                               Identifying
                                                                                                                                                                                    (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding peptide associated DNA of the invention
                                                                                                                                       ADC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 52; 105pp; English
                     subjects with a high drug metabolizing rome CYP3A5 expression for establishing
by the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 5 A; 10 C; 25 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wild-type -147A oligonucleotide
                                                                                                                                                                                                                                 98GB-00028619
                                                                                                                                                                                                                                                                            99WO-GB004380
                                                                                                                                    Armstrong M
                                                                                                                                                                                                                                                                                                                                                                                                                                                           phenotype; variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%;
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Pred. No. 1.6e+
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                     phenotype whether a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
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                     associated drug will !
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                       will be
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Disclosure, Page 31; 68pp; English

Generating new antibodies specific for immunorecessive epitopes - by selection from variegated V gene library cloned from immuno:toleranc

diagnosis, purifcn. and therapy

tolerance

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RESULT 9
AAQ74160/c
ID AAQ741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC 31-mer double stranded oligonucleotides corresponding to the cytochrome CC P450 subfamily CYP3A5 5' untranslated region containing a polymorphism at CC -147 (G) or wild-type (A) sequence were used in an electrophoretic CC mobility shift assay (EMSA). The assay showed that -147 polymorphism CC transcription regulatory regions can be screened for the presence/Absence CC of a polymorphic variant, preferably at positions -475 or -147 of the DNA CC of the 5' flanking region adjacent to the CYP3A5 coding sequence. The CC variants are present in an activator protein-3 (AP-3) motif and/or a basic transcription element (BTB). The polymorphisms cause increased CC cativity. Screening for the presence of variants cause increased CC cyp3A5 gene expression and this has been linked to drug metabolic CC cativity. Screening for the presence of variants can be used to identify Cypothrome CYP3A5 expression. Primers are used which in addition to CC hybridizing to the site of interest, are capable of introducing a CP colymorphic variants. Restriction enzyme cleavage analysis can then be used to indicate the presence or absence of the variant. The methods are cused to establish, before treatment with a drug, whether the drug will be effectively metabolized by the patient, to identify compounds and CC chanscription factors that can bind to a DNA sequence encoding CYP3A5, effects of a compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                              Barsomian G,
                                                                                                                                                                 08-DEC-1993;
06-DEC-1994;
                                                                                                                                                                                                                  08-DEC-1994;
                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                  Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab; antibody; immunotolerance; animal; variegated display library; variable region; antigen; immunorecessive; cell surface marker; foetal; cancer; stem cell; variant; therapy, Alzheimer's disease; hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse heavy chain 3' amplification primer IgG2a,b RIL.
                                                             WPI; 1995-224291/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ74160 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31
                                                                                                                                                                                                                                                    15-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                  familial hypercholesterolaemia; binding affinity; ss
                                                                                                                                 (GENZ ) GENZYME CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 CAGCIGCIGCICACCIGCITITCCA 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 5 A; 15 C; 6
                                                                                              Copeland
                                                                                                                                                               93US-00164022
94US-00350400
                                                                                                                                                                                                                  94WO-US014106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%;
                                                                                              DP,
                                                                                              Hillhouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                              Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 31;
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ABZ01168/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC Primers AAQ74153-74 are a set of degenerate primers used to amplify 90% CC of the mouse kappa chain and heavy chain Fab coding sequences from CC antibodies in an immunotolerised animal. This primer binds to the 3' of CC the heavy chain coding region. The amplified products are cloned to CC produce a variegated display library (VDL) of antibody variable regions. CC The antibodies are generated by an immunotolerant individual against an CC antigen. The VDL can be used to generate an antibody against a CC immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or CC stem cell, which can differentiate between variant or related forms of CC the antigen. The antibodies generated can be used in the diagnosis, e.g. CC detection of the immunorecessive antigen, or in therapy e.g. of cancer, CC Alzheimer's disease or familial hypercholesterolaemia. The method of CC production of the antibody allows rapid and sensitive isolation of CC antibodies produced have greater binding affinity than those produced by CC combinatorial/hybridoma methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                           New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                     Wohlgemuth J, Fry K, Matcuk G, Ly N, Woodward R, Quertermous
                                                                                                                                                                                                                                                    20-OCT-2000; 2000US-0241994P 08-JUN-2001; 2001US-0296764P
                                                                                                                                                                                                                                                                                                                                                                                                                                           T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ01168 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 42
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The invention relates to a system comprises one or two isolated DNA
                                             Claim 1; Page 361; Opp; English.
                                                                                                                                         WPI; 2002-636525/68
                                                                                                                                                                                                                                                                                                                                   25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                 WO200257414-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ01168
                                                                                                                                                                                                                                                                                                 22-OCT-2001; 2001WO-US047856
                                                                                                                                                                                                                       (BIOC-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
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                                                                                                                                                                                                                       BIOCARDIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 7 A; 13 C; 13 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression
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Pred. No. 2.
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                                                                                                                                                                         Altman P, Johnson
 for detecting gene expression, we molecules that detect expression
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                                                                                                                                                                                           Phillips
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RESULT 11
AAT971807
ID AAT97187
XX AAT97
XX AAT97
XX AAT97
XX 11-MJ
XX Vacci
XX Vacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                     This 3' primer is used with a consensus 5' primer (see AAT97179) for the PCR amplification of the human T cell receptor (TCR) alpha chain extracellular domain DNA. The 3' connection for the TCR alpha chain is made after Asn-110 of the constant region of the alpha chain. The methods of the invention allow large quantities of soluble TCR to be produced in a rapid manner. Customised tumour cell vaccines comprising soluble TCR are obtained for the treatment of lymphoma and leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T cell receptor
                                                                                                                                                                                                                                                                                                                                                          Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises least 2 different recombinant variable regions of immunoglobulin molecules derived from B cell lymphoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1996;
06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
gene amplification; immunotherapy; therapy; T cell receptor; human; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT97180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT97180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                     Example 9; Page 86; 177pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-549743/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Denney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09741244-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENI-) GENITOPE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTGCGCTTCCCCTTTCCAGTTACAGCCCCAGCCTCTTCTC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 BP; 15 A; 9 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-00644664.
96US-00761277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US007039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha chain 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
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Query Match Best Local & Matches

Similarity

75.0%; 7.98;

Score 19.2; D Pred. No. 3.1e 0; Mismatches

3.1e+04;

DB 2;

Length 39;

Indels

0;

Gaps

0

Conservative

0

Sequence

39

BP;

9

A; 7 C; 9 G; 14 T; 0 U; 0 Other;

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RESULT 13
AAV16941/c
ID AAV169
XX
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AAV16931
ID AAV16
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                                                                                                                                                             Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                  PCR primers AAV16927-44 represent sense and antisense PCR primers from a degenerate pool encoding ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) large subunit pgsilon-N-methyltransferase (protein methylase II or Rubisco LSMT) peptic peptide P18 (AAW46946). Rubisco LSMT catalyses methylation of the epsilon-amine of Lys-14 in the Rubisco large subunit. Vectors containing the LSMT gene could be used to introduce the Rubisco LSMT gene into plants that do not naturally possess it, e.g. Arabidopsis thaliana. The vector could be conjugated to agents that modulate Rubisco activity in plants. Antisense molecules based on the Rubisco activity in plants. Antisense molecules based on the gene in plants as a herbicidal measure. Probes based on the Rubisco LSMT gene sequence could be used to block expression of the gene in plants as a herbicidal measure. Probes based on the Rubisco LSMT gene sequence could be used to detect homologous genes in plants other than
                                                                                                                                                                                                                           Sequence 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated pea Rubisco LSMT gene and corresponding vectors and cDNA - used for e.g. introducing the gene into plants that do not naturally have it e.g. Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rubisco large subunit epsilon-N-methyltransferase; protein methylase III; Rubisco LSMT; peptic peptide P14; modulation; Rubisco activity; herbicide; PCR primer; amplify; ss.
                    AAV16941 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Col 11-12; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-178599/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houtz RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5723752-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sense PCR primer used to amplify Rubisco LSMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV16931 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KENT ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribulose-1,5-bisphosphate carboxylase/oxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV16931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sativum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37
                                                                                                                             39 GAGCTCCACCTCCCCAGCTGCTGCCTCACCTG 70
                                                                                                 œ
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTATCAGATACCCAACTAAAAACTGGATTCAC
                                                                                               GAACTCTGCCTCCTGGTCTGCCTTACCTG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAAACAGATACGAACCTAAACTTGGATCCAC
                                                                                                                                                                                                                             BP; 9
                                                                                                                                                             7.9%;
larity 75:0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KENTUCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00391000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00391000
                                                                                                                                                                                                                           A
                    DNA;
                                                                                                                                                                                                                         14 C; 8 G; 11 T; 0 U; 0
                    42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                    ВP
                                                                                                                                                             0
                                                                                                                                                           Score 19.2; DB 2;
Pred. No. 3.2e+04;
0; Mismatches 8
                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                         Other;
                                                                                                                                                             8
                                                                                                                                                                                           Length 42;
                                                                                                                                                             Indels
                                                                                                                                                             0
                                                                                                                                                             Gaps
                                                                                                                                                             0
RESULT 14
AAX16801
ID AAX16
XX AAX16
XX AAX16
XX 27-AP
XX Pea R
XX Pea;
KW Pea;
KW epsil
KW methy
XX methy
                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primers AAV16927-44 represent sense and antisense PCR primers from a degenerate pool encoding ribulose-1.5-bisphosphate carboxylase/oxygenase (Rubisco) large subunit epsilon-N-methyltransferase (protein methylase III or Rubisco LSMT) peptic peptide P18 (AAW46946). Rubisco LSMT catalyses methylation of the epsilon-amine of Lys-14 in the Rubisco large subunit. Vectors containing the LSMT gene could be used to introduce the Rubisco LSMT gene into plants that do not naturally possess it, e.g. Arabidopsis thaliana. The vector could be conjugated to agents that modulate Rubisco activity in plants. Antisense molecules based on the Rubisco the Rubisco activity in plants. Antisense molecules based on the Rubisco LSMT gene sequence could be used to block expression of the gene in plants as a herbicidal measure. Probes based on the Rubisco LSMT gene sequence could be used to block appression of the gene in plants as a herbicidal measure.
                               Pea; rubisco; ribulose-1,5-bisphosphate carboxylase/oxygenase; primepsilon-N-methyltransferase; PCR; amplification; methyltransferase;
                                                                                                                                              AAX16801;
                                                                                                                                                                          AAX16801 standard;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42 BP; 11 A; 8 C; 14 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated pea Rubisco LSMT gene and corresponding vectors and cDNA - used for e.g. introducing the gene into plants that do not naturally have it e.g. Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rubisco large subunit epsilon-N-methyltransferase; protein methylase III; Rubisco LSMT; peptic peptide P14; modulation; Rubisco activity;
                                                                              Pea Rubisco LSMT P18-derived
                                                                                                              27-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Col 13-14; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-178599/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribulose-1,5-bisphosphate carboxylase/oxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5723752-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense PCR primer used to amplify Rubisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV16941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sativum.
                                                                                                                                                                                                                                                         35 GAACTCTGCCTCCTGGTCTGCCTTACCTG
                                                                                                                                                                                                                                                                                      39 GAGCICCACCICCCAGCIGCIGCCICACCIG 70
                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00391000
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                                                                                                                                                                          DNA;
                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                     7.9%;
75.0%;
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                                                                                                                                                                            ₽P
                                                                                                                                                                                                                                                                                                                      0;
                                                                             degenerate primer
                                                                                                                                                                                                                                                                                                                                      Score 19.2; DB 2;
Pred. No. 3.2e+04;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                     2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LWST
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Indels

0

Gaps

0

primer;

42;

US5866394-A Synthetic. Pisum sativum.

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RESULT 15
AAX16811/c
ID AAX16811 standard; DNA; 42 BF
XX
AC AAX16811;
XC Pea Rubisco LSMT P18-derived
XX Pea; rubisco; ribulose-1,5-bi
XX Pea; rubisco; ribulose-1,5-bi
XX Pea; rubisco; ribulose-1,5-bi
XX Postion-N-methyltransferase;
XX methylation; ss.
XX Synthetic.
OS Pisum sativum.
XX Pisum sativum.
XX PN US5866394-A.
XX PN US5866394-A.
XX PN US5866394-A.
XX PN US5866394-A.
XX PS 31-OCT-1996; 96US-00741931
XX PN 31-OCT-1996; 95US-00391000
XX 21-FEB-1995; 95US-00391000
XX PN HOUTZ RL;
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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42 BP; 9 A; 14 C; 8 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a primer from a degenerate pool of primers synthesised based on the peptide P18 (AAW75489) from the pea Rubisco (Ribulose-1,5-bisphosphate carboxylase/oxygenase) large subunit epsilon-N-methyltransferase (LSMT). The primer is based on the sense strand encoding the peptide P18 and is used in the isolation of the pea Rubisco LSMT from a cDNA library. The Rubisco LSMT gene encodes a protein of 489 amino acids with a predicted molecular weight of 55 kD. Recombinant Rubisco LSMT enzyme is a methyltransferase that catalyses methylation of the epsilon-amino group of Lys-14 in the large subunit of Rubisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Rubisco LSMT methyltransferase enzyme - that methylates the lysine epsilon-amino group of Rubisco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-1999.
                                                                                                                                                                                                                                                                                                                             Pea; rubisco; ribulose-1,5-bisphosphate carboxylase/oxygenase; primer; epsilon-N-methyltransferase; PCR; amplification; methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-141928/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                               Pea Rubisco LSMT P18-derived degenerate
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                                                                           (KENT ) UNIV KENTUCKY RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GAGCTCCACCTCCCCAGCTGCTGCCTCACCTG 70
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24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAACTCTGCCTCCTGGTCTGCCTTACCTG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KENTUCKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                   primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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XFFX8X00000000XX
                                                                                          Recombinant Rubisco LSMT methyltransferase enzyme - that methylates the lysine epsilon-amino group of Rubisco.
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Example 4; Col 13-14; 28pp; English.

This sequence represents a primer from a degenerate pool of primers synthesised based on the peptide P18 (AANT5489) from the pea Rubisco (Ribulose-1,5-bisphosphate carboxylase/oxygenase) large subunit epsilon-N-methyltransferase (LSMT). The primer is based on the antisense strand encoding the peptide P18 and is used in the isolation of the pea Rubisco LSMT from a CDNA library. The Rubisco LSMT gene encodes a protein of 489 amino acids with a predicted molecular weight of 55 kD. Recombinant Rubisco LSMT enzyme is a methyltransferase that catalyses methylation of the epsilon-amino group of Lys-14 in the large subunit of Rubisco

Sequence 42 BP; 11 A; 8 C; 14 G; 9 T; 0 U; 0 Other;

Query Match Best Local S Matches 24 Local Similarity 24; Conservative 75.0%; 7.98; 0 Pred. No. Score 19.2; DB 2; Mismatches 3.2e+04 Length 42; Indels 0, Gaps 0

Search completed: October Job time: 334.623 secs ۳, 2006, 00:26:40 밁 Ş

35 39

GAGCTCCACCTCCCCAGCTGCTGCCTCACCTG 70 GAACTCTGCCTCCTGGTCTGCCTTACCTG

4

Copyright

GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.

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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                         000000
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score
         20.24
20.28
20.20
20.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is derived by analysis of the total
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/put

2: /EMC_Celerra_SIDS3/ptodata/2/put

3: /EMC_Celerra_SIDS3/ptodata/2/put

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6: /EMC_Celerra_SIDS3/ptodata/2/put

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16: /EMC_Celerra_SIDS3/ptodata/2/put

16: /EMC_Celerra_SIDS3/ptodata/2/put
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Match Length DB
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18892170 seqs, 6143817638 residues
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242
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8
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                       1.6 US-11-175-859-61985
1.6 US-11-175-859-75378
1.6 US-11-175-859-75378
1.6 US-11-175-859-94006
1.7 US-10-035-833A-1473
1.7 US-10-035-833A-3970
1.8 US-11-175-859-61890
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1.8 US-11-175-859-61830
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US-10-131-827-7899
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Sequence 40976, A
Sequence 61985, A
Sequence 61985, A
Sequence 73641, A
Sequence 94006, A
Sequence 1473, Ap
Sequence 61890, Ap
Sequence 61890, A
Sequence 61890, A
Sequence 61890, A
Sequence 61890, A
Sequence 61232, Ap
Sequence 98374, A
Sequence 98374, A
Sequence 9830, A
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4 5	44	<u>4</u>	42	41	40	39	38	37	36	35	<b>3</b>	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18
18.2	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.6	18.6	18.6	18.6	18.8	18.8	18.8	19	19	19	19	19	19	19.2	19.2	19.2	19.4	19.4	19.4
7.5	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.7	7.7	7.7		7.8	7.8		7.9	7.9	7.9	7.9		7.9	7.9			8.0	8.0	8.0
24	50	50	50	50	<u>4</u> 5	45	32	29	50	50	43	43	50	50	50	50	50	50	50	50	50	50	39	39	50	50	50
11	16	16	16	16	w	w	10	7	16	ω	9	σ	16	16	16	16	16	16	12	7	7	16	ω	w	16	16	16
US-10-310-914A-116991	US-11-175-859-89058	US-11-175-859-80567	US-11-175-859-37922	US-11-175-859-3989	US-09-794-366-12	US-09-748-131B-12	US-10-939-294A-18234	US-10-084-839-3861	US-11-175-859-66081	US-09-993-346-504	US-10-186-186-2	US-10-184-508A-2	US-11-175-859-111918	US-11-175-859-58714	US-11-175-859-4623	US-11-175-859-74739	US-11-175-859-64934	US-11-175-859-13889	US-10-499-151A-46	US-10-131-827-6784	US-10-131-827-6394	US-11-175-859-102443	US-09-925-192-35	US-09-925-664-35	US-11-175-859-100374	US-11-175-859-64743	US-11-175-859-9678
		80567.		e 3989,	Sequence 12, Appl	Sequence 12, Appl	Sequence 18234, A	Sequence 3861, Ap	Sequence 66081, A	20	Sequence 2, Appli		Sequence 111918,	Sequence 58714, A	4623,	74739,	Sequence 64934, A	Sequence 13889, A	e 46, F		Sequence 6394, Ap	Sequence 102443,	Sequence 35, Appl	Sequence 35, Appl	Sequence 100374,	Sequence 64743, A	Sequence 9678, Ap

#### ALIGNMENTS

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US-11-175-859-40976
US-11-175-859-40976
Sequence 40976, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITILE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT APPLICATION NUMBER: US 60/585,352
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
UMMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
SEQ ID NO 40976
LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
US-11-175-859-40976

Query Match
Best Local Similarity 66.0%; Pred. No. 6.3e+02;
Matches 33; Conservative 1; Mismatches 16; Indels 0; Gaps
Matches 33; Conservative 1; Mismatches 16; Indels 0; Gaps
Oy

56 CTGCTGCCTCACCTGCTTTTCCAAACCCCCTGTAAACGGTAACTACA 105
Phblication No. US20040009479A1

RESULT 2
US-10-131-827-7899
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0

GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kit,
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

TITLE OF INVENTION:

CHRONIC INFLAMMATORY DISEASES

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US-11-175-859-73641/c
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; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-61985
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US-11-175-859-61985
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-7899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                 Sequence 73641, Application US/11175859 Publication No. US20060024715A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 61985, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
SEQ ID NO 73641
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Best Local
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Best Local Similarity
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                 CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
                                                                                                                                       APPLICANT: Affymetrix, Inc.

APPLICANT: Liu, Guoying et al.

TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
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CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 506612000120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity 66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                    CCACAGCATCTGCCCTACYATCTGCTCCAATACTAACCCCTGT 49
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Pred. No. 8.8e+03;
1; Mismatches 13; Indels
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Pred. No. 8.8e+03;
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FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116551
SOFTWARE: Patentin version 3.2
SEQ ID NO 75378
LENGTH: 50
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; ORGANISM: homo sapien
US-11-175-859-75378
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US-11-175-859-73641
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US-11-175-859-75378/c
                                                                                                                                 US-11-175-859-94006
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIN version 3.2
SEQ ID NO 94006
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 94006, Application US/11175859 Publication No. US20060024715A1
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APPLICANT: Affymetrix,
APPLICANT: Liu, Guoyir
                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                   APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Affymetrix, Inc. APPLICANT: Liu, Guoying et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
                                                                                                                                               TYPE: DNA ORGANISM: homo sapien
                                                                                                                                                                                LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 AAGGCTGACTRTACTGTATCAAAAAACCAAAATAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 CTGCTTTTCCAAACCCCACCCTGTAAACGGTAACTACATTTTG 110
                               69 TGCTTTTCCAAACCCCACCCTGTAAACGGTAACTACATTTT 109
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28; Conserv
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25; Conserv
                                                                                  Similarity
TGATTTTCCAGATCTTACCCTGTTYAATATATCCAGATTTT 10
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                                                                                Score 20.2; DB 16
Pred. No. 1.4e+04;
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Pred. No. 1.4e+04;
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Pred. No. 1.4e+04;
                                                                Mismatches
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                                                                                                 DB 16;
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US-10-035-833A-1473/c

GENERAL INFORMATION:

Sequence 1473, Application US/10035833A Publication No. US20040072156A1

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APPLICANT: Saito, Osamu
APPLICANT: Saito, Osamu
TITLE OF INVENTION: Detection of Genetic Polymorphisms
FILE REFERENCE: FORS-06904
CURRENT APPLICATION NUMBER: US/10/035,833A
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 7669
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3970
LENGTH: 41
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-035-833A-3970/c
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SEQ ID NO 1473
LENGTH: 41
TYPE: DNA
ORGANISM: Homo sapiens
US-10-035-833A-1473
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Best Local !
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Best Local Similarity 68.4%;
Matches 26; Conservative
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OP INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3590.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR PELICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
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APPLICANT: Sekine, Akihiro
APPLICANT: Iida, Aritoshi
APPLICANT: Iida, Aritoshi
APPLICANT: Saito, Osamu
APPLICANT: Saito, Osamu
APPLICANT: Saito, Osamu
FITLE OF INVENTION: Detection of Genetic Polymorphisms
FILE REFERENCE: PORS-06904
CURRENT APPLICATION NUMBER: US/10/035,833A
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 7669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nakamura, Yuho
APPLICANT: Sekine, Akihiro
APPLICANT: Iida, Aritoshi
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Local Similarity 68.4%;
hes 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 21 TTTTGGTCACCTGGCTGGGAGCTCCACCTCCCCAGCTG 58
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Pred. No. 1.6e+04;
1; Mismatches 11; Indels
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Pred. No. 1.6e+04
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; ORGANISM: homo sapien
US-11-175-859-61890
                                                                                                                              ; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-20305
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US-11-175-859-20305/c
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US-11-036-317-987319
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                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEG ID NOS: 116251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20305
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Affymetrix,
APPLICANT: Liu, Guoyi
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Best Local Similarity
Matches 29; Conservat
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                                                           Matches
                                                                            Query Match
Best Local :
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CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
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APPLICANT: Blume, John
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
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TYPE: DNA
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39 GAGCTCCACCTCCCCAGCTGCTGCCTCACCTGCTTTTCCAAACCCCACC 87
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                                                         l Similarity 30; Conserv
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21; Conserv
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91.3%;
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                                                     Score 19.8; DB 16;
Pred. No. 2e+04;
1; Mismatches 18;
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Pred. No. 1.6e+04;
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Pred. No. 1.7e+04;
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                                                         Indels
                                                                                            Length 50;
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GAGCTCCCCATTCTCAAGTCCTACSTGACAAGCTGATCCCAAGCAACCC

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RESULT 14
US-11-175-859-89374
; Sequence 89374, Application US/11175859
; Publication No. US20060024715A1
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                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: Homo sapiens US-10-131-827-1159
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US-10-131-827-1159/c
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US-11-175-859-61232
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Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1159
LENGTH: 50
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                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3590.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
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APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LY, NGOC
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 116251
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                                                                                                                                                                       35 CTGGGAGCTCCACCTCCCAGCTGCTGACCTGCTTTTC 76
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Pred. No. 2e+04;
1; Mismatches 18;
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                                                                                                                                                                                                                  Score 19.6; DB 7;
Pred. No. 2.3e+04;
0; Mismatches 14;
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RESULT 15
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Search completed: October Job time: 792.816 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 89374
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 96830, Application US/11175859 Publication No. US20060024715A1 GENERAL INFORMATION:
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Best Local :
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APPLICANT: Liu, Guoying et al.

TITLE OF INVENTION: Method of Analysis of Human Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
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                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 11625:
SOFTWARE: PatentIn version
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PRIOR FILING DATE: 2004-07-02
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                                                                                                                                                                                                               LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
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Pred. No. 2.3e+04;
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Pred. No. 2.3e+04;
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#### SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%, length 10-241 nt.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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Post-processing: Minimum Match 0% | VL B
Maximum Match 100%
Listing first 35 summaries
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Perfect score:
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236
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                                US-11-348-413-1113015
US-11-217-229-168000
US-11-379-168000
US-11-078-073-81
US-11-078-073-83
US-11-078-073-83
US-11-078-073-85
US-11-078-073-86
US-11-078-073-86
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US-11-078-073-86
US-11-323-061-4
US-11-323-507-43
US-11-233-507-43
US-11-233-507-15
US-11-333-507-15
US-11-333-507-15
US-11-333-507-15
US-11-333-507-15
US-11-333-507-15
US-11-333-507-15
US-11-333-697-1540
US-11-321-991-8
US-11-321-991-8
US-11-321-991-8
US-11-325-139A-6881
US-11-320-097-1540
US-11-30-097-1541
US-11-30-097-1542
US-11-370-084-7274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications NA. News
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(without alignments)
333.232 Million cell updates/sec
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Sequence 82, Appl
Sequence 83, Appl
Sequence 84, Appl
Sequence 86, Appl
Sequence 86, Appl
Sequence 2014, Appl
Sequence 2014, Appl
Sequence 4, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 857, Appl
Sequence 857, Appl
Sequence 15001, Appl
Sequence 15001, Appl
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15, Appl
11320, A
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11320, App
14193, App
5018, App
5018, Appli
6881, Appli
6882, Appli
11764, Ap
1540, Ap
1541, App
1542, Ap
7274, Appli
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APPLICANT: Wyeth
APPLICANT: Myeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Olmsted, Stephen
IITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR RPLICATION NUMBER: PCT/US05/035471
PRIOR RPLICATION NUMBER: US 11/243,445
PRIOR RILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR APPLICATION DATE: 2004-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
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US-11-217-529-168000/c
US-91-11-217-529-168000, Application US/11217529
; Publication No. US20060099612A1
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-168000
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CTHER INFORMATION: SEQ ID NO: 14059; WANOIUQ4A_at;
CTHER INFORMATION: 0000000000000
US-11-348-413-1113015
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US-11-348-413-1113015/c
                                                                                   PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 168000
LENGTH: 25
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CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAOURA, NORIHISA
APPLICANT: NAKAOURA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
TITLE OF INVENTION: METHODS FOR ANALYZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial FEATURE: OTHER INFORMATION: probe
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cal Similarity 87.0%;
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US-11-177-646-509
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Pred. No. 4.6;
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Sequence 509, App
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US-11-348-413-779975
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               CURRENT APPLICATION NUMBER: US/11/078,073
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US 60/552,620
PRIOR FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US 60/559,824
PRIOR FILING DATE: 2004-04-05
PRIOR FILING DATE: 2004-04-05
PRIOR APPLICATION NUMBER: US 60/647,191
PRIOR APPLICATION NUMBER: US 60/647,191
PRIOR FILING DATE: 2005-01-25
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Best Local Similarity
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Best Local (
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PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 779975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT FILING DATE: 2006-02-07
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
                                                                                                                                                                                   APPLICANT: de Fougerolles, Antonin
APPLICANT: Frank-Kameneteky, Maria
APPLICANT: Manoharran, Muthiah
APPLICANT: Rajeev, Kallanthottathil G.
APPLICANT: Hadwiger, Philip
TITLE OF INVENTION: IRNA AGENTS TARGETING
FILE REFERENCE: 14174-085001
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PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
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LOCATION: (1)..(25)
COTHER INFORMATION: SEQ ID NO: 5002; WANO1PA72_at; Start 23; Stop
OTHER INFORMATION: 00000100000000
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OTHER INFORMATION: probe
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ORGANISM: Artificial
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Pred. No. 5.6;
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Pred. No. 5.6;
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APPLICANT: Hadwiger, Philipp
TITLE OF INVENTION: IRNA AGENTS TARGETING VEGF
FILE REFERENCE: 14174-085001
CURRENT APPLICATION NUMBER: US/11/078,073
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US 60/552,620
PRIOR FILING DATE: 2004-03-12
PRIOR PILING DATE: 2004-04-05
PRIOR APPLICATION NUMBER: US 60/559,824
PRIOR APPLICATION NUMBER: US 60/647,191
PRIOR PILING DATE: 2004-04-05
PRIOR APPLICATION NUMBER: US 60/647,191
PRIOR FILING DATE: 2005-01-25
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; ORGANISM: Homo
US-11-078-073-82
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; ORGANISM: Homo sapiens
US-11-078-073-81
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82
LENGTH: 23
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Publication No. US20060094032A1
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Best Local Similarity
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LENGTH: 23
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CURRENT APPLICATION NUMBER: US/11/078,073
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US 60/552,620
PRIOR FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US 60/559,824
PRIOR APPLICATION NUMBER: US 60/559,824
PRIOR FILING DATE: 2004-04-05
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APPLICANT: Frank-Kamenets
APPLICANT: Manoharan, Muti
                                                                                                                                                                                                                        APPLICANT: de Fougerolles, Antonin
APPLICANT: Frank-Kamenetsky, Maria
APPLICANT: Manoharan, Muthiah
APPLICANT: Rajeev, Kallanthottathil G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/647,191 PRIOR FILING DATE: 2005-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rajeev, Kallanthottathil G.
APPLICANT: Hadwiger, Philipp
TITLE OF INVENTION: IRNA AGENTS TARGETING VEGF
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94.7%;
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Pred. No. 5
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Pred. No. 5
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US-11-078-073-84/c
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          APPLICANT: Frank-Kamenetsky, Maria
APPLICANT: Manoharan, Muthiah
APPLICANT: Manoharan, Muthiah
APPLICANT: Hadwiger, Kallanthottathil G.
APPLICANT: Hadwiger, Philip
TITLE OF INVENTION: IRNA AGENTS TARGETING VE.
FILE REFERENCE: 14174-085001
CURRENT APPLICATION NUMBER: US/11/078,073
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US 60/552,620
PRIOR APPLICATION NUMBER: US 60/559,824
PRIOR APPLICATION NUMBER: US 60/559,824
PRIOR APPLICATION NUMBER: US 60/559,824
PRIOR APPLICATION DATE: 2004-03-12
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LENGTH: 23
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LENGTH: 23
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Best Local Similarity
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US 60/559,824
PRIOR FILING DATE: 2004-04-05
PRIOR APPLICATION NUMBER: US 60/647,191
PRIOR FILING DATE: 2005-01-25
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2005-03-11
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APPLICANT: Frank-Kamenetsky, Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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TYPE: RNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/647,191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hadwiger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manoharan, Muthiah
                                                                                                                                                                                                                                                                                                          Application US/11078073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frank-Kamenetsky, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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94.78;
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Pred. No. 5.4;
                                                                                                                                                        VEGF
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Sequence 86, Application US/11078073

Publication No. US20060094032A1

GENERAL INFORMATION:
APPLICANT: de Fougerolles, Antonin
APPLICANT: Frank-Kamenetsky, Maria
APPLICANT: Manoharan, Muthiah
APPLICANT: Rajeev, Kallanthottathil G
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-80
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APPLICANT: Hadwiger, Philipp
TITLE OF INVENTION: IRNA AGENTS TARGETING VE
FILE REFERENCE: 14174-085001
CURRENT APPLICATION NUMBER: US/11/078,073
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US 60/552,620
PRIOR FILING DATE: 2004-03-12
PRIOR PRIOR PHILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US 60/559,824
PRIOR APPLICATION NUMBER: US 60/559,824
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LENGTH: 23
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Matches
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LENGTH: 23
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PRIOR FILING DATE: 2004-04-05
PRIOR APPLICATION NUMBER: US 60/647,191
PRIOR FILING DATE: 2005-01-25
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CURRENT APPLICATION NUMBER: US/11/078,073
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US 60/552,620
PRIOR FILING DATE: 2004-03-12
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NUMBER OF SEQ ID NOS: 1061
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: IRNA AGENTS TARGETING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: de Fougerolles, Antonin
APPLICANT: Frank-Kamenetsky, Mari
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                              148 CCTTCTCCTTCTGCCATG 165
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18; Conserv
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                                                                                                                                                                Rajeev, Kallanthottathil G.
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Pred. No. 5.4;
0; Mismatches
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Pred. No. 7
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FILE REFERENCE: 17929-002001

CURRENT APPLICATION NUMBER: US/11/323,061

CURRENT FILING DATE: 2005-12-30

PRIOR APPLICATION NUMBER: US 60/640,707

PRIOR FILING DATE: 2004-12-30

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 22
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US-11-323-061-4
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GENERAL INFORMATION:
APPLICANT: Brennan, Mark David
APPLICANT: Condra, Jodi Ann
Amv Tabb
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Best Local Similarity 94.4%;
Matches 17; Conservative
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APPLICANT: EXPRESSION DIAGNOSTICS, INC.
                                                                                                                                                                                                                                                                             Sequence 2014, Application US/10511937 Publication No. US20060088836A1
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APPLICANT:
APPLICANT:
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APPLICANT: Massey, Amy Tabb
APPLICANT: Wei, Mei
APPLICANT: Neibergs, Holly
TITLE OF INVENTION: GENETIC MARKERS OF SCHIZOPHRENIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/647,191 PRIOR FILING DATE: 2005-01-25
                 APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                  APPLICANT:
PRIOR APPLICATION NUMBER: PCT/US2003/012946
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OTHER INFORMATION: Primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                 Woodward, Robert
                                                                                                                                                                                                      Fry, Kirk
                                                                                                                                                                                                                     Wohlgemuth, Jay
                                                                                                                                                                 Ly, Ngoc
                                                                                                                                                Prentice, James
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Pred. No. 7
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Pred. No. 9;
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; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR ETILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PATENTIN VERSION 3.2
; SEQ ID NO 2014
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; ORGANISM: Homo sapiens
US-10-511-937-2014
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                                                                                                                     GENERAL INFORMATION:
APPLICANT: Ommen van, Garrit-Jan B.
APPLICANT: Deutekom van, Judith C.T.
APPLICANT: Dunnen den, Johannes T.
APPLICANT: Aartsma-Rus, Annemieke
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                             Sequence 43, Application US/11233507
Publication No. US20060099616A1
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SEQ ID NO 6
LENGTH: 20
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APPLICANT: Saidman, Shlomo
APPLICANT: Saidman, Shlomo
APPLICANT: Evron, Tama
TITLE OF INVENTION: Antisense Oligonucleotide Against Human Acetylcholinesterase
TITLE OF INVENTION: (AChE) and uses thereof
TILE REFERENCE: 13122/US/01
CURRENT APPLICATION NUMBER: US/11/346,145
CURRENT FILING DATE: 2006-02-01
PRIOR APPLICATION NUMBER: IL 143379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
                                                           APPLICANT: Aartsma-Rus, Annemieke TITLE OF INVENTION: Modulation of exon recognition in pre-mRNA by TITLE OF INVENTION: interfering with the secondary RNA structure FILE REFERENCE: P63917US00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/IL02/00411
PRIOR FILING DATE: 2002-05-23
CURRENT APPLICATION NUMBER: US/11/233,507 CURRENT FILING DATE: 2005-09-21 PRIOR APPLICATION NUMBER: PCT/NL2004/00196
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Pred. No. 9.
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PRIOR APPLICATION NUMBER: 09/857,123
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: GB98263593
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 35
LENGTH: 20
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US-10-511-937-857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: h59AON2
US-11-233-507-43
                                                                                                                                                                        Sequence 857, Appli
Publication No. US2
GENERAL INFORMATION
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
                                                                                                       APPLICANT:
APPLICANT:
                                                                      APPLICANT:
                                                                                                                                                        APPLICANT: EXPRESSION DIAGNOSTICS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/223,738
CURRENT FILING DATE: 2005-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SANSEAU, Philippe
APPLICANT: TATE, SIMON NICHOLAS
TITLE OF INVENTION: HUMAN VANILLOID RECEPTORS AND THEIR USES
FILE REFERENCE: PG3606D1
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PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.1
EQ ID NO 43
       TITLE OF INVENTION:
                                        APPLICANT:
                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                      115 CTGCTCCCACTCTTGC 130
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                                                                                                                                                                                                                                                                                            2 CTGCTCCCATTCTTGC 17
                                                                                           Fry, Kirk
Woodward, Robert
                                                                                                                         Wohlgemuth, Jay
Fry, Kirk
Morris, MacDonald
Rosenberg, Steven
RENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
PENTION: AND MONITORING TRANSPLANT REJECTION
                                                                                      Ly, Ngoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/11223738
                                                                      Prentice, James
                                                                                                                                                                                        Application US/10511937 o. US20060088836A1
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Pred. No. 12;
0; Mismatches
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Pred. No. 9.
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Best Local Similarity
Matches 16; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GENSET 020CP1
CURRENT APPLICATION NUMBER: US/11/370,584
CURRENT FILING DATE: 2006-03-08
PRIOR APPLICATION NUMBER: US/10/349,143
PRIOR FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: US 09/298,850
PRIOR APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: US 60/082,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-370-584-10001/c
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CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR PRIOR FILING DATE: 2002-04-24
PRIOR PRIOR PRIOR DATE: 2002-04-24
PRIO
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SEQ ID NO 10001
LENGTH: 19
                                                                                                                                              Matches
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Best Local Similarity
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LENGTH: 19
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TITLE OF INVENTION: Biallelic markers for use
TITLE OF INVENTION: density...
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                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..19
                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: downstream amplification primer 99-8732 for SEQ 2136, OTHER INFORMATION: in complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
                                         209 CATGCTTCTTGTTCTGTCT 227
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CTTACTTCTTGTTGTCT 1
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Pred. No. 12;
0; Mismatches
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Pred. No. 1:
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RESULT 18 US-11-233-507-15 ; Sequence 15, Application US/11233507

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APPLICANT: Ommen van, Garrit-Jan B.
APPLICANT: Deutekom van, Judith C.T.
APPLICANT: Dunnen den, Johannes T.
APPLICANT: Dunnen den, Johannes T.
APPLICANT: Aartsma-Rus, Annemieke
TITLE OF INVENTION: Modulation of exon recognition in pre-mRNA by
TITLE OF INVENTION: interfering with the secondary RNA structure
FILE REFERENCE: P63917US01
CURRENT APPLICATION NUMBER: US/11/233,495
CURRENT PILING DATE: 2005-09-21
PRIOR APPLICATION NUMBER: PCT/NL2003/00214
PRIOR APPLICATION NUMBER: PCT/NL2003/00214
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NO 7
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
CTUERE TEPOENTION: MAIONI
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TITLE OF INVENTION: Modulation of exon recognition in pre-m
TITLE OF INVENTION: interfering with the secondary RNA str
TILE OF INVENTION: interfering with the secondary RNA str
TILE OF INVENTION: interfering with the secondary RNA str
TILE OF INVENTION NUMBER: US/11/233,507
CURRENT FILING DATE: 2005-09-21
PRIOR APPLICATION NUMBER: PCT/NL2004/00196
PRIOR FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: PCTPCT/NL03/00214
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-03-21
VUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 19
TYPB: RNA
ORGANISM: Artificial Sequence
FEATURE:
US-11-370-584-11320
; Sequence 11320, Application US/11370584
; Publication No. US20060177863A1
                                                                       RESULT 20
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US-11-233-495-7
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Best Local s
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APPLICANT: Deutekom vi
APPLICANT: Dunnen den
APPLICANT: Aartsma-Ru
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Best Local :
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                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: h41AON1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: h41AON1
                                                                                                                                                                                                              6.0%;
Local Similarity 47.4%;
les 9; Conservarion
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Local Similarity 47.4%;
les 9; Conservarion
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                                                                                                                                    Ommen van, Garrit-Jan B.
Deutekom van, Judith C.T.
Dunnen den, Johannes T.
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                                                                                                                                                                                                                                           Score 14.2;
Pred. No. 12;
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Pred. No. 12;
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FILE REPERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/11/370,584
CURRENT FILING DATE: 2006-03-08
PRIOR APPLICATION NUMBER: US/10/349,143
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR APPLICATION NUMBER: US 09/298,850
PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: US 60/082,614
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US-11-043-842-740
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US-11-043-842-740
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APPLICANT: COMPUSED Ltd
APPLICANT: COMPUSED Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 1847.1004
CURRENT APPLICATION NUMBER: US/11/043,842
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1028
SEQ ID NO 740
LENGTH: 20
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Publication No. US20060183131A1
                                                                                                    Matches
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APPLICANT: Blumenfeld, Ma
APPLICANT: Chumakov, Ilya
                                                                                                                                                                                                                                                      ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: downstream amplification OTHER INFORMATION: in complement
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LOCATION: 1..20
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                                                                                                  Local Similarity
nes 16; Conserv
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                                             112 CTCCTGCTCCCACTCTTGC 130
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16; Conserv
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Pred. No. 1:
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Pred. No. 1
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RESULT 22 US-11-370-584-4193/c ; Sequence 4193, Application US/11370584 ; Publication No. US20060177863A1

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APPLICANT: HELIX RESEARCH INSTITUTE
FILE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5018
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
RESULT 24
US-11-321-991-8
, Sequence 8, Application US/11321991
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FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION UNMER: US/11/370,584
CURRENT FILING DATE: 2006-03-08
PRIOR APPLICATION NUMBER: US/10/349,143
PRIOR FILING DATE: 2003-01-21
PRIOR PELICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR PELICATION NUMBER: US 09/298,850
PRIOR PELICATION NUMBER: US 09/298,850
PRIOR PELICATION NUMBER: US 09/298,850
PRIOR PELICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: US 60/082,614
PRIOR APPLICATION NUMBER: US 60/082,614
PRIOR PILING DATE: 1998-104-21
PRIOR PILING DATE: 1998-104-21
PRIOR PILING DATE: 1998-04-21
                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized
US-11-293-697-5018
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LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-13878 for SEQ
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TYPE: DNA
ORGANISM: Homo Sapiens
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15; Conserv
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Pred. No. 1
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Pred. No. 1;
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US-11-255-139A-6882/c
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US-11-255-139A-6881/c
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                                                                                                                                 Sequence 6882, Application US/11255139A Publication No. US20060154271A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 14; Conserv
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CURRENT APPLICATION NUMBER: US/11/255,139A
CURRENT FILING DATE: 2005-10-20
NUMBER OF SEQ ID NOS: 8014
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT PPLICATION NUMBER: US/11/255,139A
CURRENT FILING DATE: 2005-10-20
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CURRENT FILING DATE: 2005-12-29
PRIOR APPLICATION NUMBER: US/11/024,426
PRIOR FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 09/146,893
PRIOR FILING DATE: 1998-09-03
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APPLICANT: PAPACONSTANTINOU, JOHN
TITLE OF INVENTION: HYALIRONATE SYNTHASE GENES AND USES THEREOF
FILE REFERENCE: 35541.069
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
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Pred No. 13
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Pred. No. 13;
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Sequence 1540, Application US/11102097
Publication No. US20060160759A1
GENERAL INFORMATION:
APPLICANT: Chen, et al.
TITLE OF INVENTION: Influenza Therapeutic
FILE REFERENCE: 049261-0621
CURRENT APPLICATION UMMBER: US/11/102,097
CURRENT FILING DATE: 2005-04-08
NUMBER OF SEQ ID NOS: 2926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANTON: density...
FILTE OF INVENTION: density...
FILTE OF INVENTION: density...
FILTE REFRENCE: GENSET.020CP1
CURRENT FILLING DATE: 2006-03-08
PRIOR APPLICATION NUMBER: US/10/349,143
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILLING DATE: 1999-10-20
PRIOR PRILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 09/298,850
PRIOR PILLING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/092,614
PRIOR APPLICATION NUMBER: US 60/082,614
PRIOR FILLING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: US 60/082,614
PRIOR APPLICATION NUMBER: US 60/082,614
PRIOR FILLING DATE: 1998-04-21
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US-11-102-097-1540
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Matches
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LENGTH: 17
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SEQ ID NO 11764
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SOFTWARE: PatentIn version
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  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: downstream amplification
OTHER INFORMATION: complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
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Patent In
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version
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Pred. No. 13;
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Pred. No. 1
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APPLICANT: Chen, et al.
TITLE OF INVENTION: Influenza Therapeutic
FILE REFERENCE: 0492611-0621
CCURRENT APPLICATION NUMBER: US/11/102,097
CURRENT FILING DATE: 2005-04-08
NUMBER OF SEQ ID NOS: 2926
SOFTWARE: Patentin version 3.2
SEQ ID NO 1542
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit; OTHER INFORMATION: influenza virus.
US-11-102-097-1540
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US-11-102-097-1542
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US-11-102-097-1541
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 1541
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Best Local Similarity
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            Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/11/102,097
CURRENT FILING DATE: 2005-04-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chen, et al. TITLE OF INVENTION: Inf
                                                                           OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit OTHER INFORMATION: influenza virus.
                                                                                                        TYPE: DNA
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit OTHER INFORMATION: influenza virus.
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ORGANISM: Artificial
FEATURE:
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Score 13.4; D
Pred. No. 15;
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Pred. No. 15;
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; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-11-268-341-1
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US-11-370-584-7274/c
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PRIOR FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR APPLICATION NUMBER: US/09/298,850
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US/60/109,732
PRIOR FILING DATE: 1998-11-23
                                                   APPLICANT: AIN1, Ideris
APPLICANT: Hamzah, Hairul Aini
APPLICANT: Hamzah, Hairul Aini
TITLE OF INVENTION: (IBDY) STRAINS BY MOLECULAR BIOLOGY METHOD
FILE REFERENCE: $1436.70010US00
CURRENT FILING DATE: 2005-11-07
PRIOR APPLICATION NUMBER: WS/11/268,341
CURRENT FILING DATE: 2005-11-07
PRIOR APPLICATION NUMBER: MY PI 20044610
PRIOR APPLICATION NUMBER: MY PI 20044610
PRIOR FILING DATE: 2004-11-05
NUMBER OF SEQ ID NOS: 6
SOPTWARE: Patentin version 3.3
SEQ ID NO 1
LENGTH: 18
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Best Local Similarity
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SEQ ID NO 7274
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Publication No. US20060177863A1
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APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high
TITLE OF INVENTION: density...
FILE REFERENCE: GENSET 020CP1
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Omar, Abdul Rahman
APPLICANT: Hair-Bejo, Mohd
APPLICANT: Aini, Ideris
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NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification
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Pred. No. 19
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US-11-293-697-5010
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US-11-255-139A-3650/c
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                                                               Query Match
Best Local S
Matches 14
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PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5010
LENGTH: 18
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
CURRENT FILING DATE: 2005-12-05
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Best Local Similarity
Matches 15; Conserv
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Publication No. US20060154271A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/11/255,139A
CURRENT APPLICATION NUMBER: US/11/255,139A
CURRENT FILLING DATE: 2005-10-20
NUMBER OF SEQ ID NOS: 8014
                                                                                                                                                     TYPE: DNA
ORCANISM: Artificial Sequence
FEATURE:
FEATURE:
ORCANISM: Description
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ORGANISM: Homo sapiens
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                   134 AGACACCTGCTCCCCC 149
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ACACACCTGCTCCCAC 18
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RESULT 35 US-11-177-646-509 ; Sequence 509, Application US/11177646

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GENERAL INFORMATION:
APPLICANT: AGAN, ERIAN
APPLICANT: AGAN, ERIAN
APPLICANT: AGAN, ERIAN
APPLICANT: STENGER, DAVID
APPLICANT: STENGER, DAVID
APPLICANT: STENGER, DAVID
APPLICANT: TIBETTS, CLARK
APPLICANT: TIBETTS, CLARK
APPLICANT: WANGER, DAVID
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Maximum Match 100%

Listing first 11 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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                                              Jadhav, V.
Patent: W
                                                                             synthetic construct synthetic construct other sequences.
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CS155924
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ACCESSION: CS155924
ACCESSION: AR118904
ACCESSION: BD089856
ACCESSION: BD089856
ACCESSION: AR207191
ACCESSION: AR207191
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Sequence 58 from Patent WO0129262.
AX114935
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Patent: WO 0129262-A 58 26-APR-2001;
Orchid BioSciences, Inc. (US)
Location/Qualifiers
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Sequence 114 from Patent
CS155923
CS155923.1 GI:74271071
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                                                                                                    /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/db_xref="taxon:32630"
/note="Synthetic"
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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CS155866/c
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Sequence 57 from Patent WO2005078097.
CS155866
CS155866.1 GI:74271014
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Patent: WO 2005078097-A 57 25-AUG-2005;
Sirna Therapeutics, Inc. (US)
Location/Qualifiers
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Sirna Therapeutics, Inc. (US)
Location/Qualifiers
Unclassified.
1 (bases 1 to 20)
Uchida, K., Uchida, T., Tanaka, Y., Matsuda, Y. and Kondo, S.
                                   Unknown.
                                                                                    Sequence 30 from patent US
AR118904
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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/mol_type="unassigned RNA"
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Patent: JP 2001321190-A 2100 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEWICAL RESEA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/2100
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
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                                                                                               Synthetic at 1p36.
AB068203
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 Watanabe, N.,
             Chen, Y.Z.,
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/mol_type="genomic DNA"
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Location/Qualifiers
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             Hayashi,Y.,
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  Maekawa, K.,
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Bennett, C.Frank. and Cowsert, L.M.
Antisense modulation of talin expression
Patent: US 6372492-A 85 16-APR-2002;
Location/Qualifiers
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                                                                                                   Sequence 285 from Patent AX590845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 85 from patent AR207191
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A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1,935-p36
Genomics 74 (1), 55-70 (2001)
Cookson, W.O., Moffat, M.F., Allen, M. and Lench, N.
                                           synthetic construct synthetic construct
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                          Sugimoto,Y., Thara,N. and Takasuga,A.
Direct Submission
Submitted (04-MAR-2004) Yoshikazu Sugimoto, Shirakawa Institute of Animal Genetics; Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan (E-mail:kazusugi@siag.or.jp, Tel:81-248-25-5641,
                                                                                                                                                                                                                                                                                                                                                                                                                    Ihara,N., Takasuga,A., Mizoshita,K., Takeda,H., Sugimoto,M.,
Mizoguchi,Y., Hirano,T., Itoh,T., Watanabe,T., Reed,K.M.,
Sneiling,W.M., Kappes,S.M., Beattie,C.W., Bennett,G.L. and
Sugimoto,Y.
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                                                                                                                      /note="reverse primer for microsatellite DIK4617"
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/db_xref="taxon:32630"
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AR405844 Sequence
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                                                                           source
                                                                                          Clarke, J.H.

Direct Submission

Submitted (33-JUN-2003) Clarke J.H., John Innes Centre, Colney

Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a
single line, ET an enhancer trap dissociation transposon, GT a gene
trap dissociation transposon, MT a mis-expressor mutator
transposon. 3 denotes a sequence derived from the 3'end of the
transposon, 5 denotes a sequence derived from the 5'end of the
transposon BESRC GARNet, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: N123009.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Langham, S.,
Unpublished
                                                                                                                                                                                                                                                               EX545753.1 GI:32168986
STS; STS, sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                       Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Walsh, S., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
                                                                                                                                                                                                                                                                                                                                    tagged site.
BX545753
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Arabidopsis thaliana transposon insertion STS SM_3.36298, sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
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/variety="Columbia-0 NASC stock code
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                                                                                                                                                                                                                                             Bowles, B.,
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AR682631
CQ970252
AX516265
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CQ002636
AR682820
AX516639
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AX573414
AX746300
AR238006
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AX573414 Sequence
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AX746300 Sequence
AX746300 Sequence
E25630 RNA-DNA chi
AR682371 Sequence
CQ004681 Sequence
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I05520 Sequence
E29443 Oligonucleo
I05520 Sequence
AX682820 Sequence
AX618800 Sequence
AX518603 Sequence
AX518603 Sequence
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57 Method of
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                            Similarity 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura,Y., Sekine,A., Iida,A. and Sai
Detection of genetic polymorphisms
Patent: WO 02052044-A 2870 04-JUL-2002;
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="unassigned DN/
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                            Score 21.6; DB 2;
Pred. No. 4e+05;
1; Mismatches 10;
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Best Local Similarity 76.5%;
Matches 26; Conservative
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                                          Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:10114"
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                                                                                                       /organism="unknown"
/mol_type="genomic DNA"
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76.5%;
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TGCTCTTCCTTCATCTTCCRCCATGATTGTGAGGCCCC
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PN JP 2002514913-A/9
PD 21-MAY-2002
PF 18-DEC-1997 JP 1998528049
PR 19-DEC-1996 US 60/033684,08-AUG-1997 US
PR 18-AKER
PC C12N15/09,712M1/00,712Q1/68,712N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers. Eukaryota; Metazoa; Chordata; Craniata; Vertek Mammalia; Eutheria; Euarchontoglires; Glires; Sciurognathi; Muroidea; Muridae; Murinae. 49 bp DNA Bioreactive allosteric polynucleotide. החופהכי Bioreactive allosteric polynucleotides Patent: US 6630306-A 9 07-OCT-2003; Yale University; New Haven, CT Score 21.2; DB 2; Pred. No. 5.1e+05; 0; Mismatches 8 Score 21.2; DB 2; Pred. No. 5.1e+05; 0; Mismatches 8 DNA N 8 Vertebrata; Eut lires; Rodentia; Length Length 49; Indels linear Indels linear S 49; 60/055039 PAT PAT Euteleostomi; 0 0, 18-DEC-2003 Gaps Gaps PI 0; 0

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RESULT 8
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Sequence
141116
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Noonberg, S.B. and Hunt, C. Anthony.
In vivo oligonucleotide generator, and methods of testing the binding affinity of triplex forming oligonucleotides derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
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Noonberg, S.B. and Hunt, C. Anthony.
In vivo oligonuclectide generator, and methods of binding affinity of triplex forming oligonuclectic
                                                                                                                                                                                                                                                 Patent: US 5624803-A 20 29-APR-1997;
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   Homo sapiens (human)
                        CQ004290.1 GI:41010922
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ilarity 78.1%;
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                                                                                                                                                                                                       /organism="unknown"
/mol_type="unassigned
                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 6.9e+05;
0; Mismatches 7
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Pred. No. 6.9e+05;
0; Mismatches 7;
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AR147108/c
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Sequence 21
AR147108
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Sequence
AR681155
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1 (bases 1 to 45)
Cochran, M.D. and Junker, D.E.
Recombinant swinepox virus
                                 Unknown.
Unclassified.
                                                       Unknown
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Wohlgemuth, J., Fry, K., Woodward, R. and I Wohlgemuth, J., Fry, K., Woodward, R. and I Methods and compositions for diseases and chronic inflammatory diseases Patent: US 6905827-A 584 14-JUN-2005; Expression Diagnostics, Inc.; So. San Fx Location/Qualifiers
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Mammalia; Eutheria;
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45 bp |
210 from patent US 6221361
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/mol_type="unassigned DN
/db_xref="taxon:9606"
                                                                                                                                                                                                           /organism="unknown"
/mol_type="genomic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Nucleotide deleted between
Accession number cg43976335"
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Pred. No. 1.6e-
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Pred. No. 1.3e+06;
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AR158296/c
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AR267871/c
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AR267871
AR267871.1
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AR158296
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Cochran,M.D. and Junker,D.E.
Recombinant swinepox virus
Patent: US 6497882-A 210 24-DEC-2002;
Syntro Corporation; San Diego, CA
Location/Qualifiers
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Location/Qualifiers
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Cochran, M.D. and Junker, D.E.
Recombinant swinepox virus
Patent: US 6251403-A 210 26-JUN-2001;
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/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
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                                               Score 19.4; DB 2;
Pred. No. 1.8e+06;
0; Mismatches 11;
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Pred. No. 1.8e+06;
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AR684817
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AR684983
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AR365906
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Sequence
AR684983
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1 (bases 1 to 50)

1 (bases 1 to 50)

Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.

Wethods and compositions for disgnosing or monitorial and chronic inflammatory diseases

Patent: US 6905827-A 4246 14-JUN-2005;

Expression Diagnostics, Inc.; So. San Francisco, CA

Location/Qualifiers
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Cochran,M.D. and Junker,D.E.
Recombinant swinepox virus
Patent: US 6328975-A 210 11-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown.
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Location/Qualifiers
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nilarity 70.3%;
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210 from patent US 6
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
                                   GI:74466753
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Pred. No. 1.8e+06;
0; Mismatches 6,
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Pred. No. 1.8e+06;
0; Mismatches 11
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Unclassified.

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AUTHORS Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.
TITLE Methods and compositions for disposing or monitoring auto immune and chronic inflammatory diseases

JOURNAL Patent: US 6905827-A 4412 14-JUN-2005;
EXPRESSION Diagnostics, Inc.; So. San Francisco, CA

FEATURES

SOURCE

1. 50

/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

OUERY Match
Best Local Similarity 79.3%; Pred. No. 1.8e+06;
Best Local Similarity 79.3%; Pred. No. 1.8e+06;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps Db

10 TTCTCCTGCTTCCACTTCTGCATGAGACA 138

Db

11 TTATCCTGCTTCCACTTATAGCATGAATCA 41

Search completed: October 1, 2006, 01:33:51

Job time: 1977.39 secs
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## GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:36:33; Search time 0.001 Seconds (without alignments) 696.476 Million cell updates/sec

Title: Perfect score: US-10-642-946-6\_1967-2208 242

ttctccagcacagcactgga.....ccaactaaaactggattcac 242

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 0.5

Searched: 79 seqs, 1439 residues

Total number of hits satisfying chosen parameters:

Jssud-Patents - NA

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 79 summaries

Database : issdb1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

US-09-396-196G-18892

Sequence 18892, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Mack

INFORMATION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT APPLICATION UNMBER: 09-15

PRIOR APPLICATION UNMBER: 60/100,678

PRIOR APPLICATION UNMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FRASTSEQ for Windows Version 4.0

SEQ ID NO 18892

TENET: DATE: 198 ; TYPE: DNA ; ORGANISM: Mus musculus US-09-396-196G-18892

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RESULT 3
US-10-085-612A-23
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-768
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                            APPLICANT: PETFOS, WILLIAM
APPLICANT: Colvin, Oliver
APPLICANT: Vredenburgh, James
APPLICANT: Vredenburgh, James
APPLICANT: Warks, Jeffrey
TITLE OF INVENTION: METHODS FOR EVALUATING THE ABILITY TO METABOLIZE PHARMACEUTICALS
FILE REFERENCE: DNA-5-C1
CURRENT APPLICATION NUMBER: US/10/085,612A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR APPLICATION NUMBER: 60/771,630
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VETBION 3.2
SEQ ID NO 23
LENGTH: 22
TYPE: NNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 768
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Best Local
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Patent No. 6929912
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APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
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                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lander, Eric
ORGANISM: Homo sapiens
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l Similarity 81.0%;
17; Conservation
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Ireland, James S.
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87.0%;
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Pred. No. 4.7;
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                                        US-09-526-193A-240
                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/124,702
PRIOR FILING DATE: 1999-03-15
PRIOR PELICATION NUMBER: 60/138,048
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/151,977
PRIOR FILING DATE: 1999-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 240, Application US/0:
Patent No. 6617122
GENERAL INFORMATION:
APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, An;
APPLICANT: Pimstone, Simon N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 262, Application No. 6514694
GENERAL INFORMATION:
                                                                                                            NUMBER OF SEQ ID NOS: 287
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 240
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 262
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Query Match
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                                                                                                                                                                                                                                                                                                                APPLICANT: Pimstone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
TITLE OF INVENTION: CHOLESTEROL LEVELS
FILE REFERENCE: 50110/002005
CURRENT APPLICATION NUMBER: US/09/526,193A
CURRENT FILING DATE: 2000-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/216,393B
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THERF
FILE REFERENCE: TX-1-C2
                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial sequence FEATURE:
                                                                                            LENGTH:
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18; Conserv
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Pred. No. 12;
0; Mismatches
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Pred. No. 11;
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Best Local Similarity

6.3%; 85.0%;

Score 15.2; Pred. No. 13;

DB 1;

Length 21;

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US-09-617-871-32
                                                                                                                       RESULT 7
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            # Sequence 32, Applic
# Patent No. 6355434
# GENERAL INFORMATIO
# APPLICANT: Draz
# APPLICANT: In M
# APPLICANT: Asan
                                                                                                                                                                                                                                                                                         US-08-846-020A-32
                                                                                                                                                                                                                                             Query Match
Best Local :
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GENERAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 248 4000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JAITEL Ph.D., Brenda H.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 0092662
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "primer" IMMEDIATE SOURCE: CLONE: Exon 9 sense primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,020A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Polymorphisms and Their Use in Classifying Patients
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Grobholz, James
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 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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ZIP: 02109-2891
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                                                            INFORMATION:
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                                                                                       Application US/09617871
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Drazen M.D., Jeffrey M.
In M.D., Kwang-Ho
Asano M.D., Koichiro
Beier, David
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Beier, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drazen M.D., Jeffrey M.
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GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Daley, George Q.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jarrell Ph.D., Brenda H.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 0092662
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
TELEPAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                              Sequence 1850, Appli
Patent No. 6727063
GENERAL INFORMATION:
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                                                                       APPLICANT: Daley, George Q.
APPLICANT: McCarchy, Jeanette J.
APPLICANT: McCarchy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR PILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
                                                            PRIOR FILING DATE: 2000-07-26
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DESCRIPTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/617,871
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: CHOATE, HALL & STEWART
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence
TITLE OF INVENTION: Polymorphisms and Their Use in Classifying Patients
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.2%; Score 15;
100.0%; Pred. No.
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Mismatches (
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; ORGANISM: Homo sapiens
US-09-657-472-1850
                                                                                                         JS-09-021-701-404
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                                                    Matches
                                                                 Best Local
                                                                            Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                      MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: JUVU
CITY: Palo Alto
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/021,701
                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 650-236-2386
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                                                                                                                                                              STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10-FEB-1998
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                           124 TCGTTTCCATCTCTTTGGA 142
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TCCTTTCCATCCCTGTGGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delenstarr, Glenda C.
Webb, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shannon, Karen Wolber, Paul K.
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                                                   0; Mismatches
                                                                            Score 14.2;
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Pred. No. 14;
                                                                 Pred.
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RESULT 10

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                                          CURRENT APPLICATION NUMBER: US/09/487,368A
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 97
LENGTH: 20
TYPE: DNA
                                                                                                                                                                                                                           Sequence 97, Application US/09487368A
Patent No. 6261840
                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                            TITLE OF INVENTION: ANTI
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 10-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 1097
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
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               ORGANISM: Artificial Sequence FEATURE:
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HYPOTHETICAL: N
ANTI-SENSE: NO
OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
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TITLE OF INVENTION: probe sequences
TITLE OF CHOUENCES: 1165
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DEDNESS: single
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3000 Hanover Street
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Webb, Peter G.
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Pred. No. 1
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US-09-487-368A-97

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APPLICANT: ROBERT MCKAY

TITLE OF INVENTION: ANTISENSE MODULATION OF PTE
FILE REFERENCE: ISPH-0478
; CURRENT APPLICATION NUMBER: US/09/629,644A
; CURRENT FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR PILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 242
SEQ ID NO 97
LENGTH: 20
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Best Local (
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SEQ ID NO 97
LENGTH: 20
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APPLICANT:
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Patent No. b
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CURRENT FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lex M. Cowsert APPLICANT: Jacqueline Wy.
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APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
TITLE OF INVENTION: ANTISENSE MODULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lex M. Cowsert APPLICANT: Jacqueline Wy: APPLICANT: Susan M. Frei
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                                                                                                 OTHER INFORMATION:
                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                  TYPE: DNA
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5. 6492345
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Susan M. Preier
Brett P. Monia
Madeline M. Butler
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Brett P. Monia
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                                                                                             Antisense Oligonucleotide
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      5.9%;
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   Score 14.2;
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Pred. No. 18
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Length 20;
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                                                                                                        RESULT 16
US-09-495-714C-138/c
                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Chlamydia pneumoniae US-09-198-452A-6637
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US-09-198-452A-6637/c
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US-09-198-452A-3809/c
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Sequence 138, Application US/09495714C
Patent No. 6670465
GENERAL INFORMATION:
APPLICANT: University Technologies International Inc.
TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1
FILE REFERENCE: 45499.4 (formerly 45074.6)
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 6637
LENGTH: 20
TYPE: DNA
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CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 3809
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Griffais, R.
APPLICANT: INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides,
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnos
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Griffals, R. TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnos TITLE OF INVENTION: and treatment of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 CCTCGTTTCCATCTCTTTG 140
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                                                                                                                                                                                                                                                16;
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Pred. No. 1
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Pred. No. 18
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); Mismatches
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                    (ALPHA) 1F-SUBUNIT GENE
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CURRENT FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PatentIn version 3.1
SEQ ID NO 138
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-726-345-2
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                                                         Sequence 2, Application US/09726345

Patent No. 6855521

GENERAL INFORMATION:

APPLICANT: Naval Medical Research Center

TITLE OF INVENTION: Serotype and Dengue Group Specific Flurogenic |

TITLE OF INVENTION: (TagMan) Assays Against the Respective C and |

TITLE OF INVENTION: No. 685521-Coding Regions of Dengue Virus

FILE REFERENCE: NC 82197

CURRENT APPLICATION NUMBER: US/09/726,345

CURRENT FILING DATE: 2000-12-01

NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
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Matches
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Best Local S
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LENGTH: 20
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APPLICANT: Mizuno, Yoshikuni
TITLE OF INVENTION: Isolated DNA or Gene Responsible for FILE REFERENCE: 0652.2110000
CURRENT APPLICATION NUMBER: US/09/601,844B
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR APPLICATION SUMBER: PCT/JP99/00545
PRIOR FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Intron
LOCATION: (11)..(20)
OTHER INFORMATION: Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Exon 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(10)
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Pred. No. 18;
0; Mismatches
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Pred. No. 1
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NS5 Genomic
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; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Antisense Oligonucleotide US-10-209-405-27
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US-10-209-405-27/c
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US-10-209-405-96
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US-09-726-345-2
                                                                                                                  US-10-209-405-96
                                                                                                                                                                                                                                                                              Sequence 96, Application US/10209405
Patent No. 6906186
GENERAL INFORMATION:
APPLICANT: Jacqueline Wyatt
APPLICANT: Susan M. Freier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: RTS-0131
CURRENT APPLICATION NUMBER: US/10/209,405
CURRENT FILLNG DATE: 2002-07-30
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 27
LENGTH: 20
TYPE: DNA
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Patent No. 6906186
GENERAL INFORMATION:
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SEQ ID NO 96
LENGTH: 20
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Best Local Similarity
Matches 16; Conserv
                                                         Matches
                                                                                    Query Match
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FILE REFERENCE: RTS-0131
CURRENT APPLICATION NUMBER: US/10/209,405
CURRENT FILING DATE: 2002-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jacqueline Wyatt
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF POLO-LIKE KINASE EXPRESSION
                                                                                                                                TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
                                                       Local Similarity
nes 16; Conserv
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                           148 TCTCACGTGGAGCTGAACA 166
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ilarity 84.2%;
Conservative
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84.2%;
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Pred. No. 18;
                                                                       Score 14.2;
Pred. No. 18;
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Pred. No. 18;
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RESULT 21 US-09-422-978-6418/c

Sequence 6418, Application US/09422978 Patent No. 6537751

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CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 6418
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                                                                                                                                                                  RESULT 23
US-10-156-306B-6889/c
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306B-6888
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APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKX-Gamma and PKR
TITLE OF INVENTION: Levels of IKX-Gamma and PKR
FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306B
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6888
                                                                                                  Sequence 6889, Application US/10156306B Patent No. 7022828
GENERAL INFORMATION:
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        APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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TITLE OF INVENTION: Biallelic markers for use
FILE REFERENCE: GENSET 020CP1
FILE REFERENCE: MBHB01-664-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
PEATURE:
NAME/KEY: primer_bind
LOCATION: 1.19
OTHER INFORMATION: upstream amplification primer 99-11313 for SEQ
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Local Similarity 88.2%;
es 15; Conservation
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                                                                                                                                                                                                                                                                                           38 GGAGCTCCACCTCCC 52
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                                                                                                                                                                                                                                                                                                                                          14; Conservative
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Chumakov, Ilya
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                                                                                                                                                                                                                                                                                                                                                           Score 13.4;
Pred. No. 2
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Pred. No. 2
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NUMBER OF SEQ ID NOS: 8014

SOFTWARE: PatentIn version 3.0

SEQ ID NO 6889

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens
US-10-156-306B-6889
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                                                              US-08-632-673B-9
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Matches
           Query Match
Best Local Similarity
 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                             TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,673B
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/156,306B CURRENT FILING DATE: 2002-05-28
                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION UNMBER: 30,223
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
                                                                         MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS
TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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CITY: San Francisco
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nes 14; Conserv
                                                                                                                      TOPOLOGY:
                                                                                                                                   STRANDEDNESS:
                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Thomas, Winston J.
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                                                                                                                        linear
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16-APR-1996
N: '7"
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                5.5%;
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                Score 13.4;
Pred. No. 22;
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Pred. No. 21
 Mismatches
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MARKERS AND DIAGNOSTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                       Version
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RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION FILE REFERENCE: RTS-0027 CURRENT SPLICATION NUMBER: US/09/357,072 CURRENT FILING DATE: 1999-07-19 NUMBER OF SEQ ID NOS: 87 SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Appearent No. 6025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17,
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APPLICANT: Brett P. Monia
APPLICANT: Brenda F. Baker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIOM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
         ATTORNEY/AGINT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TITLE OF IN
                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                    APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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14; Conservative
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INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                               California
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                                                                                                                                                                                                                                                                                                                                                   E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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 (415)
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576-0300
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93.3%;
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Pred. No. 22;
0; Mismatches
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Best Local Similarity
                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10336-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
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APPLICANT:
                        APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-ARR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-ARR-1996
                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                             STREET: 1155 A
CITY: New York
STATE: New Yor
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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OTHER INFORMATION:
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OTHER INFORMATION:
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Jav. David
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JENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
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Feder, John N.
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/note= "N = 5'-phosphorylated cytosine
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Pred. No. 22;
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US-09-503-444A-17/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                       APPLICATION NUMBER: 08/6 FILING DATE: 23-May-1996 PRIOR APPLICATION DATA:
                                                                                                                                           SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
                                                                                       PRIOR APPLICATION DATA:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
              APPLICATION NUMBER: 08/632,673 FILING DATE: 16-Apr-1996
                                                                                                    FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                 STREET:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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APPLICATION DATA:
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Similarity 93.3%; Pred. No. 2:
14; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09503444A
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                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                          Tsuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas, Winston J. Drayna, Dennis T. Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gnirke, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                        Ruddy,
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                                                                                                                   14-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                        David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mod_base= OTHER
/note= "N = 3'-digoxigenin-conjugated
guanine (G-dig) "
                                                                                                                                                                                                                                                                                                                                                           Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                              44
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/note= "N = 5'-phosphorylated cytosine
                                                                      08/652,265
                                                                                                                                                                                                                                                                                                               Edmonds LLP
                                                                                                                                 US/09/503,444A
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                                                                                                                                        US-09-341-700A-294
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CURRENT FILING DATE: 1990-09-24
PRIOR APPLICATION NUMBER: PCT/EP98/00497
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: EP 97 101 531.8
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 1764
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-341-700A-294/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-503-444A-17
                                                                                                                                                                                                                            SEQ ID NO 294
LENGTH: 18
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6972171
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Brysch, Wolfgang
TITLE OF INVENTION: ANTISENSE OLIGONUCLE
FILE REFERENCE: 10496/P63763USO
                                                                  Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 294, Application US/09341700A
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                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: antisense oligonucleotide
                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
FEATURE:
NAME/KEY: modified_base
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REGISTRATION NUMBER: 26,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
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FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 18
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = 3'-digoxigenin-conjugated
OTHER INFORMATION: guanine (G-dig)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: OTHER INFORMATION:
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                                 52 CCAGCTGCTGCCTCA 66
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                                                                    Conservative
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                                                                                   5.5%;
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/note= "N = 5'-phosphorylated cytosine
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                                                                  Score 13.4; D
Pred. No. 22;
0; Mismatches
                                                                                                   DB 1;
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RESULT 31
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; MOLECULE TYPE:
US-08-546-130A-24
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Patent No. 5892010
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                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY, AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546,130A
FILING DATE: 20-CCT-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gray, Joe W.
APPLICANT: Collins, Colin
APPLICANT: Pinkel, Daniel
APPLICANT: Kallioniemi, Olli-Pekka
APPLICANT: Tanner, Minna M.
TITLE OF INVENTION: Amplifications of Chromosomal Region
TITLE OF INVENTION: 20013 as a Prognostic Indicator in Breast Cancer
                                                                                                                                                                                    APPLICANT:
                                   NUMBER OF SEQUENCES: 4
                                                                       APPLICANT: Rommens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
TITLE OF INVENTION: Uses
                                                                                                                            APPLICANT: Collins, Colina APPLICANT: Hwang, Soo-in APPLICANT: Godfrey, Tony APPLICANT: Kowbel, David
                                                                                                                                                                                                        APPLICANT:
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CITY: San Francisco
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                     ADDRESSEE:
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14; Conservative
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3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                    Gray, Joe W.
Collins, Colin
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Pred. No. 23;
0; Mismatches
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APPLICANT: GRAY, JOE W
APPLICANT: COLLINS, COLIN
APPLICANT: COLLINS, COLIN
APPLICANT: RINKEL, DANIEL
APPLICANT: KALLIONIEMI, OLLI-PEKKA
APPLICANT: TANUER, MINNA M
APPLICANT: TANUER, MINNA M
APPLICANT: TANUER, MINNA M
TITLE OF INVENTION: AMPLIFICATIONS OF CHROMSOMAL REGION 20Q13 AS ;
TITLE OF INVENTION: PROGNOSTIC INDICATOR IN BREAST CANCER
FILE REFERENCE: 2500.136US2 20Q13
CURRENT APPLICATION NUMBER: U20066,641
CURRENT APPLICATION NUMBER: U309/066,641
CURRENT FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: 08/546,130
EARLIER FILING DATE: 1995-10-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Pacentin Ver. 2.0
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US-09-066-641-31/c
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FILING DATE: 15-7UL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 023070-068900US
REFERENCE/DOCKET NUMBER: 023070-068900US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
                                                                                                                          US-09-066-641-31
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                                           Matches
                                                                                  Query Match
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                                                                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: primer
                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                        ENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 TTCTCCACCACAGCA
                                           14;
  1 TTCTCCAGCACAGCA 15
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                                                            93.3%;
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93.3%; Pred. No. 23;
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                                           0; Mismatches
                                                              Score 13.4;
Pred. No. 23
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APPLICANT: Rommens, Johanna
TITLE OF INVENTION: GENES FROM THE 20Q13 AMPLICON AND THEIR USES
FILE REFERENCE: 2500.124US3
CURRENT APPLICATION NUMBER: US/08/892,695A
CURRENT FILING DATE: 1997-07-15
EARLIER APPLICATION NUMBER: 08/785,532
EEARLIER FILING DATE: 1997-01-17
EARLIER APPLICATION NUMBER: 08/731,499
EARLIER FILING DATE: 1997-01-16
EARLIER FILING DATE: 1996-10-16
EARLIER FILING DATE: 1996-10-16
EARLIER FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/08892695A Patent No. 6808878
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APPLICANT:
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APPLICANT: Collins, Colli
APPLICANT: Hwang, Soo In
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APPLICANT: Kowel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2Q ID NO 45
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/572,126
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              APPLICANT: Lizonova, Alena
TITLE OF INVENTION: COMPLEMENTARY ADENOVIRAL VECTOR SYSTEMS
TITLE OF INVENTION: AND CELL LINES
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 TTCTCCACCACAGCA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TTCTCCAGCACAGCA 15
                                                                                                                                                                                    60601
                                                                                                                                                                                                                                         Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 93.3%;
                                                                                                                                                                                                                     Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08572126
                                                                                                                                                                                                                                                        E: Leydig, Voit & Mayer, Ltd.
Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                   Brough, Douglas E. McVey, Duncan L. Bruder, Joseph T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kovesdi, Imre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tony
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                                                                                                                                                                                                                                                                                                                                                                                                                             Douglas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 13.4; D; Pred. No. 23; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 19;
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Query Match
Best Local Similarity
Thes 15; Conserva
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                                                                              ; MOLECULE TYPE: cDNA US-09-003-199-17
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US-09-003-199-17
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                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft word 5.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (312) 616-56
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                     TELEFAX: (908)298-538
INFORMATION FOR SEQ ID NO:
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thampoe, Immac J.
REGISTRATION NUMBER: 36,322
REFERENCE/DOCKET NUMBER: CN
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION | 10F0RMATION:
TELEPHONE: (908)298-5061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CH
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Parker, Eric M
APPLICANT: Strader, Catherine D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 3076
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rudinski, Mark S
TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2000 Gail
CITY: Kenilworth
                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/003,199 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 5.5%; Score 13.2; Local Similarity 83.3%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/258416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Schering-Plough Corporation
2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                Conservative
                                                                                                                                                                                                           (908) 298-5388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                           single
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                              5.5%;
83.3%;
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                              Score 13.2;
Pred. No. 2
                Mismatches
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                                             DB 1;
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                                             Length 18;
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156

GGAGCTGAACAGAACGAC 173

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RESULT 37
US-08-757-023A-3
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US-09-003-199-19
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TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-003-199-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19,
                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (908)298-5388
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                    APPLICANT: Brough, Do
APPLICANT: McVey, Dur
APPLICANT: Bruder, Jo
APPLICANT: Lizonova,
TITLE OF INVENTION: C
TITLE OF INVENTION: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Parker, Eric M
APPLICANT: Strader, Catherine D
APPLICANT: Rudinski, Mark S
TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Thampoe, Immac J.
REGISTRATION NUMBER: 36,322
REFERENCE/DOCKET NUMBER: CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)298-5061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,199
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Schering-Plough Corporation STREET: 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                               156 GGAGCTGAACAGAACGAC 173
                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 83.3
Chicago
                                                                                                                                                                                                                                                                                                                          GGAGCAAAACAGGACGAC 18
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                                                                                                                    Lizonova,
                                                                                                                                Brough, Douglas E. McVey, Duncan L. Bruder, Joseph T.
                                                                                                                                                                                   Kovesdi,
                                                                                                                                                                                                                                                                                                                                                                                                         5.5%;
83.3%;
                                                                                                                                                                     Douglas E.
                                                                                  COMPLEMENTARY ADENOVIRAL VECTOR SYSTEMS AND CELL LINES
                                                                                                                                                                                        Imre
                                                                                                                  Alena
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Pred. No. 24;
O; Mismatches
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US-08-651-155B-1
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NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 7427.
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 616-5600
TELECAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 hose airs
              ZIP: 80302

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/651,155B
FILING DATE: 17-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PETERSEN MY., STEVEN C.
REGISTRATION NUMBER: 36,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08651155B Patent No. 6365401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Mahan D
APPLICANT: Conner |
APPLICANT: Hiethof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPERTY NO.

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chrisman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 15; Conserv
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                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 20
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/757,023A FILING DATE: 26-NOV-1996
REFERENCE/DOCKET NUMBER: 17060.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 GCTGCCTCACCTGCTTT 75
                                                                                                                                                                                                                                                                                                                  Boulder
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                                                                                                                                                                                                                                                                                                                                     1900 Fifteenth Street
                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hiethoff Mr., Douglas M.
VENTION: METHOD AND PROBES FOR THE IDENTIFICATION
VENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mahan Dr., Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conner Mr., Christopher P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                   INFECTION
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Pred. No. 24;
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TELECOMMUNICATION INFORMATION:

ELEPHONE:

303/546-1300

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RESULT 39
US-09-321-797-3
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Patent No. 6482616
GENERAL INFORMATION:
APPLICANT: Kovesdi, Imre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: ABA1475
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
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                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/321,797
FILING DATE: 27-May-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/757,023A
FILLING DATE: 26-NOV-1996
APPLICATION NUMBER: US 08/258416
FILING DATE: 10-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REGRERENCE/DOCKET NUMBER: 74273
TELEPHONE: (312) 616-5600
TELEPHONE: (312) 616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TOPOLOGY: linear MOLECULE TYPE: DNA (synthetic) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lizonova, Alena
TITLE OF INVENTION: COMPLEMENTARY ADENOVIRAL VECTOR SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 CATTTTGTGCCCACTACG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTGGGTGCCCAGTACG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                   LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303/449-5426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other nucleic acid
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                                                                                                                                             616-5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND CELL LINES
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Pred. No. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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US-10-006-937-7
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US-09-194-036B-1
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                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09194036
Patent No. 6548246
GENERAL INFORMATION:
APPLICANT: Mahan, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thonart, Philippe
APPLICANT: Dauvrin, Thierry
TITLE OF INVENTION: ENZYME OR CELL PREPARATION WITH
TITLE OF INVENTION: INULINASE ACTIVITY
FILE REFERENCE: VANM237.001AUS
CURRENT APPLICATION NUMBER: US/10/006,937
CURRENT PILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jonniaux, APPLICANT: Rauw, Ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: primer for sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,036B
FILING DATE: 17-No. 6548246-1998
                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST
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                                                                                                                                                   STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCCTGCTAAGCACTGG 18
                                                                                                                                                                                  CITY: Mountain View
                                                                                                                                                                                                  STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09194036B
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Pred. No. 2
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Pred. No. 2;
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                                                                                                                                                        PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9217, Application US/09866108A Patent No. 6686188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US/60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 494-0 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US97/08208
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 08/651,155
FILING DATE: 1996-05-17
                        APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                    APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
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REFERENCE/DOCKET NUMBER: 220002060601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5995
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15; Conserv
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Yonggang
ENN, Sharron G.
Pavid K.
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    data removed
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Pred. No. 24;
0; Mismatches
See File Wrapper or PALM.
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; SEQ ID NO 9217
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                                                                                        US-09-866-108A-9218
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US-09-866-108A-9218/c
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                                                                           Best
                                                            Matches
                                                                                                                                                                                   Patent No. 668
SEQ ID NO 9218
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Best Local Similarity
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/866,108A CURRENT FILING DATE: 2001-05-25 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
APPLICANT: GU, Yizhong
                                                                                                                                                                                                                              Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 15755
                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                     LENGTH: 17
                                                                           Local
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00669
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                            31 CTGGCTGGGAGCT 43
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                                                            13;
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6686188
                                                                           Similarity
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HANZEL, David
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                                                                         Score 13;
Pred. No.
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Pred. No.
                                                            Mismatches
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                                                                           DB 1;
24;
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24;
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RESULT 45
US-09-866-108A-9220/c
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Best Local 8
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Patent No. 6686188
SEQ ID NO 9219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                           APPLICANT: PENN, SHERRON G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
TITLE OP INVENTION: MYOSKIL-LIKE GENE EXPRESSED
FILE REFERENCE: ABOMICA-7
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                 CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
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APPLICANT: JI, Yongga
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GU, Yizhong
APPLICANT: JI, Yongga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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Local Similarity 100.0%; Pred. No.
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
APPLICATION NUMBER: US 60/207,456
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APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION UNMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR PLING DATE: 2000-05-26
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9220
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SEQ ID NO 9220
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                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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                      APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00669
                                                                            APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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5. 6686188
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l Similarity 100.0%;
l3; Conservative (
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See File Wrapper or PALM
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US-08-584-040-5754
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Patent No. 9221
SEQ ID NO 9221
                                                                US-08-584-040-5754
   Matches
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                                 Query Match
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TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
-09-866-108A-9221
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                                                                                                                                                                                                                                                        CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/005,974

FILING DATE: October 26, 1995

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327
                                                                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: tocrage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: BECOBEdO, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: CONDITIONS GELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                               TELEPHONE: (213) 955-0440
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nes 13; Conserv
                                                                                                     TYPE: nucleic acid
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STATE: California
                                                                                 STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: Januar
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l Similarity
12; Conserv
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633 West Fifth Street
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 5.3%;
ilarity 75.0%;
Conservative
                                                                          linear
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Y 11, 1996
Score 12.8; D
Pred. No. 26;
2; Mismatches
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                                 DB 1;
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US-09-371-772B-2633
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APPLICANT: Sweedler, David
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and
FILE REFERENCE: MBHB00-831-B (247/276)
CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR PILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
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US-09-474-432B-580
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                                            PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2633
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2633, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: PatentIn version 3.0
SEQ ID NO 580
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                         TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
ERIOR APPLICATION NUMBER: US 60/005,974
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
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TYPE: RNA
ORGANISM: Homo sapiens
ORGANISM: Mus sp
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Pred. No. 26;
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US-09-866-108A-119
; Sequence 119, Application US/09866108A
; Patent No. 668618B
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; ORGANISM: Homo sapiens
US-09-476-387-579
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Best Local S
Matches 11
                                                                                                                                                            APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggan;
APPLICANT: PENN, Sharr;
APPLICANT: HANZEL, David
APPLICANT: RANK, David
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APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
FILE REFERENCE: MBHB00-331-C (249/073)
CURRENT APPLICATION NUMBER: US/09/476,387
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
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SOFTWARE: PatentIn version 3.0
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FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                              APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/064,866 PRIOR FILING DATE: 1997-11-05
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PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 60/083,727
PRIOR FILING DATE: 1998-04-29
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Adamic, Jasenka Matulic
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Beaudry, Amber
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75.0%;
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Pred. No. 2
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-119
                      RESULT 52
US-09-866-108A-120
                                                                                                                                                                                            Matches
                                                                                                                                                                                                              Query Match 5.3%;
Best Local Similarity 87.5%;
                                                                                                                                                                                                                                                                                                                                                                Patent No. 66
SEQ ID NO 119
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed -
NUMBER OF SEO ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: US
FILING DATE: 2000-09-27
120,
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  Application US/09866108A
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Pred. No. 2
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US-09-866-108A-120
US-09-866-108A-120
Sequence 120, Application US/09866108A
Fatent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
APPLICANT: SHANNON, Mark
CURRENT FILING DATE: 2001-05-25
FRIDR REFERENCE: AEDMICA-7
CURRENT FILING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 0236,359
PRIOR APPLICATION NUMBER: GB 0236,359
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669

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                                                                     Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                   Patent No. 6680
SEQ ID NO 1319
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ORGANISM: Homo sapiens
-09-866-108A-120
                                                                                                                                              ORGANISM: Homo sapiens -09-866-108A-1319
                                                                                                                                                                                                                                                        SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 15755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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APPLICANT: CHAN, Mensheng
APPLICANT: SEANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-866-108A-1319/c
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SOFTWARE: Aeomica Sequence
                                                                                                                                                                                 LENGTH: 17
TYPE: DNA
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APPLICANT: JI, Yongga
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OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00667
OR APPLICATION NUMBER: PCT/USO1/00664
OR APPLICATION NUMBER: PCT/USO1/00664
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00665
OR APPLICATION NUMBER: PCT/USO1/00665
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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                                  CTCACCTGCTTTTCCA 78
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                                                                       Conservative
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NN, Sharron
NZEL, David
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                                                                                        Score 12.8;
Pred. No. 26;
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Pred. No. 2
                                                                         Mismatches
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; ORGANISM: Homo sapiens
US-09-866-108A-1320
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                                                                                                                                                                       Sequence 5889, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, YIZhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Aeomica
Patent No. 6686188
SEQ ID NO 1320
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
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              CURRENT APPLICATION NUMBER: US/09/866,108A CURRENT FILING DATE: 2001-05-25 PRIOR APPLICATION NUMBER: US 60/207,456
                                                                         APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 15755
                                                                                                                                     APPLICANT:
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PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/236,359
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APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/00665
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FILING DATE: 2000-05-26
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Similarity 87.5%;
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Pred. No. 2
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RESULT 56
US-09-866-108A-5890
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US-09-866-108A-5889
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Best Local
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SOFTWARE: Acomica Sequence Listing Engine Patent No. 6686188
SEQ ID NO 5889
                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
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OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR RETLING DATE: 2001-01-30
OR RPLICATION NUMBER: PCT/US01/00667
OR RPLICATION NUMBER: PCT/US01/00667
OR RPLICATION NUMBER: PCT/US01/00667
OR RILING DATE: 2001-01-30
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                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
                                       APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
                   APPLICATION NUMBER: PCT/US01/00668
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LING DATE: 2001-01-30
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T: CHEN, Wensheng
T: SHANNON, MARK
INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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ilarity 87.5%;
Conservative
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Pred. No. 26;
0; Mismatches
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APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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; SEQ ID NO 7503
; LENGTH: 17
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 5890
LENGTH: 17
                                                                                     Matches
                                                                                                                              Query Match
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ORGANISM: Homo sapiens
-09-866-108A-5890
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PRIOR FILING DATE: 2001-01-30
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APPLICANT: JI, Yongga
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00663
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HANZEL, David K.
                                                                                     Conservative
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87.5%;
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Pred. No. 2
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Pred. No. 2
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RESULT 58
US-09-866-108A-7504/c
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-09-27
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PRILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Accomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 7504
LENGTH: 17
                                                                                                                                                                                                                                                                                            Sequence 2633, Application US/09685664B Patent No. 6818447 GENERAL INFORMATION:
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                                       APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Re
FILE REFERENCE: MBHB00-876-K (400/021)
CURRENT APPLICATION NUMBER: US/09/685,664B
CURRENT FILING DATE: 2000-10-10
                                                                                                                                                                                                                   APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
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ORGANISM: Homo sapiens
-09-866-108A-7504
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEONICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
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APPLICANT: JI, Yongga
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                       APPLICATION NUMBER: US 60/005,974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RANK, David R. CHEN, Wensheng
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1995-10-26
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Pred. No. 26;
0; Mismatches
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306B
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8014
SOPTWARE: PatentIn version 3.0
SEQ ID NO 4949
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US-10-138-674B-2633
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                                                                   NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2633
                                                                                                                                                                                                                                                                                                            Patent No. 7034009
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
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NUMBER OF SEQ ID NOS: 8231
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2633
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Best Local Similarity
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                                                                                                                          APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
                                                                                                                                                                                                                   APPLICANT: Sirna Therapeutics,
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
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ORGANISM: Mus musculus
           TYPE: RNA
ORGANISM: Mus musculus
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5. 7034009
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Pred. No. 26;
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Pred. No. 26;
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APPLICANT: C. Frank Bennett
APPLICANT: Bert W. O'Malley
TITLE OF INVENTION: ANTIENSE MODULATION OF SRA EXPRESSION
FILE REFERENCE: RTS-0048
CURRENT APPLICATION NUMBER: US/09/280,409
CURRENT FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 127
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
RESULT 64
US-09-474-922A-42/c
; Sequence 42, Application US/09474922A
; Patent No. 6187586
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US-09-280-409-127/c
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US-09-280-409-127
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APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF integrin beta 3 EXPRESSION
FILE REFERENCE: RTS-0070
CURRENT APPLICATION NUMBER: US/09/344,520
CURRENT PILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 29
LENGTH: 18
TYPE: DNA
TYPE: DNA
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APPLICANT: Lex M. Cowsert
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Best Local
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                                                                                                                                                                                                                                                                   FEATURE:
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5. 6037176
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87.5%; Pred. No. 28;
tive 0; Mismatches
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87.5%; Pred. No. 28;
tive 0; Mismatches 2;
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Pred. No. 26;
2; Mismatches
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APPLICANT: Carrill, John P.
APPLICANT: Little, Randall D.
APPLICANT: Little, Randall D.
APPLICANT: Recker, Robert R.
APPLICANT: Johnson, Mark L.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-013
CURRENT APPLICATION NUMBER: US/09/544,398B
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: US 60/071,449
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-13
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US-09-544-398B-406/c
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; ORGANISM: human
US-09-475-947A-333
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                                                                                                                                                                                                                Sequence 406, Application US/09544398B Patent No. 6770461
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brett APPLICANT: Lex M. CC APPLICANT: Richard J. TITLE OF INVENTION: FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 18
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APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Folymorphic Repeats in Human
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
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APPLICATION NUMBER: US 60/105,511
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Richard A. Roth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.8; D
Pred. No. 28;
0; Mismatches
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Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
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CURRENT APPLICATION NUMBER: US/09/543,771B
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 1999-01-13
PRIOR APPLICATION NUMBER: US 60/071,449
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: US 60/105,511
PRIOR APPLICATION NUMBER: US 60/105,511
PRIOR APPLICATION NUMBER: US 60/105,511
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEO ID NOS: 641
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 406
                                                                                                                                                                                                                                                                                                     RESULT 68
US-08-758-306-691/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 641
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 406
LENGTH: 18
                                                                                                                                                                                                                                                                      Sequence 691, Application US/08758306 Patent No. 5807743
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.3%;
Best Local Similarity 87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 406, Appl
Patent No. 6780609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Carulli, John P.
APPLICANT: Little, Randall D.
APPLICANT: Recker, Robert R.
APPLICANT: Johnson, Mark L.
TITLE OF INVENTION: High bone mass gene of 11q13.3
FILE REFERENCE: 032796-014
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                          APPLICANT: Stinchcomb,
APPLICANT: McSwiggen,
TITLE OF INVENTION: TRI
TITLE OF INVENTION: AS:
                                                                                                                          TITLE OF INVENTION:
                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                           NUMBER OF SEQUENCES:
                                                    STREET:
                                   STREET:
                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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SSSEE: Lyon & Lyon
T7: 633 West Fifth Street
ST: Suite 4700
Los Angeles
S: California
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nilarity 87.5%;
Conservative
                                                                                                                                           Stinchcomb, Dan T.

MCSWiggen, James A.

WENTION: METHOD AND REAGENT FOR THE
VENTION: TREATMENT OF DISEASES
VENTION: ASSOCIATED WITH
VENTION: INTERLEUKIN-2 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                            GAMMA-CHAIN EXPRESSION
                                                                                                           1379
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Pred. No. 2
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1715, Apparent No. 583754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                            COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ITITLE OF INVENTION: IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/758
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSeq Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 13; Conserv
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APPLICATION NUMBER: US/08/292,620A FILING DATE: August 17, 1994
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                                                                                                                                                                                                                                                                                                                                                                                 Kenneth G. Draper
MENTION: RIBOZYME TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                     Sean Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dan T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     James McSwiggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Susan Grimm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.1%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stinchcomb
                                                                                                                                                                                                                                                                                                                                DISEASES OR CONDITIONS RELATED TO LEVELS OF INTRACELLULAR ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM P.C
                                                                                                                                                                                                                                                                                                               MOLECULE-1 (I-CAM-1)
                                                                                                                                                                                                                                                                                                2390
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Pred. No. 3
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US-08-292-620A-1918
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 499-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1715:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1918, Application US/08292620A Patent No. 5837542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 11; Conserv
  CLASSIFICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION NUMBER: 08/008,895
APPLICATION NUMBER: 19,1993
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILLING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILLING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: RIBOZYME TREATMENT OF INTENTION: DISEASES OR CONDITIONS TITLE OF INVENTION: RELATED TO LEVELS OF INTENTION: INTRACELLULAR ADHESION TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                APPLICATION NUMBER:
FILING DATE: August
CLASSIFICATION: 435
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                     90071-2066
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Dan T. Stinchcomb
James McSwiggen
Sean Sullivan
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                                                                                                          US/08/292,620A
: August 17, 1994
CON: 435
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January 19, 1993
MBER: 07/989,849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2390
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Pred. No. 30;
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US-08-292-620A-1952
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Best Local Similarity 78.6%;
Matches 11; Conservative
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: Including apprior APPLICATION DATA: described belapplication NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
APPLICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION INDMER: 32,327
REGISTRATION INDMER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ITTLE OF INVENTION: INVENTION: INVENTION: ITTLE OF SEQUENCES:
                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: December 7
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
STREET: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 CCACCTCCCCAGCT 57
                                                                                                                                                                                                                                                                                                                                                                                                                90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sean Sullivan
Kenneth G: Draper
VENTION: RIBOZYME TREATMENT OF
VENTION: DISEASES OR CONDITIONS
VENTION: RELATED TO LEVELS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dan T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08292620A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Susan Grimm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      December 7, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE-1 (I-CAM-1)
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                                                                                                                                                                                                                                                                                                                    .C. DOS 5.0
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Pred. No. 3
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Best Local
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                                                                                                                                                                                                                        SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg Bichard 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                      TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                             NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                  SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADJESSION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Anna 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 5.1%;
Local Similarity 78.6%;
es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                James McSwiggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09071845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dan T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Susan Grimm
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                                                                            1715:
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Pred. No. 3
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US-09-071-845-1918
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                                                                                 US-09-071-845-1918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1918, App
Patent No. 6132967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Query Match 5.1%;
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTMARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,621
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WARDLURG, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                 TELEPHONE: (213) 489-160
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 63 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 CCACCTCCCCAGCT 57
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                                                                                                     linear
                                                                                                                                                                                                                                                           (213) 489-1600
                                                                                                                     single
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78.6%;
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                                                                                                                                                                                                                                                                                                  208/149
    Score 12.4; D
Pred. No. 30;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.4;
Pred. No. 30;
                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                        1; Length 17;
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RESULT 75
US-08-834-497A-49
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                                                                                                                                             Query Match
Best Local :
                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMER: US/08/292,620
FILING DATE: AUGUST 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ITILE OF INVENTION: ITILE OF INVENTION: ITILE OF INVENTION: ITILE OF INVENTION:
                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071-2006
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
Tom Compatible
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
STREET:
CITY: L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                          Match 5.1%; Local Similarity 78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                            44 CCACCTCCCCAGCT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Los Angeles
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INVENTION: RIBOZYME TREATMENT OF INVENTION: DISEASES OR CONDITIONS
                                                          CCACCUCCCCACCU 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACCTCCCCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Susan Grimm
Dan T. Stin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sean Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dan T. Stinchcomb
James McSwiggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09071845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE-1 (I-CAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM P.C. DOS 5.0
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                                                                                                                                          Score 12.4;
Pred. No. 3
                                                                                                                           Mismatches
                                                                                                                                           30;
                                                                                                                                                           DB 1;
                                                                                                                                                         Length 17;
                                                                                                                           Indels
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RESULT 76
                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic) US-08-834-497A-49
                                                                                                                           Query Match 5.1%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 13-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 16-APR-1996
FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49, Application US/08834497A Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                               36 TGGGAGCTCCACCT 49
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                                                       TGGGTGCTCCACCT 14
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T: Ruddy, David
T: Ruddy, David
T: Tsuchihashi, Zenta
T: Wolff, Roger K.
INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
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                                                                                                                                                                                                                                                                                                 17 base pairs
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Feder, John N.
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                                                                                                                                                 Score 12.4;
Pred. No. 3
                                                                                                                             ed. No. 30;
Mismatches
                                                                                                                                                                 DB 1; Length 17;
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US-08-834-497A-50

Sequence 50, Application US/08834497A Patent No. 6140305 GENERAL INFORMATION: APPLICANT: Thomas, Winston J. APPLICANT: Drayna, Dennis T.

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RESULT 77
US-09-866-108A-5891
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                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE:
US-08-834-497A-50
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                            GENERAL INFORMATION:
                                                                                                                           Sequence 5891, Application US/09866108A Patent No. 6686188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/834,497A

PILING DATE: 04-APR-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/834,497A

FILING DATE: 04-APR-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/652,265

FILING DATE: 23-MAY-1996

CLASSIFICATION NUMBER: US 08/632,673

PRIOR APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

CLASSIFICATION: 514

PRIOR APPLICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,912

FILING DATE: 04-APR-1996

CLASSIFICATION: 514

PRIOR APPLICATION: 514

CLASSIFICATION: 514
                                                          APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron
               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                              APPLICANT:
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION UNMBER: 28,462
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleach STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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RANK, David R. CHEN, Wensheng SHANNON, Mark
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                                              HANZEL,
                                                                                                                                                                                                                                                                                                                                                                                                                                    17 base pairs
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Tsuchihashi, Zenta
Wolff, Roger K.
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IBM PC compatible
SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650-493-4935
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                            Sharron G.
L, David K.
David R.
                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                        Score 12.4;
Pred. No. 3
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                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                         Gaps
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Query Match
Best Local Similarity
Matches 13; Conserve
                                        FILE REFERENCE: AEOMICA-7
CCURRENT APPLICATION NUMBER: US/09/866,108A
CCURRENT FILING DATES 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5891
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; SEQ ID NO 5891
; SEQ TRACTH: 17
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PRILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00663
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Patent No. bocc-
Patent INFORMATION:
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APPLICANT:
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Aeomica Sequence Listing Engine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 2001-01-30
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FILING DATE:
                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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92.9%;
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Pred. No. 30;
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RESULT 79
US-10-156-306B-5820/c
Sequence 5820, Application US/10156306B
Patent No. 7022828
Patent No. 7022828
Patent No. 7022828
PAPLICANT: RLBozyme Pharmaceuticals, Inc.
PAPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE ACID INVENTION UNMBER: US/10/156,306B
CURRENT APPLICATION NUMBER: US/10/156,306B
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5820
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-156-306B-5820
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Search completed: October 2, 2006, 15:36:33 Job time: 0.001 secs
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NUMBER OF SEO ID NOS: 15755

SOFTWARE: Acomica Sequence Listing Engine

Patent No. 6686188

SEO ID NO 5892

LENGTH: 17

TYPE: DNA

ORGANISM: Homo sapiens

S-09-866-108A-5892
                                                                                                                                                                                                       Query Match 5.1%; Score 12.4; DB 1; Length 17; Best Local Similarity 92.9%; Pred. No. 30; Matches 13; Conservative 0; Mismatches 1; Indels
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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Minimum
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                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                         Run on:
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                                                                                                                                              Scoring table:
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DB seq length: 0
DB seq length: 200000000
                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 0.5
                                                                                         58 seqs, 1209 residues
                                                                                                                                                                                                   US-10-642-946-6_1967-2208
242
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                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                     2006, 15:44:33 ;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database

ngedb1:\*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 58 summaries

N. Genesex

Maximum

## SUMMARIES

c 33	32	31	c 30	29	c 28	27	c 26	25	24	23	22	21	20	19	18	17	c 16	c 15	14	c 13	12	11	10	9	8	7	c 6	<sub>5</sub>	c 4	ω	2	,	Result
14.8	15	15	15.2				15.2			٠	15.2	٠	•	•	'n	5	15.8	ŗ	ŗ	15.8	٠	•	٠		ა	•	•	•	•	18.2	18.4	18.6	Score
6.1			6.3						٠			٠		6.4	6.4	٠	6.5	6.5		6.5	6.7	6.7	6.7	6.7	6.7	6.7	٠	6.8	7.1	7.5	7.6	7.7	Query
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AEE10387	ADJ95475	AAV13327	AEC03076	ADW72414	ADW72412	ADU66202	AAH62254	AAC69341	ADP78412	ADG17312	AAS42716	AAX91393	AAF26513	AEA33500	AAD45780	ACL46978	ACL46620	ACL46980	ACL46618	ADL24990	ADX84489	ADX84073	ADH49242	ABT05734	918	ABS59191	AAF96003	ADR46326	AAD31117	ADO23704	ABL40677	AEB90482	ID
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Maize gamma-zein P	œ,	-		Mitochondrial poly	rial	kinase	inhit	Ω	imeric	T. gondii sequenci		Primer for RT-PCR	n SRC-3	ssion s	n promoter -1	target	SÍRNA	3 sir	3 target	estinal		DNA detection exte	NOV85 PCR primer,	related		G-pro	Human gene single	۲÷.	⊏	Microorganism tran	syndr	127B probe for det	cription

WPI; 2005-564577/57.

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14.4	14.4	14.4	14.4	14.8	14.8	14.8	14.8	14.8	14.8		14.8	14.8	14.8	14.8		14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	
6.0	6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	
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Melanoma associate			Dog genomic marker	<pre>Up-regulated renal</pre>	Mitochondrial	FOLH1 target oligo	ENPP3 siRNA sense	FOLH1 siRNA sense			FOLH1 target oligo	FOLH1 siRNA sense	FOLH1 siRNA antise	Human Alstrom's	Primer F2 for H.py	Skin permeabilizat	Human phosphodies	Human phosphodiest	Solanum glycosylas	Human MD-1 RP105-a	Human MD-1 RP105-a	Chimeric phosphoro	Chimeric phosphoro	

## ALIGNMENTS

Middleton RP, AEB90482; 02-FEB-2004; 2004US-0541346P 02-FEB-2005; 2005WO-US003375. 18-AUG-2005 WO2005075685-A1 Canis familiaris. osteoarthritis; antiarthritic; osteopathic; diagnosis; drug screening; pharmaceutical; ss; probe. 127B probe for detection of osteoarthritis gene, SEQ ID NO:1578. 20-OCT-2005 (first entry) AEB90482 standard; DNA; 25 BP. (NEST ) NESTEC SA. Hannah

The present invention relates to degenerative joint diseases, such as osteoarthritis and new compositions, devices and methods based on unique profiles of gene expression associated with osteoarthritis. Specifically claimed is a combination (A) comprising polynucleotide molecules (I), where (I) are differentially expressed in an osteoarthritic or in a pressteoarthritic subject compared to expression in subjects which are not osteoarthritic or pre-osteoarthritic. Also given is a method of detecting (M1) differential expression of nucleic acids in a sample; detecting (M2) Polymucleotides differentially expressed in canine osteoarthritis, useful in diagnosing and prognosticating osteoarthritis in mammals, and in identifying compounds useful for treating the disease. Example 5; SEQ ID NO 1578; 170pp; English.

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Best Local Similarity
                                                                                                                                     protein 13.31. The protein can be expressed by standard DNA recombination. The Parkinson syndrome associated protein 13.31 and encoding polynucleotides are useful for treating diseases such as cerebral cortex function disorder. The present sequence represents the human Parkinson syndrome associated protein 13.31 cDNA isolating RT-PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed in osteoarthritis, diagnosing or prognosticating (M4) osteoarthritis by measuring the production of transcription or translation products of one or more genes comprising any of SEQ ID NOs 1-1558 in a sample from the subject; a kit for detecting osteoarthritis by oligonucleotides of at least 10 consecutive bases comprising any of SEQ ID NOs 1-1558 or their fragments, and modulating (M5) osteoarthritis-arthritis associated gene expression in a cell by administering a compound that affects the expression of at least one gene comprising a sequence selected from SEQ ID NOs 1-1588. In M5 the compound is a vitamin preferably 1 alpha, 25-dihydroxy vitamin procession of the compound control succession of the compound compound that affects the expression of at least one gene comprising a sequence selected from SEQ ID NOs 1-1588. In M5 the compound is a vitamin procession of the compound com
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                                                                                                                                                                                                                                                                                                                          The invention relates to a novel human Parkinson syndrome associated protein 13.31. The protein can be expressed by standard DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide-human Parkinson syndrome associated protein 13.31 and polynucleotide encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2000; 2000CN-00116476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkinson syndrome associated protein 13.31; human; anti-Parkinson;
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                                                                                                   RFC-1 primer used in production of heterozygous mutant RFC mouse
                                                                                                                                                                                   21-AUG-2002
                                                                                                                                                                                                                                                                                                                                     AAD31117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 BP; 5 A; 9 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and producing a DNA fragment. The current sequence is that of a PCR primer of the invention which is related to microorganism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for preparing a DNA fragment from a microorganism transformation. The method comprises preparing DNA units which have a structure enabling them to connect DNA fragments for homologous recombination, connecting these DNA units with a DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparing DNA fragment from microorganism transformation, by preparing DNA units which have structure for connecting DNA fragment for homology cecombination, connecting DNA units with DNA fragment, and producing Directions of the connecting DNA units with DNA fragment, and producing Directions of the connecting DNA units with DNA fragment, and producing DNA units with DNA fragment for homology DNA units with DNA fragment for homology DNA units with DNA fragment, and producing DNA units with DNA fragment for homology DNA units with DNA units with DNA fragment for homology DNA units with DNA fragment for homology DNA units with D
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ilarity 87.0%;
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Pred. No. 7
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Pred. No. 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to genetically modified non-human animal comprising CC modification in at least one allele of endogenous reduced folate carrier CC (rfc) gene in the animal, where genetic modification results in reduction in endogenous RFC expression or biological activity in animal. The non-CC in endogenous RFC expression or biological activity in animal. The non-CC human animal optionally is further modified by introduction into genome, CC a nucleic acid sequence encoding biologically active human RFC. The CC compounds for treating cancer, for studying the molecular and biochemical CC events associated with folate transport and for identifying compounds CC useful for treating conditions associated with defective folate CC transport. Furthermore, a compound which binds to RFC with a higher CC transport. Furthermore, a compound which binds to RFC with a higher CC treating a neural tube defect, Parkinson's disease, Alzheimer's disease, CC cardiovascular disease, stroke, cleft palate. In the genetically modified CC animal, expression level of human rfc can be varied, as desired, to compound end of the present CC sequence is a PCR primer used in production of heterozygous mutant RFC compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                              Homo sapiens
                                                                                         Microsatellite marker; Bex4; ovarian cancer; cytostatic; human; gene therapy; tumour suppressor protein; PCR; primer; ss.
                                                                                                                                                                                         Microsatellite marker PCR primer 19-R.
                                                                                                                                                                                                                                                                 18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                ADR46326 standard; DNA; 19
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86.4%;
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Pred. No. 11
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RESULT 6
AAF96003/c
ID AAF960
XX AAF960
XX 18-NOV
DT 18-NOV
DT 06-JUN
XX
Human
XX
Human;
KW polymo
KW polymo
KW pulmon
XX
Homo g
OS Homo g
OS Uniden
XX
FT Variat
FT
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KW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marker within BAC CIT-B-470f8 on 19q14.3. PCR was performed on genomic CC DNA from 15 early-stage and 18 late-stage ovarian tumours of different histologies. LOH analysis was performed to identify potential candidate tumour suppressor genes involved in ovarian carcinogenesis. The invention CC chromosome X (PAPX) ADR46296 is down-regulated in cancer cells. Claimed methods for killing a tumour cell comprise administering to the tumour cell a nucleic acid that encodes a Bex4 polypeptide, a vector comprising the nucleic acid, or a Bex4 polypeptide. The tumour cell can ovarian, cervical, brain, breast, prostate and hepatic tumour cells in a sample indicates a predisposition of an individual to develop cancer. A CC sample indicates a predisposition of an individual to develop cancer. A CC claimed method for detecting cancer recurrence in an individual diagnosed with and treated for cancer comprises measuring the level of bex4 gene methylation. The presence of hypermethylation indicates recurrence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                              Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
                                                                                                                                                                                                                                                                                           18-NOV-2004
06-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New vector comprising an isolated nucleic acid encoding a Bex4 polypeptide, useful for treating cancer, e.g. ovarian, cervica breast, prostate or liver cancer.
                                                        variation
                                                                                                             Homo sapiens
Unidentified
                                                                                                                                                             pulmonary embolism; paternity test; ds.
                                                                                                                                                                                                                                                        Human gene single nucleotide polymorphism #764.
                                                                                                                                                                                                                                                                                                                                                                                    AAF96003 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 2 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of PCR primer 19-R for a microsatellite marker within BAC CIT-B-470f8 on 19q14.3. PCR was performed on genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-2003; 2003US-0446877P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 CCAGCTGCTGCCTCACCT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGCTGCTGGCTCACCT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovarian, breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 39; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%;
nilarity 94.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chien J;
                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                         Location/Qualifiers
                                     *tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, e.g. ovarian, cervical, brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 19;
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/standard\_name= "Single nucleotide polymorphism"

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ABS59177 7
ABS59101 ID ABS55 XX XX ABS55 XX XX Huma XXX Huma XXX definition of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
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26-JUL-2000;
16-AUG-2000;
                                                                                                                                                                                                                                      diabetes; cell signal processing; metabolic pathway modulation; can adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma; immune response; neurodegenerative disorder; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Revised record issued on 18-NOV-2004 : The variantion incorrectly given a captial \ensuremath{\mathbf{V}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, mycoardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                                                                                                                                                                                                                             Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis; diabetes; cell signal processing; metabolic pathway modulation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2000; 2000WO-US024503
                              01-AUG-2002
                                                                                                                                       Homo
                                                                                                                                                                                                                     Crohn's
                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABS59191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABS59191 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis.
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                                                                                   WO200259313-A2
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                                                                                                                                                                                                             rohn's disease;
                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                             G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                         PCR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCAGCACAGCACTGGATTT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        вÞ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     given a captial V
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2000US-0220947P.
2000US-0225724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
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                                                                                                                                                                                                                                                                                                                                                                             coupled receptor, reverse primer #113.
                                                                                                                                                                                                                  multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
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                                                                                                                                                                                                                     sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΒP
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Pred. No. 1
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                                                                                                                                                                                                                  Albright hereditary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ß
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                                                                                                                                                                                                                  osteodystrophy;
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RESULT 8
ABN89181
ID ABN8
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AC ABN8
XX
AC ABN8
XX
AC ABN8
XX
XX

standard;

DNA;

22 ВÞ

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28-AUG-2002 ABN89181; ABN89181

(first entry)

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                                                                                                                                                                      cc diabetes, or a disorder related to cell signal processing and metabolic cc pathway modulation. The GPCR polypeptide and nucleic acid are also useful cf or diagnosting the presence of or predisposition to a disease associated co with altered levels of GPCR, particularly cancer. The GPCR nucleic acid are also useful cand polypeptide are especially useful in therapeutic or prophylactic applications for disorders associated with aberrant GPCR expression or activity. The DNA encoding the protein is useful in gene therapy for treating the above conditions. Furthermore, the nucleic acids and colypeptides are useful in treating adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, neurodegenerative disorders, casthma, inflammatory disorders, Crohn's disease, multiple sclerosis or Albright hereditary osteodystrophy. These are also useful in developing a cowerful assay system for functional analysis of various human disorders, cas well as in diagnostic applications. ABS58747-ABS59231 represent human cases of GPCR coding sequences, primers and probes of the invention
                                                                       Matches
                                                                                           Best
                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel isolated G-protein coupled receptor (GPCR) polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid and antibody are useful for treating, preventing or alleviating a GPCR-associated disorder or a pathological state in a subject, particularly a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New G protein coupled receptor polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li L, Ballinger RA, Pa
Casman SJ, Vernet CAM,
Gerlach V, Smithson G,
Peyman JA, Ellerman K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001; 2001US-0267464P.
22-FEB-2001; 2001US-02791021P.
14-MAR-2001; 2001US-0275946P.
23-MAR-2001; 2001US-0278150P.
18-APR-2001; 2001US-0284591P.
                                                                                                                                            Sequence 22 BP; 3 A; 9 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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16-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001; 2001WO-US049394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-)
                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-599789/64.
                                     133 TCTCTTTGGAGCACCTCTCAC 153
                                                                       18;
N
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                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page
   TCTCTTTAGAGCCCCTTTCAC
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0299327P
2001US-0312902P
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2001US-0259743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            586; 685pp; English
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                                                                                        6.7%;
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NM, Shenoy SG, Gusev V,

G, Stone DJ, Sciore P,

K, Gangolli EA, Millet
                                                                       0;
                                                                                          Score 16.2;
Pred. No. 1
                                                                       Mismatches
                                                                                           16;
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Malyankar UM, Edinger S
Macdougall JR, Gunther
                                                                                                          Length 22
                                                                         Indels
                                                                       0,
                                                                       Gaps
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CC (GPCRX) proteins given in ABB1440 to ABB81458. GPCRX proteins can have (GPCRX) proteins given in ABB81440 to ABB81458. GPCRX proteins can have cc antiatherosclerotic, anorectic, antibacterial, fungicide, protozoacide, cv inucide, analgesic, cytostatic, immunomodulator, metabolic, hypotensive, cc antiasthmatic, antiparkinsonian, hypertensive, osteopathic, anti-HIV, cc antiinflammatory, antiinferrility, neuroprotective, antianginal, cc antidepressant, antimanic, anticonvulsant, haemostatic, hepacotropic, cc fumunosuppressive, cerebroprotective, dermatological, antiaddictive, cc enhypotropic and gynaecological activities, and can be used in vaccines complete therapy. GPCRX proteins and polynucleotides can be used for creating or preventing a GPCRX-associated disorder such as creating or preventing a GPCRX-associated disorder related to cell signal cc and polynucleotides can also be used in the manufacture of a medicament for preventing or treating disorders or syndromes including developmental disorders, cardiomyopathy, atherosclerosis, cancer, neurodegenerative cd absorders, autoimmune disorders, infectious diseases and diabetes.
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26-FEB-2001;
27-SEP-2001;
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28-SEP-2000;
03-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                 Novel G-protein coupled-receptor polypeptides and nucleic acids diagnosing, treating cardiomyopathy, atherosclerosis, cancer, neurodegenerative, autoimmune disorders, infectious diseases and
                                                                                                                                                                                                                                                                                                                                                Example 1; Page 198; 213pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-499868/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spaderna SK, s
Macdougall JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JAN-2001;
24-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001;
18-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-2001; 2001WO-US030552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200226985-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPCR9 reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲Ţ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 2000US-0237581P.

2000US-02387359.

2000US-02407359.

2001US-0260019.

2001US-0260389.

2001US-02621569.

2001US-02631339.

2001US-0263691P.

2001US-0263691P.

2001US-0263691P.

2001US-02636929.

2001US-02636329.

2001US-02636322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Casman S,
, Shenoy S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPCRX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0236284P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          man S, Padigaru M,
henoy S, Gerlach V,
Smithson G, Li L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer SEQ ID NO:121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dickson K, Ve
, Ellerman K,
Malyankar UM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vernet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiatherosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edinger
Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ü
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gunther E;
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autoimmune disorders, in

The invention relates to a novel isolated G-protein coupled receptor X (GPCRX) polypeptide. The isolated protein, its encoding polynucleotide and the antibody of the isolated protein is useful for treating or preventing a GPCRX-associated disorder in a subject, preferably human, where the disorder is cardiomyopathy, atherosclerosis or diabetes. The isolated protein, its encoding polynucleotide and the antibody of the isolated protein is useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, anorexia,

Example 2;

Page 226; 264pp; English.

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Best Local S
Matches 18
                                                                                                                                                                                                                                 05-DEC-2000;
29-DEC-2000;
04-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiparkinsonian; cardiant; antiarteriosclerotic; immunosuppressive; hypotensive; haemostatic; antifertility; antiasthmatic; antiinflammatory; anti-HTV; G-protesin coupled receptor X; cardiomyopathy; atherosclerosis; diabetes; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidaemia; parkinson's disorder; immune disorder; Alzheimer's disease; dyslipidaemia; congenital of the strong disorder; cancer; hypertension; neoplasm; congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma; transplantation; adrenoleukodystroph; congenital adrenal hyperplasia; prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency; graft versus host disease; AIDS; bronchial asthma; Crohn's disease; multiple sclerosis; chromosomal mapping; tissue typing; forensic biology; gene therapy; transgenic animal; PCR; primer; ss.
                                                                                                                                                     Novel isolated G-protein coupled receptor polypeptide, designated NOVX, useful for treating or preventing in human receptor-associated disorders e.g. cardiomyopathy, atherosclerosis or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22 BP; 3 A;
                                                                                                                                                                                                                WPI; 2002-537559/57.
                                                                                                                                                                                                                                                                                                                                                                                      05-DEC-2001; 2001WO-US046530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200246229-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPCR related reverse PCR primer SEQ ID No 187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABT05734 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention
                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCTTTGGAGCACCTCTCAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCTTTAGAGCCCCTTTCAC 22
                                                                                                                                                                                                                                         Padigaru M,
, Mayotte JE,
KS, Ballinger
                                                                                                                                                                                                                                                                                                                           ; 2000US-0251459P.
; 2000US-0259007P.
; 2001US-00005041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; anorectic; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                       Burgess CE, Shimkets RA, UBaumgartner JC, Mishra V, RA, Wolenc AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                        Spytek KA;
, Vernet CAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٥,
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for

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RESULT 10
ADH49242
ID 4DH49242
XX ADH49
XX ADH49
XX ADH49
XX ADH49
XX Human
XW Human
XW hypot
XW Drime
OS Homo
XX WO200
XX WO200
XX WO200
XX BOS Homo
XX WO200
XX WO2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC immune disorders, haematopoietic disorders, and various dyslipidaemias, CC immune disorders, haematopoietic disorders, and various dyslipidaemias, CC metabolic disturbances associated with obesity, the metabolic syndrome X, CC wasting disorders associated with chronic diseases, and cancer. The CC disorders also include cardiomyopathy, atherosclerosis, hypertension, CC congenital heart defects, aortic stenosis, subaortic stenosis, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer, CC fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial CC asthma, Crohm's disease, and multiple sclerosis. The isolated protein, CC its encoding polymucleotide and the antibody of the isolated protein is CC useful in screening assays, detection assays (e.g., chromosomal mapping, CC tissue typing, forensic biology). The isolated protein, to detect GPCRX mRNA or a genetic lesion in a GPCRX gene, and to modulate GPCRX activity. The CC cell of the invention is useful for producing non-human transgenic CC animals. This polymucleotide sequence represents a reverse PCR primer of CC a GPCRX protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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Best Local Similarity
Matches 18; Conserv
                                                                           28-FEB-2001;
28-FEB-2001;
28-FEB-2001;
02-MAR-2001;
02-MAR-2001;
02-MAR-2001;
02-MAR-2001;
16-MAR-2001;
20-MAR-2001;
20-MAR-2001;
30-MAR-2001;
30-MAR-2001;
12-APR-2001;
12-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001;
27-FEB-2001;
28-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic; hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV85; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOV85 PCR primer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH49242;
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2001US-0271646P.
2001US-0271840P.
2001US-027240SP.
2001US-0272410P.
2001US-0272410P.
2001US-027241P.
2001US-0273048P.
2001US-0273048P.
2001US-0273048P.
2001US-0273049P.
2001US-0277324P.
2001US-0277324P.
2001US-0277324P.
2001US-0288039P.
2001US-0288034P.
2001US-02883443P.
2001US-0288696P.
2001US-0288696P.
2001US-0288696P.
2001US-0288696P.
2001US-0288696P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002WO-US005910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 C; 2 G; 8 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.2;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
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Ginns EI,

06-AUG-2003; 2003US-0493238P. 07-MAY-2004; 2004US-0568958P. 06-AUG-2004; 2004WO-US025526

(UYMA-) UNIV MASSACHUSETTS

17-FEB-2005 WO2005014850-A2 Analysis; mass

spectroscopy; PCR; primer; ss

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RESULT 11
ADX84073
ID ADX84
XX ADX84
AC ADX84
AC ADX84
DT 05-MA
XX DNA d
XX Analy
XX Analy
XX Analy
XX Analy
XX Analy
OS Synth
XX WO200
XX I17-FE
XX I7-FE
XX 06-AU
PR 07-MA
XX UYMA
PA (UYMA
XX Ginne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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31-MAY-2001; 2001US-0294634P.
20-JUN-2001; 2001US-0299645P.
21-JUN-2001; 2001US-0299845P.
05-JUL-2001; 2001US-0203242P.
13-AUG-2001; 2001US-0311981P.
16-AUG-2001; 2001US-0311858P.
17-AUG-2001; 2001US-0312864P.
17-AUG-2001; 2001US-0312818P.
17-SEP-2001; 2001US-0312818P.
25-FEB-2002; 2002US-00322818P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Casman SJ,
Gorman L, G
Miller CE,
Rastelli L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel human NOVX proteins, where X is any number from 1 to 91 and their coding sequences (see ADH48717-ADH48930). The proteins and coding sequences are useful for preventing treating disorders or syndromes e.g. atherosclerosis, hypertension, obesity or cancer. The present sequence was used in an example from the
                                                                                                                                                                                                                               DNA detection extension primer #48
                                                                                                                                                                                                                                                          05-MAY-2005
                                                                                                                                                                                                                                                                                     ADX84073;
                                                                                                                                                                                                                                                                                                                ADX84073 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22 BP; 3 A; 9 C; 2 G; 8 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 882; 923pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NOVX polypeptides or polynucleotides, useful for preventing treating disorders or syndromes e.g., atherosclerosis, hyperten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-698672/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alsobrook JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taupier RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                133 TCTCTTTGGAGCACCTCTCAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%;
85.7%;
                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.2;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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WPI; 2005-195764/20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC sample, comprising a central controller programmed to exchange and exchange information about the biological sample with an outside system or CC database and exchange information about the biological sample with one or CC more modules of the system, a sample transfer module for transferring a portion of the sample to a first container, a nucleic acid extraction CC module for extracting nucleic acids from cells within the portion and for transferring the portion from the first container to a second container, CC a nucleic acid measurement module for measuring the concentration of CC nucleic acids in the portion, a PCR preparation module for adding PCR CC reaction materials to the portion, a thermocycling module for amplifying CC a target sequence and extending a primer in the portion, a primer CC extension preparation module for adding primer extension reaction CC materials to the portion, a mass spectrometry preparation module for removing a sample of the portion from the second container to a support CC or analysis by mass spectrometry and a mass spectrometry module for analyzing the sample. The invention also relates to an automated method CC analyzing the sample. The virus is a virus of the family Herpesviridae, CC preferably Cytomegalovirus (CMV). The sample. The pathogen is a virus, batterium or fungus. The virus is a virus of the family Herpesviridae, CC preferably Cytomegalovirus (CMV). The system enables high accurate assays on nucleic acid sequences (e.g. clinically relevant nucleic acid cetection extension primer used in the scope of the invention.
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Best Local (
               Ginns EI,
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                                                                                                                                                                                                                                                                                                                                                                                                         ADX84489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                            06-AUG-2004; 2004WO-US025526
                                                                                                                                                                                                                      WO2005014850-A2
                                                                                                                                                                                                                                                                                           Analysis; mass spectroscopy; ss.
                                                                                                                                                                                                                                                                                                                                DNA target sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADX84489 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22 BP; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID NO 144; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analyzing sample.
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                                                    (UYMA-) UNIV MASSACHUSETTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 GTTTCCATCTCTTTGGAGCAC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
               Galdzicka M;
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                                                                                      2003US-0493238P.
2004US-0568958P.
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           relates to a system for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; 5 C; 3 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.2;
Pred. No. 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 22;
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materials to the portion, a mass spectrometry preparation module for removing a sample of the portion from the second container to a support for analysis by mass spectrometry and a mass spectrometry module for analyzing the sample. The invention also relates to an automated method for detecting mutations in a target gene. The diagnostic assay is an assay for detecting a pathogen in the sample. The pathogen is a virus, bacterium or fungus. The virus is a virus of the family Herpesviridae, preferably Cytomegalovirus (CMV). The system enables high accurate assays on nucleic acid sequences (e.g. clinically relevant nucleic acid.
                                                                                                                                                                                                                                                                                                                                                             more modules of the Bystem, a sample transfer module for transferring a portion of the sample to a first container, a nucleic acid extraction module for extracting nucleic acids from cells within the portion and for transferring the portion from the first container to a second container, a nucleic acid measurement module for measuring the concentration of nucleic acid in the portion, a PCR preparation module for adding PCR reaction materials to the portion, a thermocycling module for amplifying a target sequence and extending a primer in the portion, a primer extension preparation module for adding primer extension reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sample, comprising a central controller programmed to exchange information about the biological sample with an outside system or database and exchange information about the biological sample with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clinical assay system for assaying sample, has central controller, sample transfer module, nucleic acid extraction and measurement module, thermocycling module, primer extension module, mass spectrometry module analyzing sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a system for performing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 562; 207pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an assay on a biological
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Query Match Best Local Similarity Sequence 23 BP; ហ Ą 6.7%; 6 C; 3 G; 9 T; Score 16.2; Pred. No. 19 0 U; 15; 0 Other; DB 1; Length 23;

sequences) using mass spectrometry. This sequence represents sequence used in the scope of the invention.

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밁
                        8
                        126 GTTTCCATCTCTTTGGAGCAC 146
1 GTTTCCATCTATTTGGTACAC 21
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Matches

18;

Conservative

0,

Mismatches

ω --

Indels

٥,

Gaps

0

RESULT 13
ADL24990/c
ID ADL249
XX ADL249
XX ADL249
XX Intest
XX Intest
XX intest
XX intest
XX inflam
XX autoim
XX autoim
XX inflam
XX in ADL24990 standard; DNA; 19

20-MAY-2004 (first entry)

Intestinal epithelium/geyer's patch M cell-associated PCR primer #135.

inflammatory bowel disease; glutenenteropathy; infectious diseasutoimmune disease; haemolytic anaemia; rheumatoid arthritis; carave's disease; multiple sclerosis; allergy; asthma; diabetic immune system disorder; hypersensitivity; anaphylaxis; blood group incompatibility; ss; human; PCR; primer. intestinal epithelium cell development; peyer's patch M cell development; dermatitis; mellitus;

WO200280852-A2

17-OCT-2002

04-APR-2002; 2002WO-US010873

04-APR-2001; 2001US-0281416P

(DIGI-) DIGITAL GENE TECHNOLOGIES

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RESULT 14
ACL46618
ID ACL46618
AC ACL46
XX ACL46
AC ACL46
AC CHP3
XX CYTOS
XX CYTOS
XX HOMO
OS HOMO
OS HOMO
OS HOMO
OS HOMO
PR WO200
XX ACL46
PF 19-M2
XX HOMO
PR 20-M3
XX AMHI
PT BE X,
XX AMHI
PT EXPT
PT ACL11
PS Clair
XX The 1
PG Comport
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises DNA sequences which are associated with intestinal epithelium and peyer's patch M cells. The DNA sequences of the invention are useful for assessing, modifying, modulating or regulating intestinal epithelium or M cell development. The DNA sequences of the disease, glutenenteropathy, infectious diseases, autoimmune diseases (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's disease, multiple sclerosis, allergy, asthma and diabetic mellitus), anaphylaxis, and blood group incompatibility. The present DNA sequence represents a PCR primer that was used to amplify an intestinal epithelium/peyer's patch M cell-associated DNA sequence of the invention
                                                                                             Pharmaceutical composition comprising an agent capable of modulating expression level or protein activity of a gene, e.g. ABCC4, or a T constituted by the polypeptide or antibody, and a carrier, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated or purified polypeptide encoded by genes associated with intestinal epithelium or M cell development, differentiation or function, useful for treating autoimmune diseases and infectious diseases.
                                                      Claim 3; SEQ ID NO 7690; 113pp; English
                                                                                                                                                                                                                                     20-MAY-2003; 2003US-0471729P
                                                                                                                                                                                                                                                                19-MAY-2004; 2004WO-US015645
                                                                                                                                                                                                                                                                                           06-JAN-2005
                                                                                                                                                                                                                                                                                                                     WO2005001092-A2
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                  ENPP3 target oligonucleotide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACL46618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.5%;
nilarity 89.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                 Slonim DK,
                                                                                                                                                                                                                                                                                                                                                                        therapy; Vaccine;
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Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                          RNA Interference; cancer;
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cell
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protein comprising: The present

ing: (a) an a

agent capable of n f a cancer-related

a novel pharmaceutical composition of modulating an expression level

transmembrane

protein (CRTP) or gene

cancer, lung cancer, breast cancer, prostate

cancer,

liver cancer,

kidney

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invention relates to

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ARESULT 15
ACL469BO/C
ID ACL469
XX ACL469
XX CYLOST
XW CYCOST
XW Short
XX Synthe
PN W02005
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PN W02005
XX Synthe
PN TO-MAY
XX 19-MAY
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                        The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAR-2005
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                                                                                                                                                                                                                                                                                                                                                                Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                    treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-2003; 2003US-0471729P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENPP3 siRNA antisense sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2005-075568/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 AACAGAACGACCTGTTAAG 181
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 8052; 113pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                       cancer.
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                                      The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or gene protein activity of a cancer related transmembrane protein (CRTP) or gene (C) an antibody specific for a CRTP, or a T cell activated by a CRTP; and (C) a carrier. The pharmaceutical composition may also comprise a composition may also comprise a composition protein composition may also comprise a composition protein composition may also comprise a composition of the cRTP by RNA interference or an antisense mechanism. The CRTPs of the craft of cancer, breast cancer, prostate cancer, liver cancer, kidney craft for the short interfering RNAs (siRNA) oligonucleotide. Note: The sequence craft cate or this patent did not form part of the printed specification, but created on electronic format directly from WIPO at
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                             was obtained in electronic ftp.wipo.int/pub/published_
                                                                                                                                                                                                                                                                                                                     Claim 3;
                                                                                                                                                                                                                                                                                                                                                    treating cancer.
                                                                                                                                                                                                                                                                                                                                                                Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
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Query Match

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RESULT 18

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Matches
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                                                                                                                                                                                        cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a target oligonucleotide from one such CRTP for which short interfering RNAs (sirNA) were produced. Note: The sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
                                                                                                                  Sequence
                                                                                                                                                ftp.wipo.int/pub/published
                                                                                                                                                              not form part of the printed specification, electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 8050; 113pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule useful for identifying polymorphisms associated with CYP3A4, CYP3A5 or GSTM1 substrates which influence breast cancer treatments, comprises at least one base variation from human CYP3A4 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytochrome P450; CYP3A4; CYP3A5; glutathione S-transferase; polymorphism; GSTM1; breast cancer; therapy; chemotherapeutic agendrug-drug interaction; drug adverse effect; anti-cancer agent; enz
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Expression system associated primer SEQ ID NO
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                                                         AEA33500;
                                                                                    AEA33500 standard; DNA; 22 BP
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nilarity 81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colvin OM,
                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agent;
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RESULT 20
AAF26513
ID AAF26
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a DNA construct (I) comprising a mammalian beta actin promoter being functionally coupled to the enhancer. Also described are: a vector (II) comprising (I); a cell (III) comprising (II); a tripotent cell comprising (II); and increasing (M1) an expression of a DNA, comprising integrating beta actin promoter to the upstream of the DNA, where the promoter is obtained from a host cell, in which the DNA exist. (II) is useful for expressing a DNA in a host cell such as mammalian cell e.g. rodent cell. (III) is useful for producing protein which involves culturing (III) in a culture medium and recovering protein e.g. antibody or treating ADS or cancer. (I) enables to produce large quantities of protein e.g. antibody. This sequence represents a DNA construct associated primer.
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acquired immune deficiency syndrome; immune disorder; cancer;
protein production; antibody production; PCR; primer; ss.
                                                                                                                                                                                                                                                                      Steroid receptor coactivator-3; SRC-3; antisense; inflammation; tumour; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF26513 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel DNA construct comprising mammalian beta actin promoter being functionally coupled to enhancer, useful for producing protein e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-425413/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-2004; 2004WO-JP018006
                                                                                                                                                                                                                                                                                                                                                                 Human SRC-3
                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody or treating AIDS or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsunoda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Habu K;
                                                                                                                                                                                                                                                                                                                                                                 antisense oligonucleotide #17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 4 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.8%;
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); Mismatches
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Pred. No. 19
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                                                                                                                                                                                                                                                                                                         infection;
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15-NOV-1999;

99US-00440612

05-DEC-2000.

Homo sapiens

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Best Local Similarity
Matches 16; Conserv
                                                                                 New isolated Toxoplasma gondii nucleic acids used, infection caused by this microorganism.
                                                                                                                                                                                                                                                                                                                            Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium Toxoplasma oocyst; RT-PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to an antisense oligonucleotide, targeted to a nucleic acid molecule encoding human steroid receptor coactivator-3 (SRC-3). The invention is useful for inhibiting the expression of SRC-3 in human cells or tissues in vitro. It is useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. It is useful prophylactically, to prevent or delay infection, inflammation or tumor
The invention provides isolated Toxoplasma gondii nucleic acids that encode immunogenic polypeptides. The T. gondii nucleic acid molecule immunogenic proteins and antibodies to the proteins can be used to inhibit T. gondii occyst shedding in a cat due to infection with T.
                                                                                                                       WPI; 1999-418930/35
                                                                                                                                                                                                                      18-DEC-1998;
                                                                                                                                                                                                                                             01-JUL-1999
                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                       (HESK-) HESKA
                                                                                                                                                                                              19-DEC-1997;
                                                                                                                                                                                                                                                                     WO9932633-A1
                                                                                                                                                                                                                                                                                           Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                               Primer for RT-PCR analysis of T.
                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX91393 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antisense compound useful to prevent or delay infection, inflammation or tumor formation, specifically hybridizes with an inhibits the expression of human steroid receptor coactivator-3.
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                                                                                                                                               Lutz
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                                                           381pp;
                                                                                                                                               SB,
                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%;
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                                                            English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                             gondii immunogenic protein
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                                                                                                                                                                                                                                                                                                                                           cat;
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RESULT 22
AAS42716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                         The invention relates to detection of parasite oocysts or cysts in a faeces sample comprising contacting the sample with a solid support, drying and then washing the sample with an aqueous wash solution, addir an aqueous elution solution and eluting DNA from the sample by heating and amplifying by PCR oocyst/cyst-specific DNA and detecting parasite amplification products. The method is useful for detecting parasite ocysts e.g., enteric apicomplexa oocysts such as Cryptosporidium oocysts. The method is also useful for developing vaccines to prevent cysts. The method is also useful for developing vaccines to prevent ocytts shedding in cats. The present sequence is a PCR primer used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gondii. They can be used for preventing T. gondii infection and for preventing the spread of T. gondii infection. They can also be used for preventing T. gondii infection. They can also be used for detecting T. gondii infection. The detection method can be used to detect parasite cysts or occysts in feces, e.g. from enteric apicomplexa occysts such as Cryptosporidium occysts and Toxoplasma occysts. Sequences AAX91276-395 primers used in RT-PCR analysis of nucleic acid sequences encoding immunogenic T. gondii proteins
                                                                                                                                                                                                                                                                Detecting parasite oocysts or cysts in feces, comprises eluting DNA from sample into aqueous solution by heating, amplifying DNA with primers specific for oocysts or cysts being detected, and detecting amplification
                                                                                                                                                                                                                                                                                                                                                                Milhausen MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic protein; oocyst; faeces; ss; enteric apicomplexa oocyst; Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine; oocyte shedding; PCR primer.
                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                 WPI; 2001-529100/58
                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxoplasma gondii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-1998;
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                             DNAs
                                                                                                                                                                                                                     2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCTGTTTGGGTTGTCTGG
                                                                                                                                                                                                                  Page 25; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                           encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             97US-00994825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 C; 9
                           immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein PCR primer nTG78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Pred. No. 23;
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                           proteins from Toxoplasma gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 Other;
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                                                                                                                                                     adding
                                                                                        oocysts
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Best Loc Matches Query Match Best Local

ch 6.3%; l Similarity 85.0%; 17; Conservative

Score 15.2; D Pred. No. 23; 0; Mismatches

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AC ADP7
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                                                                                                                                 RESULT 24
                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                   The invention relates to an isolated Toxoplasma gondii protein. The protein is useful for inhibit occyst shedding by cats infected with Toxoplasma gondii. The protein is useful for preventing or ameliorating diseases caused by infection with T. gondii. The nucleic acid can be used as genetic vaccine which encodes the protein. The protein and the nucleic acid are used as diagnostic respents for detection of T. gondii infection. The present sequence is used in the exemplification of the
          GFAT; Antidiabetic; Cardiant;
Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
                                           Chimeric phosphorothioate oligonucleotide
                                                                                                                                                                                                                                                     Sequence 20
                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 262; 198pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               Novel immunogenic Toxoplasma gondii proteins useful for inhibiting oocyst shedding by cats infected with Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-899768/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1997;
18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG17312 standard; DNA;
                                                                 12-AUG-2004
                                                                                       ADP78412;
                                                                                                           ADP78412 standard;
                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-2002; 2002US-00321856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILH/) MILHAUSEN M J
                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gondii sequencing primer #118
                                                                                                                                                                                       189
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Best Local
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             Human ABC1 cholesterol transporter; chromosome 9q31; ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangier disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
                                                                                      Human ABC1
                                                                                                                   29-JAN-2001
                                                                                                                                                                            AAC69341 standard;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotides inhibit human GFAT expression.
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e= "2-methoxyethyl
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peripheral vascular disease;

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GCAGCCTCACCCGCTCTTCC 20

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CC disease, particularly coronary artery disease, but also cerebrovascular CC disease, coronary restenosis, and peripheral vascular disease. CC Conversely, a high level of HDL has protective effects against CC cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic cardiovascular disease comprising the administration of an expression of CC cardiovascular disease comprising the administration of an expression cc vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which minic ABC1 activity, compounds which cc stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an CC increased risk for cardiovascular disease due to polymorphisms in the CC area of the forman ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, coronary artery disease, associated CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick CC disease. They may also be used in the treatment of disease seconiar activity, such as Alzheimer's disease, Niemann-Pick CC disease. They may also be used in the treatment of disease associated CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick CC disease. The ABC1 because acceptance of Cansank Accession No. CAN10005. and X75026. and the nucleic company and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol trafficking in monocytes and fibroblasts, being located on chromosome 931, and mutations in this gene encoding ABC1 is located on chromosome 931, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders. Tangier disease (TD) and familial HDL deficiency (FHA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease.
                                               sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The present sequence represents a polymorphic site of the human ABC1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the human ABC1 cholesterol transporter protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New ABC1
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01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1999;
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N BIORESEARCH INC.
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99US-0138048P.
99US-0139600P.
99US-0151977P.
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Query Match Best Local ( Matches

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AAH62254/c
ID AAH62254 standard; DNA; 21
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                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid segments of the human genome, particularly from genes including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis.
                                                                                                                                                                                Revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 42; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cargill M,
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Unidentified
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12-SEP-2001
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/standard_name= "single nucleotide polymorphism"
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30-APR-2003;
23-MAY-2003;
23-OCT-2003;
24-NOV-2003;
                                                                                                                                                                                                                                                                         The invention relates to a chemically synthesized double stranded short interfering nucleic acid (siNA) molecule (I) that directs cleavage of a county of the through RNA interference (RNAi), where one strand of the siNA molecule comprises nucleotide sequence having sufficient complementarity to the c-JUN RNA for the siNA molecule to direct cleavage of the c-JUN RNA through RNA interference. (I) is useful for inhibiting mitogen activated protein kinase gene (e.g., c-JUN, JNK1, JNK2, p38, ERK1 or ERK2) expression associated with diseases e.g., inflammatory disease, autoimmune disease, allergy, cancer. (I) exhibits improved RNA interference activity and nuclease resistance. The present sequence represents a human MAP kinase 8/JNK1 modified siRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel short interfering nucleic acid molecule useful for inhibiting mitogen activated protein kinase gene expression e.g., c-UUN associated with diseases e.g., inflammatory disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA interference; mitogen activated protein kinase inhibitor; inflammation; immunosuppressive; immune disorder; autoimmune di allergy; antialnergic; cytostatic; neoplasm; cancer; ss; siRNA; gene silencing; small interfering RNA; MAP kinase inhibitor.
                                                      ADW72412;
                                                                              ADW72412 standard;
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Polisky B;
                            24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
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; 2003US-00720448.
; 2004US-00757803.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1705; 322pp; English.
                                                                                                                                                                                               Conservative
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                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8/JNK1 modified siRNA
                                                                                                                                                                                                                                                   A,
                                                                              DNA;
                                                                                                                                                                                                            55.0%;
                                                                                                                                                                                                                                                   3 C;
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G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usman
                                                                                                                                                                                                             Score 15.2;
Pred. No. 2:
                                                                                                                                                                                                                                                    2 T;
                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                   6 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haeberli P,
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                                                                                                                                                                                                                                                    0 Other;
                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                         Length
                                                                                                                                                                                                 Indels
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Claim

SEQ ID NO 370;

98pp; English.

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Cell transduction; organelle; chloroplast; mitochondria; Alpers Disease; carnitine deficiency; pyruvate carboxylase deficiency; mitochondrial cytopathy; mitochondrial DNA depletion; mitochondrial encephalopathy; mitochondrial myopathy; neuropathy; ataxia retinitis pigmentosa; pyruvate dehydrogenase deficiency; Alzheimers disease; Parkinsons disease; diabetes; aging; heart disease; mitochondrial polymerase; PolG; muscular-gen; ophthalmological; cerebroprotective; anticonvulsant; antiparkinsonian; nootropic;
New polynucleotide encoding a polypeptide having an organelle or chloroplast localization signal, and a protein transduction domain, useful for treating diseases with defective mitochondrial function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-2003; 2003US-0482603P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-2004; 2004WO-US020454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; cardiovascular-gen.; antidiabetic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2005001062-A2
                                                                                                                                                                                                    2005-075550/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuropathy; ataxia;
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Considerable to a polymicide control a recombinant control particle relates to a polymicide comprising an organelle and/or chloroplast localization also relates to a comparish particle comprising an bacteriophage, a method of transfecting careful comprising a bacteriophage, a method of transfecting careful comprising a bacteriophage, a method of transfecting careful comprising a protein transduction domain and an organelle comprising contacting the cell with a vector operably linked to a collypeptide having a protein transduction domain and an organelle careful carefu The invention relates to a polynucleotide encoding a

Mitochondrial polymerase PolG target DNA #59

dehydrogenase deficiency, Alzheimers disease, Parkinsons disease, diabetes, aging and heart disease. This sequence represents mitochondrial polymerase PolG target DNA used in the scope of the invention.

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RESULT 29
ADW72414
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Best Local :
polypeptide comprising an organelle and/or chloroplast localization algunal and a protein transduction domain. The invention also relates to a recombinant viral vector comprising the polynucleotide, a cell comprising a modified organelle comprising a bacteriophage, a method of transfecting a cell comprising contacting the cell with a vector operably linked to a polypeptide having a protein transduction domain and an organelle comprising transfecting the cell with a recombinant lambdaphage, the recombinant lambdaphage comprising a polynucleotide encoding an organelle comprising lambdaphage comprising a polynucleotide encoding an organelle protein, where the organelle localization signal operably linked to a bacteriophage lambda surface protein, where the organelle localization signal is displayed on a surface of the recombinant lambdaphage and directs the recombinant lambdaphage to the organelle, and where the recombinant lambdaphage introduces a polynucleotide into the organelle, a composition comprising
                                                                                                                                                                                                                                                                                                                                                        New polynucleotide encoding a polypeptide having an organelle or chloroplast localization signal, and a protein transduction domain, useful for treating diseases with defective mitochondrial function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      retinitis pigmentosa; pyruvate dehydrogenase deficiency;
Alzheimers disease; Parkinsons disease; diabetes; aging; heart disease;
mitochondrial polymerase; PolG; muscular-gen.; ophthalmological;
cerebroprotective; anticonvulsant; antiparkinsonian; nootropic;
neuroprotective; cardiovascular-gen.; antidiabetic; ss;
short interfering RNA; siRNA; RNA interference; gene silencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell transduction; organelle; chloroplast; mitochondria; Alpers Disease; carnitine deficiency; pyruvate carboxylase deficiency; mitochondrial cytopathy; mitochondrial DNA depletion; mitochondrial encephalopathy; mitochondrial myopathy; neuropathy; ataxia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JAN-2005.
                                                                                                                                                                                                                                                                               The invention relates to a polynucleotide encoding a recombinant
                                                                                                                                                                                                                                                                                                                    Claim 96; SEQ ID NO 372; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENC-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADW72414 standard; RNA; 21
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85.0%;
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Pred. No. 22
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RESULT 30
AEC03076/c
ID AEC03
XX AEC03
XX AEC03
AC AEC04

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Best Local
Watson JD,
Abernethy N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immediate type hypersensitivity; immunosuppressive; asthma; antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory; ear, nose, throat disease; inflammation; respiratory disease; immune disorder; IgB; short interfering nucleic acid; siNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IgE short interfering nucleic acid SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEC03076 standard; DNA;
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                                                                                                                                                                                  20-FEB-2004; 2004US-0546434P
                                                                                                                                                                                                                                                        21-FEB-2005; 2005WO-NZ000021
                                                                                                                                                                                                                                                                                                                                                                                                            WO2005080410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive; expression; RNA interference; allergy; atopic dermatitis; urticaria; dermatological; dermatological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiallergic; antiinflammatory; antiasthmatic; dermatological;
immunosuppressive; expression; RNA interference; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            silencing;
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                                                                                                            GENESIS RES & DEV CORP LTD.
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Murison GJ,
, Webster G;
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                                  Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.2;
Pred. No. 2
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                                      Havukkala
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RESULT 31
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inflammatory disease; polymorphism; 5-lipoxygenase; asthma; ulcerative colitis; bronchitis; sinusitis; psoriasis; rhinitis; arthritis; diagnosis; treatment; PCR primer; ss.
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                        Classifying patients with inflammatory disease, specifically according to polymorphisms in 5-lipoxygenase gene regulatory
                                                                                                                                                                                                                                                                    06-MAY-1996;
25-APR-1997;
     according to
to identify
                                                                                                                                                                                                                                                                                                                                             29-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sense primer
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                                                                                                            WPI; 1997-558997/51.
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                                                                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL.
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17; Conserv
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  to polymorphisms
fy candidates for
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97US-00846020.
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     lipoxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.2; D
Pred. No. 22;
0; Mismatches
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                                                                                                                                                             Beier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-lipoxygenase gene
                                                                                                                                                             Ò
                                                                                                                                                             Grobholz
  inhibitor treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 Other;
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                                                      asthma
                             region,
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atopic
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The present sequence was used in the development of a novel method for classifying patients suffering from an inflammatory disease. The method comprises identifying in DNA from at least 1 patient a sequence polymorphism, as compared with the normal 5-lipoxygenase (5-LOX) gene (AAT88431), in a 5-LOX regulatory gene sequence. The method can be applied to subjects with asthma, ulcerative colitis, bronchitis, sinusitis, psoriasis, allergic and non-allergic rhinitis, lupus or rheumatoid arthritis. Specifically it can be used to diagnose asthma or susceptibility to disease, identify treatments suitable for individual
                                                                                                                                                                                                                                                                                                             Example 1;
                                                                                                                                                                                                                                                                                                             Page 19; 56pp; English.
                                                                                            asthma or
                                                                                                                                                                                                                                         method
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S
                             Query Match
Best Local S
Matches 15
                                                              Sequence 18
              47
                               15;
                                       Similarity
             CCTCCCCAGCTGCTG
                                                               BP; 1 A; 9 C; 4 G; 4 T; 0 U; 0 Other;
                              larity 100.0%;
Conservative
                                              6.2%;
16
              61
                              0
                                      Score 15;
Pred. No.
                               Mismatches
                                       DB 1;
26;
                              0
                                              Length 18;
                               Indels
                              0,
                             Gaps
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patients or assess the likely success of treatment

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N

CCTCCCCAGCTGCTG

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Equine herpesvirus type 1-related PCR primer
                         06-MAY-2004
                                                 ADJ95475;
                                                                          ADJ95475 standard;
                         (first
                                                                          DNA;
                         entry)
                                                                          18
                                                                          ВP
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Equine herpesvirus type 4; genetic ma virucide; vaccine; EHV-1 strain V592 neurovirulence; herpesvirus disease; virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4; Equine herpesvirus type 4; genetic marker; ORF30-ml region marker; polymerase ORF30-ml PCR; primer; ss. region;

Equine herpesvirus 1. WO2004011677-A2

26-JUL-2002; 2002US-0398576P 23-JUL-2003; 2003WO-GB003279

(ANIM-) ANIMAL HEALTH TRUST.

Poynter N, Nugent ŗ, Birch-Machin I, Allen ດ

WPI; 2004-143877/14.

treating herpe to an ORF30-ml Assessing the virulence of a herpesvirus isolate, useful in preventing or treating herpesvirus infection, by using virulence marker corresponding region.

Claim 24; Page 60; 63pp; English.

RESULT 32
RD395475
ID 95475
ID 95475
AC ADJ95
AC This invention relates to a novel method of assessing the virulence of a herpesvirus isolate, for example Equine herpesvirus type 1 (EHV-1) or type 4 (EHV-4), which comprises using a genetic marker, especially an ORF30-ml region marker. The invention may be useful for the production of compounds with a virucide activity or for the development of a vaccine. The method, kit and sequence of the EHV-1 strain V592 polymerase ORF30-ml region are useful for assessing the virulence of a herpesvirus or neurovirulence. The vaccine is useful for immunising a host against a herpesvirus disease and for treating disease. The present sequence is that of a PCR primer which was used in the exemplification of the invention.

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RESULT 33
AEE10387/
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                                                            The invention relates to a new nucleotide sequence which comprises: a CC first nucleic acid sequence encoding a signal peptide that localizes a CC protein of interest fused to the signal peptide to an endoplasmic CC reticulum-derived protein body within a cell; a second nucleic acid sequence encoding the protein of interest; and a regulatory element CC sequence encoding the protein of interest; and a regulatory element CC than one of the first nucleic acid, the second nucleic acid and the CC regulatory element, is heterologous with respect to one or more than one of first nucleic acid, the second nucleic acid and the regulatory CC element. Also described are: a nucleotide sequence comprising, a gamma-cc zein regulatory element operatively linked with a nucleic acid sequence ce encoding a gamma-zein signal peptide fused to a heterologous protein of interest, and a gamma-zein 3' UTR operatively linked to the nucleic acid sequence; a plant comprising the nucleotide sequence; a plant comprising the protein of interest; and an cxpression construct comprising the protein of interest; and an expression construct comprising the following operatively linked elements CC protein of lanterest comprising the following operatively linked elements cut to the nucleotide sequence is useful for producing cut transcenic plants and seeds having heterologous protein. Such as gamma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a gamma-zein signal protein of interest; transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleotide sequence comprising a first nucleic acid sequence encoding a gamma-zein signal peptide, a second nucleic acid sequence encoding the protein of interest; and a regulatory element, useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize gamma-zein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18
                                     zein peptide,
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15; Conserv
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plants and seeds having heterologous protein, such as gam
de, localized to the endoplasmic reticulum protein bodies
enic plant. The produced proteins are useful in treatment
somal diseases such as mucopolysaccharidosis. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2;
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metabolic disorder.
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ilarity 100.0%;
Conservative (
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2004US-0598428P.
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Pred. No.
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26;
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RESULT 34
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                      This invention relates to a novel nucleic acid that encodes the polycystic kidney and hepatic disease | (PRHD1) polypeptide. It has been identified that a mutation in the PKHD1 gene is associated with autosomal recessive polycystic kidney disease (ARPKD), which is characterised by enlarged kidneys and congenital hepatic fibrosis, and is most commonly observed in children and infants. The present invention describes the identification of the PKHD1 gene, mapped to human chromosome 6p21.1-p12, and splice variants thereof. The PKHD1 polynucleotides and polypeptides are useful in diagnostic testing and for developing targeted therapeutic interventions for patients with ARPKD. Furthermore, they exhibit proliferation, cellular adhesion and repulsion. This oligonucleotide sequence is a PCR primer used to amplify human PKHD1 exons for mutation analysis, in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                Germino
Furu VM;
                                                                                                                                                                                                                                                                                                   New polycystic kidney and hepatic disease 1 polynucleotides and polypeptides, useful in diagnostic testing and for developing targeted therapeutic interventions for patients with autosomal recessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR; ss; polycystic kidney and hepatic disease 1; PKHD1; autosomal recessive polycystic kidney disease; ARPKD; congenital hepatic fibrosis; human; nephrotropic; cell proliferation; cellular adhesion; repulsion; primer.
                                                                                                                                                                                                                                                      Disclosure; Page 40; 41pp;
                                                                                                                                                                                                                                                                                    polycystic kidney disease.
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-877030/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2003; 2003WO-US003410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a PCR primer used with primer AEE10386 to amplify and clone the 5'UTR and signal peptide-encoding sequences of gamma-zein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (UABR-) UAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer used to amplify human PKHD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                             Nagasawa Y,
                                                                                                                                                                                                                                                        English.
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Pred. No. 2
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Query Match Best Local S Matches 16

l Similarity

Conservative

0,

Mismatches

2.

Indels

0,

Gaps

0

6.1%;

Score 14.8; Pred. No. 2:

25; DB 1;

Length 20;

Sequence

20

B₽;

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7 C;

3 G; 4 T; 0 U; 0 Other;

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ARESULT 35
ADP78946
ID ADP78
AC ADP78
AC ADP78
AC ADP78
AC Chime
AC Chime
AC GFAT;
AC GFAT;
AC GFAT;
AC GFAT;
AC CHIME
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                                                                               Query Match
Best Local
                                                        Matches
                                                                                                                                                                                                           The present invention relates to a compound which specifically hybridizes with a nucleic acid molecule encoding GFAT, and inhibits the expression of GFAT, Specifically claimed are antisense oligonucleotides capable of modulating the expression of GFAT, and which comprise any of the 3063 sequences of 20 base pairs, given in the specification. The compound, composition and methods are useful for treating a disease or condition associated with GFAT, such as a disease or condition, e.g. diabetes, a cardiovascular or neurological disorder, ischemia/reperfusion injury. They are also useful in research and diagnostics for modulating the expression of GFAT. The present sequence represents a chimeric phosphorothicate oligonucleotide with 2'-MOE wings and a deoxy gap, these oligonucleotides inhibit human GFAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase (GFAT), for treating diabetes, a cardiovascular or neurologic disorder
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Broschat KO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2002; 2002US-0419268P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ischemia/reperfusion injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2003; 2003WO-US033332.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reperfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric phosphorothioate oligonucleotide #2745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP78946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP78946 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHAA )
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                                                        16;
                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHARMACIA CORP.
                                                                                                                                                                20
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                                                                                                                                                              BP;
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 2745; 175pp; English.
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/note= "2-methoxyethyl wing"
17. 20
/*tag= b
/mod_base= other
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1. .4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "2-methoxyethyl wing"
                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cardiant;
                                                                            6.1%;
                                                                                                                                                              6 C; 4 G; 7 T; 0 U;
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                                                  0;
                                                                               Score 14.8;
Pred. No. 2
                                                     Mismatches
                                                                                 25;
                                                                                                                                                              0 Other;
                                                                                                     DB 1; Length 20;
                                                     <u>ب</u>
                                                     Indels
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                                                  Query Match
Best Local S
Matches 16
                                                                                                                        The present invention relates to a compound which specifically hybridizes with a nucleic acid molecule encoding GPAT, and inhibits the expression of GFAT. Specifically claimed are antisense oligonucleotides capable of modulating the expression of GFAT, and which comprise any of the 3063 sequences of 20 base pairs, given in the specification. The compound, composition and methods are useful for treating a disease or condition associated with GFAT, such as a disease or condition, e.g. diabetes, a cardiovascular or neurological disorder, ischemia/reperfusion injury. They are also useful in research and diagnostics for modulating the expression of GFAT. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these oligonucleotides inhibit human GFAT expression.
                                                                                                                                                                                                                                                                                                                         New compounds, particularly antisense oligonucleotides targete nucleic acid encoding glutamine-fructose-6-phosphate amidotrar (GFAT), for treating diabetes, a cardiovascular or neurologic ischemia/reperfusion injury.
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 2738; 175pp;
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-348453/32.
                                                                                                                                                                                                                                                                                                                                                                                                                    Broschat KO, Crosby SD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFAT; Antidiabetic; Cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric phosphorothioate oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHAA ) PHARMACIA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reperfusion;
                         56
                                                  16; Conserv
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                CTGCTGCCTCACCTGCTT 73
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CTGCTGTCTCACCTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                    BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
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/note= "2-methoxyethyl wing"
17. .20
/*tag= b
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/note= "2-methoxyethyl wing"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                            6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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19
                                                               Score 14.8;
Pred. No. 2
                                                   Mismatches
                                                                                                                                                                                                                                                                                                 English.
                                                                25;
                                                                           DB
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                                                  <u>ب</u>
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amidotransferase
eurologic disorder,
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                                                  Gaps
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                                                                                         RESULT 37
ADP81801/c
ID ADP81801 standard;
                                            Query Match
Best Local S
Matches 16
                                                                                        Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                        preparing a composition for treating autoimmune disorder. It useful in gene therapy. The present sequence is an antisense oligonucleotide targeted to human MD-1 RP105-associated DNA.
                                                                                                                                                         The invention relates to compounds, compositions and methods for modulating the expression of MD-1 RP105-associated (also called as MD-1 and MD1) DNA. The composition comprise antisense oligonucleotides targeted to MD-1 RP105-associated DNA. The compound is useful for
                                                                                                                                                                                                                   Example 15;
                                                                                                                                                                                                                                         disorder.
                                                                                                                                                                                                                                                  New oligonucleotide compound that inhibits expression of MD-1 RP105-
associated, useful for preparing a composition for treating autoimmu
                                                                                                                                                                                                                                                                                       WPI, 2004-440335/41.
                                                                                                                                                                                                                                                                                                              Dobie KW,
                                                                                                                                                                                                                                                                                                                                                        09-DEC-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MD-1 RP105-associated; MD-1; MD1; autoimmune disorder; gene therapy; human; antisense; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MD-1 RP105-associated antisense oligo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                       10-JUN-2004.
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                                                       Local Similarity
18
                     59
CAGACTCACCTGCTTTTC 1
                     CIGCCICACCIGCITITC 76
                                                                                                               is used to illustrate the method of the invention.
                                             Conservative
                                                                                                                                                                                                                  SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                          2002US-00316242.
                                                                                                                                                                                                                                                                                                                                                                                2002US-00316242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/note= "2'-methoxyethyl
16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "Phosphorothicate backbone
residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "2'-methoxyethyl (2'-MOE) bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                     6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               base- OTHER
                                                                                                                                                                                                                40; 63pp; English.
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                                         0
                                                     Score 14.8;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (2'-MOE) bases"
                                                                 DB 1; Length 20;
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                                            Indels
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                                                                                                                                               It is also
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RESULT 38
ADP81821
ID ADP81
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AC ADP81
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preparing a composition for treating autoimmune disorder. It is also useful in gene therapy. The present sequence is human MD-1 RP105-associated DNA target region. This sequence is used to illustrate the
                                                                             Synthetic.
                                                                                                                                                          glycosylase; enzyme; saccharide; pharmaceutical; food
industrial raw material; PCR; primer; ss; plant.
                                                                                                                                                                                                                                          Solanum glycosylase related PCR primer SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                          ADR70686 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to compounds, compositions and methods for modulating the expression of MD-1 RP105-associated (also called as and MD1) DNA. The composition comprise antisense oligonucleotides and mD1) DNA. The composition comprise and modulating to the composition of the composition of the composition of the compound is useful for targeted to MD-1 RP105-associated DNA. The compound is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New oligonucleotide compound that inhibits expression of MD-1 RP105-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-440335/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MD-1 RP105-associated DNA target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGACTCACCTGCTTTTC
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                                                                                                                                                                                                                                                                                                entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G; 6 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.8;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a glycosylase protein (I) having a sequence of SEQ ID NO:1, 3, 7, 9 or 11 (S1) (ADB70664, ADB70666, ADB70672 or ADB70672 or ADB70670, a sequence comprising (S1) in which one or more amino acids are deleted, substituted and/or added, or a sequence exhibite slycosylase activity. Also described: (1) a gene (II) encoding (I); (2) a recombinant vector (III) containing (II); (3) a transformed host (IV) comprising (II) or (III); and (4) producing (I), using (IV). (I) is useful for combining a saccharide with a substrate, which involves used in manufacturing pharmaceuticals, food additive or as industrial raw material. (I) has high substrate specificity. The present sequence represents a PCR primer for a Solanum glycosylase protein, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAR-2003; 2003JP-00055468.
31-MAR-2003; 2003JP-00093642.
                                                                                                                                                                                                                                                                                          14-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New glycosylase protein derived from Solanaceae plant, useful for manufacturing pharmaceuticals and food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAR-2004; 2004WO-JP002675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-SEP-2004.
            WPI; 2005-345404/35
                                     Bennett CF,
                                                               (ISIS-)
                                                                                        11-DEC-2002;
                                                                                                                  11-DEC-2002; 2002US-00317869.
                                                                                                                                             12-MAY-2005.
                                                                                                                                                                      US2005101000-A1.
                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                         expression;
                                                                                                                                                                                                                                     88; antisense; phosphodiesterase 4b; PDE 4b; immunosuppressive;
                                                                                                                                                                                                                                                              Human phosphodiesterase 4B antisense oligo target site SEQ ID NO:113
                                                                                                                                                                                                                                                                                                                    ADZ47085
                                                                                                                                                                                                                                                                                                                                             ADZ47085 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; SEQ ID NO 23; 61pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-662429/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muranaka T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                            38 GGAGCTCCACCTCCCCAG 55
                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                               SISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            GGAGCTCAACATCCCCAG
                                                                                                                                                                                                                         autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                      Dobie KW
                                                               PHARM INC
                                                                                        2002US-00317869
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P
                                                                                                                                                                                                                         disease;
                                                                                                                                                                                                                                                                                                                                             ВÞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.8;
Pred. No. 2
                                                                                                                                                                                                                          immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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The invention relates to a novel compound 8-80 nucleotides in length targeted to a nucleic acid molecule encoding phosphodiesterase 4B, where the compound specifically hybridizes with the nucleic acid molecule encoding phosphodiesterase 4B (ADZ46976) and inhibits the expression of phosphodiesterase 4B. A compound of the invention has immunosuppressive activity. The compound is useful for modulating the expression of phosphodiesterase 4B. It is useful for modulating the expression of phosphodiesterase 4B. It is useful for diagnosing or treating diseases associated with expression of phosphodiesterase 4B, including autoimmune disease. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New compound 8-80 nucleobases in length targeted to a nucleic acid molecule encoding phosphodiesterase 4B, useful for diagnosing or treating diseases associated with expression of phosphodiesterase 4B, e.g.
Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                          Example 15; SEQ ID NO 113; 25pp; English.
                                                         invention.
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Query Match
Best Local :
                                 Matches
        61 GCCTCACCTGCTTTTCCA 78
                                16;
1 GCCTCACATGCTTTTCTA 18
                                       Similarity
                                Conservative
                                      6.1%;
                               0
                                       Score 14.8;
Pred. No. 25;
                                 Mismatches
                                                BB
                                               1; Length
                                ν,
                                 Indels
                                                 20
                                0
                                Gaps
                                0
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RESULT 41
ADZ47045/c
ID ADZ47045 standard; DNA; 20 BE
XX
AC ADZ47045;
XX
AC ADZ47045;
XX
DT 14-JUL-2005 (first entry)
DT 14-JUL-2005 (first entry)
XX
DE Human phosphodiesterase 4B ar
XX
BE Human phosphodiester
KW expression; autoimmune diseas
XX
Homo sapiens.
XX
Homo sapiens.
XX
FH Key Location/Qual
FT modified_base 1..20
FT /*tag= b
FT /mod_base= O7
FT modified_base 1..5
FT /mod_base= O7
FT modified_base 1..5
FT /*tag= a
FT /mod_base= O7
FT /*tag= a
FT //note= "2-met
FT modified_base 15..20
FT /*tag= c
FT /mod_base= O7
FT //note= "2-met
XX
PN US2005101000-A1.
XX
PD 12-MAY-2005.
XX
PD 11-DEC-2002; 2002US-00317869
XX
DR WPI; 2005-345404/35.
XX
DR WPI; 2005-345404/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; antisense; phosphodiesterase 4b; PDE 4b; immunosuppressive;
                                                                                                                                                                                                       11-DEC-2002; 2002US-00317869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression; autoimmune disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human phosphodiesterase 4B antisense oligonucleotide SEQ ID NO:73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "OTHER=phosphorothioate backbone.
are 5-methylcitidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       note= "2-methoxyethyl nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                              base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                               base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                         "2-methoxyethyl nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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11-DEC-2002; 2002US-00317869

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RESULT 42
AEC80212/c
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Best Local (
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pouring a solution containing percutaneous drug is assayed subcutaneous tissue side and epidermal side, injecting polyhydric alcol containing solution into the epidermal side, and measuring the degree permeability mediated by a dermal transporter. Also described is a methodo of screening for an inhibitory substance, which involves performing comparative evaluation showing the extent of skin
                                                                                                                                                                                                                                                                                                                                                                                                                                              grug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel compound 8-80 nucleotides in length targeted to a nucleic acid molecule encoding phosphodiesterase 4B, where the compound specifically hybridizes with the nucleic acid molecule encoding phosphodiesterase 4B (ADZ46976) and inhibits the expression of phosphodiesterase 4B. A compound of the invention has immunosuppressive activity. The compound is useful for modulating the expression of
                                                                                                                                                   Estimation of percutaneous drug permeability, involves pouring drug solution into chamber having subcutaneous tissue side and epidermal injecting specific solution, and measuring permeability mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skin
                                                                                                                    Example
                                                                                                                                                                                                                                   Tsuji A,
                                                                                                                                                                                                                                                                                                 10-MAR-2004; 2004JP-00068249
                                                                                                                                                                                                                                                                                                                            10-SEP-2004; 2004WO-JP013219
                                                                                                                                                                                                                                                                                                                                                                                WO2005088299-A1
                                                                                                                                                                                                                                                                                                                                                                                                        Mue ep
                                                                                                                                                                                                                                                                                                                                                                                                                                  primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEC80212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEC80212 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphodiesterase 4B. It is useful for diagnosing or treating diseases associated with expression of phosphodiesterase 4B, including autoimmune disease. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 15; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound 8-80 nucleobases in ler molecule encoding phosphodiesterase diseases associated with expression autoimmune disease.
                                                                                                                                                                                                          2005-676484/69
                                                                                                                                                                                                                                                                                                                                                                                                                                              delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      permeabilization associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                   1, SEQ
                                                                                                                                                                                                                                                                         HISAMITSU MEDICAL CO LTD
                                                                                                                                                                                                                                                              VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTCACCTGCTTTTCCA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTCACATGCTTTTCTA 3
                                                                                                                                                                                                                                   Kato M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 9
                                                                                                                                                                                                                                                             KANAZAWA TECHNOLOGY LICENSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                              permeabilization;
                                                                                                                    占
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleobases in length targeted to a nucleic acid phosphodiesterase 4B, useful for diagnosing or treating ed with expression of phosphodiesterase 4B, e.g.
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                                                                                                                                                                                                                                    Sai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
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                                                                                                              37pp; Japanese
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ţ,
                                                                                                                                                                                                                                                                                                                                                                                                                                            reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse gene RT-PCR primer SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               명
                                                                                                                                                                                                                                                             ORG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                            RT-PCR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR;
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RESULT 43
AAV25273/c
ID AAV252
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AC AAV252
XX
XX
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
This sequence represents a primer for the H.pylori gly gene. The amplified sequence was used to compare homology of the coding sequences of the invention with other known proteins. The protein encoded by the DNA of the invention may be used in a vaccine to prevent or treat useful as potential H.pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H.pylori in a sample and the diagnosis of H.pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H.pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H.pylori-specific antigens. The genomic sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            permeability. The method is useful for assaying permeability of a percutaneous drugs e.g. indomethacin. The skin permeability of a percutaneous drug can be assayed more efficiently. This sequence represents a mouse gene specific primer associated with skin permeability to a percutaneous drug. Note: This sequence is also available in electronic format directly from wipo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                   Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacteria; life cycle; inhibitor; duodenal ulcer disease; chronic gastritis; di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                           Example; Page 108; 1145pp;
                                                                                                                                                                                                                      diagnosis
                                                                                                                                                                                                                                                                              WPI; 1997-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-1996;
02-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV25273
                                                                                                                                                                                                                                                                                                                                      (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTATCAGGTACCCAACCA
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                                                                                                                                                                                                                                                                                                           Alm
                                                                                                                                                                                                                   of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for H.pylori gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%;
llarity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                           RA.
                                                                                                                                                                                                                                                                                                                                                                                             96US-00625811.
96US-00758731.
96US-00736905.
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96US-00761318
                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US005223
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                                                                                                                                                                                           English.
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Pred. No. 25;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                envelope;
activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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                                                                                            RESULT 44
ADH77769/c
ID ADH77769 standard; DNA; 21
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Best Local S
Matches 16
                                             Best Loc
Matches
                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H.pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H.pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H.pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                           The invention comprises the amino acid and coding sequence of the human protein ALMS1 which is associated with Alstrom's syndrome. The DNA and protein sequences of the invention are useful in the diagnosis of Alstrom's syndrome. The present DNA sequence represents a PCR primer fo
                                                                                                                                                                                                                                                                                                           (HOFF )
                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                           Sequence
                                                                                                                                                                                      Example; SEQ ID NO 12; 71pp; French.
                                                                                                                                                                                                                        New DNA associated with Alstrom syndrome, useful for diagnosis and identification of carriers, also related polypeptides, antibodies
                                                                                                                                                                                                                                                                                   Collin GB
                                                                                                                                                                                                                                                                                                                                             09-NOV-2001; 2001US-0345883P
                                                                                                                                                                                                                                                                                                                                                                    12-NOV-2002; 2002FR-00014097.
                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                  FR2832420-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Alstrom's syndrome-related gene (ALMS1) PCR primer #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH77769;
                                                         Local
                                                                                                                 human ALMS1 gene.
                                                                                                                                                                                                                                                             2003-610292/58
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21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALMS1;
                                                                                                                                                                                                                                                                                                           JACKSON LAB
                                                                                                                                                                                                                                                                                                                      HOFFMANN LA
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCACCTGCTTTTCCAAAC
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                      GCACTGGATTTTGGTCAC 30
                                                                                            21
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                                                                                                                                                                                                              animals.
                                                                                                                                                                                                                                                                                   Marshall J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 4 A;
                                                                                           BP; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alstrom's
                                                                                           A; 4 C;
                                                                                                                                                                                                                                                                                                                      ROCHE & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.1%;
88.9%;
                                                      6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 C; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                               syndrome;
                                                                                                                                                                                                                                                                                   Martin ML,
                                                                                            7
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                                            Score 14.8; D
Pred. No. 24;
0; Mismatches
                                                                                           G;
3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.8;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                           T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR;
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                                                                                                                                                                                                                                                                                  Naggert JK, Nishina MP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             88; primer
                                                                                            0 Other
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                                                                  DB 1; Length 21;
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RESULT 46
ACL48194/c
ID ACL481
XX
AC ACL481
XX
AC ACL481
XX
DT 24-MAR
XX

ACL48194;

ACL48194

standard;

RNA;

21

ВΡ

24-MAR-2005

(first entry)

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RESULT 45
ACL48195
ID ACL48
XX ACL48
XX ACL48
XX CYto8
XW CYto8
XW Short
XX Synth
XX Synth
XX Synth
XX I9-M9
PF 19-M9
XX I9-M9
XX I9-M9
XX IP-M9
XX
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                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or comprising: (a) an agent capable of modulating an expression level or comprising: (a) an agent capable of comprise and comprise
                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pharmaceutical composition comprising an agent capable of modulating expression level or protein activity of a gene, e.g. ABCC4, or a T control of the polypeptide or antibody, and a carrier, useful for
                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 4 A; 7 C; 3 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JAN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 9267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-2003; 2003US-0471729P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOLH1 siRNA antisense sequence,
                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMHP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2005-075568/08
                                                                                                                                                     12;
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                                                                            1 TTCTCCAGCACAGCACTG 18
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                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer.
UUCUCCACCACAGCAGUG 18
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Slonim DK,
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                                                                                                                                                                                      6.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene silencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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Pred. No. 24;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH;
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cell
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RESULT 47
ACL48196/c
ID ACL481
XX ACL481
XX ACL481
XX CYCAR
DE FOLH1
XX CYCOST
XX CYCOST
XX HOMO S
XX WO2005
XX WO2005
XX O6-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC protein activity of a cancer related transmembrane protein (CRTP) or gene (C); an antibody specific for a CRTP, or a T cell activated by a CRTP; and (CC) a carrier. The pharmaceutical composition may also comprise a (CRTP) by RNA interference or an antisense mechanism. The CRTPs of the CC RTP by RNA interference or an antisense mechanism. The CRTPs of the CC invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENP3, CF L111856, GPR54, HAVCR1, SLCGA3, SLC30A4, TRG, and TRPM4. The CRTPs of the CC pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CCRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence cancer this patent did not form part of the printed specification, but the obtained in electronic format directly from WIPO at the probabilished_pct_sequences
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Best Local
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                                                                                                 Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; 88.
                                                                                                                                                                   24-MAR-2005
                                                                                                                                                                                                    ACL48196;
                                                                                                                                                                                                                                   ACL48196 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
                                WO2005001092-A2
                                                                                                                                  FOLH1 target oligonucleotide, SEQ ID 9268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 9266; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-075568/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Be X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAY-2003; 2003US-0471729P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOLH1 siRNA sense sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wei L,
                                                                                                                                                                                                                                                                                                                                        TTCTCCAGCACAGCACTG 18
                                                                                                                                                                                                                                                                                                                     TTCTCCACCACAGCAGTG 2
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Slonim DK, Howes SH;
                                                                                                                                                                                                                                                                                                                                                                                                   6.1%;
                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                   2:
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06-JAN-2005.

Be X,

Wei L,

Slonim DK,

Howes SH;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not form part of the printed specification, but was electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a target oligonucleotide from one such CRTP for which short interfering RNAs (siRNA) were produced. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                    ACL48430 standard; DNA; 21 BP
                                                                                                      19-MAY-2004; 2004WO-US015645
                                                                                                                                          06-JAN-2005
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                     Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer;
                                                                                                                                                                                                                                                                                                    24-MAR-2005
                                                                                                                                                                                                                                                                                                                                      ACL48430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or generated transmembrane protein (CRTP) and an antibody specific for a CRTP, or a T cell activated by a CRTP; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
                                             (AMHP ) WYETH
                                                                         20-MAY-2003; 2003US-0471729P
                                                                                                                                                                        WO2005001092-A2
                                                                                                                                                                                                                                                                    FOLH1 target oligonucleotide, SEQ ID 9502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID NO 9268; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-075568/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a novel pharmaceutical composition
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WPI; 2005-075568/08

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                                                                                    Pharmaceutical composition comprising an agent capable of modulating expression level or protein activity of a gene, e.g. ABCC4, or a T co activated by the polypeptide or antibody, and a carrier, useful for
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Claim 3; SEQ ID NO 9270; 113pp; English

invention are

selected from ABCC4,

C20orf103,

CACNAID,

CDH6,

CST, ENPP3

gene

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RESULT 50
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RESULT 51
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                    The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a colonucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the city that the capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the city that the capable of inhibiting or decreasing the expression of the CRTPs of the CRTPs of the city that the capable of the city that the capable of the city that the cancer, e.g. colon colon colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, breast cancer, prostate cancer. The present sequence is a CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence colon cata for this patent did not form part of the printed specification, but the other cancer in the electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENPP3 siRNA sense sequence,
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Pred. No. 24;
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Best Local Matches 1

Similarity

Conservative

Mismatches

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RESULT 52
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                                                                                                      comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or gene, an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polymucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a target oligonucleotide from one such CRTP for which short interfering RNAs (siRNA) were produced. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 8 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                          Pharmaceutical composition comprising an agent capable of modulating expression level or protein activity of a gene, e.g. ABCC4, or a T constituted by the polypeptide or antibody, and a carrier, useful for
                                               Sequence
                                                                          electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                               The present invention relates to a novel pharmaceutical composition
                                                                                                                                                                                                                                                                                                                                                               Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Be X,
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                                                                                                                                                                                                                                                                                                                                                                                             treating cancer.
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                                                BP; 7
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                                                A; 3 C; 7 G; 4 T; 0 U;
6.1%;
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 Score 14.8;
Pred. No. 2
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                                                0 Other,
                DB 1;
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                Length 21;
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RESULT 53
ADW72413/c
ID ADW72413 standard; RNA;
CC polypstide comprising an organelle and/or chloroplast localization consisting an organelle and/or chloroplast localization consisting an organelle and/or chloroplast localization consisting the polynuclectide, a cell comprising contacting the polynuclectide, a cell comprising contacting the cell with a vector operably linked to a cell comprising a portein transduction domain and an organelle comprising a potential principle comprising contacting the cell with a vector operably linked to a cell comprising contacting the cell with a vector operably linked to a polypoptide having a protein transduction domain and an organelle comprising contacting the cell with a recombinant lambdaphage, the recombinant contacting the recombinant lambdaphage and directs the recombinant contacting the organelle localization signal is displayed on a contactin, where the organelle, and where the recombinant lambdaphage introduces a polynuclectide into the organelle, a composition comprising contacting the metabolism of a cell comprising contacting the cell with a recombinant vector displaying a recombinant, where the recombinant contacting the metabolism of a cell comprising contacting the cell with a recombinant vector displaying a recombinant component to a polynucleotide comprising a contacting a polynucleotide component component vector comprising a polynucleotide component component when expressed by the cell, a method for modifying cytochrome oxidase activity in a cell, and amethod of treating a mitochondrial disease in a host, comprising contacting a host described contacting contacting contacting and contacting a mitochondrial disease in a host, comprising contacting a bolynucleotide contacting a method of treating contacting contacting a contacting a method for condition component when expressed by the cell, a method for condition component when expressed by the cell, a method of treating contacting a host, comprising contacting contacting contacting contacting contacting contacting contacting contacting contacting contac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide encoding a polypeptide having an organelle or chloroplast localization signal, and a protein transduction doma:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 96; SEQ ID NO 371; 98pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to a polynucleotide encoding
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vector displaying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain,
comprising
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CC transduction domain, the recombinant vector encoding a functional committee of the host's mitochondrial polypeptide, where the recombinant vector transfects at complete the functional mitochondrial polypeptide in the host's cell to express the functional mitochondrial polypeptide in the at least one transfected committee of the mitochondrial mitorial polypeptide in the at least one transfected committee of the mitochondrial and compositions are useful for transfecting cells and organelle DNA in living cells directly, in particular for transfecting mitochondria and chloroplasts, and for treating diseases crelated to organelle dysfunction, such as Alpers Disease, carnithe deficiency, pyruvate deficiency, mitochondrial carboxylase deficiency, mitochondrial carboxylase deficiency, mitochondrial cytopathy, mitochondrial DNA depletion, mitochondrial encephalopathy, mitochondrial composity, neuropathy, ataxia, retinitis pigmentosa, pyruvate dehydrogenase deficiency, Alzeimers disease, Parkinsons disease, C diabetes, aging and heart disease. This sequence represents mitochondrial compositions of the invention. a mitochondrial localization signal operably linked to functional

Sequence 21 BP; 6 A; 4 C; 8 G; 2 T; 1 U; 0 Other;

밁 S Matches Query Match Local 53 CAGCTGCTGCCTCACCTG 16; Similarity Conservative 6.1%; 70 Н 0, Pred. No. Score 14.8; Mismatches BB 1. 2 Length 21; Indels 0 Gaps 0

ADY33887 standard; DNA; ВP

19-MAY-2005

(first entry)

Up-regulated renal cell carcinoma gene, RT-PCR primer SEQ Ħ No:54

primer; diagnosis; renal cell carcinoma; gene expression; gene silencing; interference; vaccine; cytostatic; reverse 88. transcriptase-PCR; RT-PCR;

Homo sapiens

WO2005019475-A2

03-MAR-2005.

20-AUG-2004; 2004WO-JP012411.

20-AUG-2003; 2003US-0496552P 27-FEB-2004; 2004US-0548201P

Nakamura Y, (ONCO-) ONCOTHERAPY (UYTY ) UNIV TOKYO. Katagiri H

SCI

WPI; 2005-202667/21.

pragnosing renal cell carcinoma (RCC), comprises determining an increased expression level of an RCC-associated gene, in a biological sample derived from a subject, compared to a normal control level of the gene.

Example 1; SEQ ID NO 54; 122pp; English.

ARSSULT 54
ADY33887/c
ID ADY338
AC ADY34
AC The invention relates to a method (M1) of diagnosing renal cell carcinon (RCC) or a predisposition for developing RCC in a subject. The method comprises determining in a biological sample derived from a subject, an expression level of an RCC-associated gene chosen from genes of RCCX 1-32, where an increase in the level as compared to a normal control level of the gene indicates that the subject suffers from or is at risk of developing RCC. Also described are (i) an RCC reference expression profile, comprising a pattern of gene expression of two or more genes carcinoma

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compound with realing pripreventing ECC (1-32, (ii) a method (M2) screening for a compound with realing siperventing ECC (1-32, detecting the binding activity between the Silpsprilate and compound with realing the binding activity between the Silpsprilate and compound and selecting the binding activity between the Silpsprilate and compound that compound that the Silpsprilate and compound that compound that before the selecting the selecting the call appressing one compression of the selecting a candidate compound with a cell appressing one compound that pressing one compound that produces the selecting the anticlate compound with a polypspide encoded by a cartivity of the polypspide of the control of the sepression level of one or more marker genes chosen from the genes of RCCX 1-32, and selecting the candidate compound with a cell into which a cartivity of the polypspide of the control of the transcriptional regulatory region has been introduced, where one creat acompound that reporter gene that is expressed under the control of the transcriptional regulatory region has been introduced, where one candidate compound that reporter gene, when the marker genes is an up-regulatory region of one or more marker genes, when the marker genes is an up-regulatory region of one or more marker genes, when the marker genes is an up-regulatory region of one or more marker gene, when the marker gene that is expressed under the control of the transcriptional regulatory region and selecting the activity or expression level of the reporter gene, and selecting the control of the transcriptional regulatory region of one or more marker genes, and regulatory region has been introduced, where one catalytic profits of RCCX 1-32 and activity or expression for the service of RCCX 1-32 and activity or expression of the control of the transcriptional regulatory region in the selection transcription of the subject, and activity or expression of the control of RCCX 1-32 and activity or expression of the control of RCCX 1-32 and activity ore
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59 CTGCCTCACCTGCTTTTC 16; Conservative Similarity

Matches Query Match

Local

6.1%; C; 8

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2

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Gaps

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Length 21; Indels

Sequence 21

BP; 6

A 2

G; 5 T; 0 U; 0 Other; Score 14.8; DB 1; Pred. No. 24; Mismatches

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Dog genomic marker oligonucleotide sequence SEQ ID NO:393.
                                   09-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New radiation hybrid map of the dog, Canine familiaris, for e.g. identifying genes implicated in phenotypic and or in genetic diseases and for studying dog pedigrees.
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                                                                                                    AAA66531 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 5 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galibert F, Andre C;
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                                                                                                                                                                                                                        149 CTCACGTGGAGCTGAA 164
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                                                                                                                                                                                                                                                                                                                         7 C; 4 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                       Length 20;
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RESULT 57
ADP10727/c
ID ADP107
XX ADP107
XX ADP107
XX I -AUG
CT 12-AUG
CT 12
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                                                                                                                                                                                                                                                                                       transplant rejection; immune system; rheumatoid arthritis; inflammatory bowel disease; multiple sclerosis; HIV; AIDS;
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  24-APR-2002; 2002US-00131831
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                                                           24-APR-2003; 2003WO-US012946.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New radiation hybrid map of the dog, Canine familiaris, for e.g. identifying genes implicated in phenotypic and or in genetic diseases and for studying dog pedigrees.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for isolating corresponding human gene sequences e.g. genes involved in genetic diseases
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                                                                                                                                                                                                                                                                                                                                                                             PCR primer for marker probe #72.
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93.8%;
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behavioral traits
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selected
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RESULT 58
ADX81409/c
ID ADX814
XX ADX814
XX ADX814
XX Melano
XX Primer
XX Mozoo5
XX Homo 8
XX Wozoo5
XX Homo 8
XX Wozoo5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a primer for a 50 mer oligonucleotide marker for diagnosis and monitoring of allograft rejection and other disorders.
                                                                                      23-JUL-2003; 2003US-0489703P

06-NOV-2003; 2003US-00703789

06-NOV-2003; 2003US-00703817

06-NOV-2003; 2003US-00704513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                              Roth RB,
                                                                                                                                                              05-MAY-2004; 2004WO-US014238
                                                                                                                                                                                           24-FEB-2005
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                                                                                                                                                                                                                                                                              primer;
                                                                                                                                                                                                                                                                                            melanoma;
                                                                                                                                                                                                                                                                                                                      Melanoma associated SNP allelotyping primer,
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                                                                                                                                                                                                                                                  Homo sapiens
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                                                         (SEQU-)
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15; Conserv
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                            Nelson MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                           polymorphism; SNP detection; cytostatic;
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Pred. No. 28;
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an

Identifying a subject at risk of melanoma by detecting presence or absence of a polymorphic variation associated with melanoma, where the presence of polymorphic variations is indicative of the subject being at risk of melanoma.

Example 7; Page 119; 418pp; English.

The invention relates to a novel method for identifying a subject at risk of melanoma. The method comprises detecting the presence or absence of a coplymorphic variation associated with melanoma, where the presence of the cone or more polymorphic variations is indicative of the subject being at cidentifying a polymorphic variation associated with melanoma; an isolated concident polymorphic variation associated with melanoma; an isolated concletc acid which comprises a portion of or all of a nucleotide sequence comprising fully defined 68400-213300 base pairs sequences (SEQ ID NO. 3, 4, 5, 6, and/or 7) given in the specification, and comprises one or more comprising fully defined 68400-213300 base pairs sequence (SEQ ID NO. 3, 4, 5, 6, and/or 7) given in the specification, and comprises one or more comprising fully defined for in the specification, and comprises one or more comprision of the nucleotide sequence above, comprision and comprising a nucleotide comprision and comprision of the nucleotide sequence above, considered to a polymorphic consideration, and comprision to a polymorphic consideration, and comprision of the nucleotide sequence above, consideration, and comprision of the nucleotide sequence above, consideration, and comprision the isolated nucleic acid linked to a cold sequence; genotyping a nucleic encoded by the isolated nucleic consideration, and treating melanoma consideration and subject. The methods and sequences have cytostatic activity. The collymucleotides may be used in gene thorapy. The methods are useful for identifying a subject at risk of melanoma, treating melanoma in a collection of the collectide in the exemplification of the collectide in the exemplificati

Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match Best Local ( Matches 15; Conservative h 6.0%; Score 14.4; I Similarity 93.8%; Pred. No. 28; 15; Conservative 0; Mismatches DB 1; Length 20; 1: Indels 0, Gaps

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147 CTCTCACGTGGAGCTG 162 ||||||||||||| 16 CTCTCACGTGGACCTG 1

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Search completed: October 2, 2006, 15:44:33 Job time : 0.001 secs

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RESULT 2
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; ORGANISM: Mus musculus
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APPLICANT: Williams, John
APPLICANT: Blume, John
APPLICANT: Blume, John
APPLICANT: Blume, John
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 987319
LENGTH: 25
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Publication No. US20050214823A1
GENERAL INFORMATION:
                             SOFTWARE: PatentIn version 3.3
SEQ ID NO 116991
LENGTH: 24
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                                                            APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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US-10-310-914A-893921
US-10-310-914A-800173
US-10-708-204-2661
US-10-708-204-2661
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US-10-310-914A-97874
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US-10-310-914A-419337
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US-10-310-914A-197383
US-10-310-914A-977383
US-10-310-914A-979354
US-10-310-914A-993524
US-10-310-914A-9134411
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GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: David Lockhart

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 310.1

CURRENT APPLICATION NUMBER: US/10/809,189

CURRENT FILING DATE: 2004-03-25

PRIOR APPLICATION NUMBER: US/09/396,196

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

INTERED DE ESO ID NOS. 137806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-18892
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                                                                                                                                                                             APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2004-01-13
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 87349
LENGTH: 25
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Publication No. US20050048531A1
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Pred. No. 21;
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Sequence 392205, Application US/11036317
Publication No. US20050214823A1
GENERAL INFONMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Al
FILE REFERENCE: 3654.1
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION UMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-987321
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-392205
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PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 987321
                                                                                                                                                         Sequence 1204416, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 392205
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Best Local
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      APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
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SEQ ID NOS:
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; ORGANISM: probe
US-11-060-756-146184
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US-11-060-756-146184
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-915497
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                                                                                                                                                                                    APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031895-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 146184
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CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 915497
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Best Local Similarity
Matches 19; Conserv
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APPLICANT: Wyeth
APPLICANT: Mounts,
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
                                                                                                                                                           LENGTH:
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ORGANISM: Human
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Pred. No. 2
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Pred. No. 2
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RESULT 12
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US-11-060-756-165160
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US-11-060-756-165160
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US-11-060-756-162607
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Matches
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SEQ ID NO 165160
LENGTH: 25
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CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 162607
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Best Local Similarity
Matches 19; Conser
         APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AMIO1083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
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APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AMIO1083 (031896-042000)
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TITLE OF INVENTION: Nucleic Acid Arrays fo
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101.083 (031896-04200)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
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NUMBER OF SEQ ID NOS:
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TYPE: DNA
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: Pred. No. 22;
0; Mismatches
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Pred. No. 22;
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                                                                                       Monitoring Expression Profiles
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; TYPE: DNA
; ORGANISM: probe
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US-11-121-849-3059
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Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 3059
LENGTH: 25
TYPE: DNA
TYPE: DNA
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SOFTWARE: Microarray Probe S
SEQ ID NO 615502
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LENGTH: 25
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
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                                                                                                                                       TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                        LENGTH:
                                                                            Local
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CCAGCACATCACTGGATCATGGGC
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Pred. No. 24;
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Pred. No. 22
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RESULT 17
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US-10-719-900-767611
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-767611
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-729485
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PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 767611
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Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528:1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
CURRENT FILING DATE: 2003-11-20
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PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 729485
                                                                              APPLICANT: NAKAO,
APPLICANT: NAKAMU
APPLICANT: KODAMA
APPLICANT: FUJIMU
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Matches 20; Conservative
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
CURRENT FILING DATE: 2003-11-20
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
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KODAMA, YUKIKO
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                                                                                                               ; TYPE: DNA; ORGANISM: Mus musculus US-11-036-317-651088
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; ORGANISM: E. coli
US-10-933-982-210405
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                                                                                                                                                                         APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splici
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 651088
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 49117
LENGTH: 25
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CURRENT APPLICATION NUMBER: US/10/933,982
CURRENT FILING DATE: 2004-09-03
NUMBER OF SEQ ID NOS: 224976
SOFTWARE: Microarray Probe Sequence Listing
SEQ ID NO 210405
                                                         Matches
                                                                        Best Local Similarity
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Publication No. US20050214823A1
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TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
                                                                                                                                                                                                                                                                                                                 APPLICANT: Williams, Alan APPLICANT: Blume, John
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RESULT 22
US-10-310-914A-529952/c
; Sequence 529952, Application US/10310914A
; Publication No. US20060003322A1
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; ORGANISM: Mus musculus
US-11-036-317-678385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 938357
LENGTH: 22
TYPE: RNA
ORGANISM: Human
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 678385
LENGTH: 25
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
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Best Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable (
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION UNDER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 78.9
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Pred. No. 2
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Pred. No. 24;
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
ITILE OF INVENTION: Bioinformatically detectable gro
ITILE OF INVENTION: Bioinformatically detectable gro
ITILE OF INVENTION: uses thereof
ITILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 59879
LENGTH: 22
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Best Local Similarity
Watches 15; Conservi
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; ORGANISM: Human
US-10-310-914A-529952
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Sequence 59879, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
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US-10-310-914A-938303
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087,0200,CPUSO1

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: US/10/310,914A

SEQ ID NO 938303

SEQ ID NO 938303

LENGTH: 23

SERGIB: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 938303
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 529952
LENGTH: 23
                                                                     Matches
                                                                                                      Query Match
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TYPE: RNA
                                                                                                                                                           TYPE: RNA
ORGANISM: Human
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                                                                   l Similarity 72.
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18; Conser
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CCCUCCCAGCUCCUGCCUCACC
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Pred. No. 30;
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Pred. No. 27;
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Pred. No. 27;
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LENGTH: 22
TYPE: RNA
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                   NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/084,839
                                                                                                                                                                                          FILE REFERENCE: FORS-06666
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OTHER INFORMATION: Synthetic .0-084-839-3863
                                               TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Human
                                FEATURE:
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Kwiatkowski, Jr., Rol
Lukowiak, Andrew A.
Lyamichev, Victor
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Vedvik, R
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Hall, Jeff G.
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Curtis, Michelle L.
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Argue, Brad T
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Skrzypczynski, Zbigniew
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son-Munoz, Marilyn C.
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on, Lisa C.
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Pred. No. 30;
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US-10-310-914A-392849
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                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CCPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                SEQ ID NO 392849
                                                                                                                                                                                                                                                                                                                                          Sequence 392849, Application US/10310914A
Publication No. US20060003322A1
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                 Query Match
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Patent No. US20020092034A1
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CURRENT APPLICATION NUMBER: US/09/962,290
CURRENT FILING DATE: 2001-09-24
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APPLICANT: Underhill, T. Michael
APPLICANT: Williams, Frederick
TITLE OF INVENTION: No. US20020092034A1-Human Model of Gestational and Adult Folate
TITLE OF INVENTION: Thereof"
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                                                                                            LENGTH: 24
TYPE: RNA
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NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                      SOFTWARE: PatentIn version 3.3
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TYPE: DNA
ORGANISM: Artificial sequence
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NAME/KEY: misc_feature
LOCATION: (1)...(24)
OTHER INFORMATION: primer
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                                                                           ORGANISM: Human
Local Similarity
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86.4%;
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Pred. No. 29;
0; Mismatches
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Pred. No. 2
Score 17.2;
Pred. No. 27;
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                 DB 1;
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                 Length 24;
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US-10-310-914A-1324851/c
Sequence 1324851, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
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US-10-310-914A-471177
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US-10-310-914A-382552
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Sentwich, Isaac
APPLICANT: Sentwich, Vuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 471177
TENDE: Name
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 382552
LENGTH: 19
TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 382552, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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Best Local
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                         Local Similarity
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Pred. No. 27;
4; Mismatches
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Pred. No.
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Sequence 1180613, Application US/10310914A
Publication No. US/20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable gro
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1180613
LENGTH: 20
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US-10-310-914A-178653/c
US-10-310-914A-178653/c
Sequence 178653, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CDUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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US-10-310-914A-1180613
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Matches
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CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1384402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1324851
                                                                                                                               NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 178653
LENGTH: 21
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Best Local S
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TYPE: RNA
ORGANISM: Human
                                                                                                                 TYPE: RNA
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                                                                                           ORGANISM: Human
Local Similarity 90.0%;
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l Similarity 70.0%;
14; Conservative
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100.0%; Pred. No.
Score 16.8; Depred. No. 35; O; Mismatches
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Pred. No. 37;
4; Mismatches
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                                   Length 21;
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RESULT 34
US-10-310-914A-185040/c
US-10-310-914A-185040, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
                                                                                 RESULT 36
US-10-310-914A-931759
J Sequence 931759, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
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Sequence 1124039, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 185040
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Best Local Similarity
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 23
TYPE: RNA
ORGANISM: Human
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
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ORGANISM: Human
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Pred. No. 32;
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Pred. No. 35;
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Best Local S
Matches 15
                                                                                                                                                                                          CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3864
LENGTH: 23
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CURRENT FILING DATE: 2002-12-06
NUMBER: OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 931759
LENGTH: 24
                                                         Matches
                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/084,839
                                                                                                                                                                                                                                                                                   FILE REFERENCE: FORS-06666
                                                                                                                               FEATURE:
OTHER INFORMATION: Synthetic
                                                                                                                                                       LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                APPLICANT: Vedvik, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
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ORGANISM: Human
                                                         Local Similarity
les 19; Conserv
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mes 15; Conserv
                           114 CCACTACGCCTCGTTTCCATCTC 136
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Olson-Munoz, Marilyn C.
                                                                                                                                                                                                                                                                                                                                           Schaefer, James J.
Skrzypczynski, Zbigniew
Takova, Tsetska Y.
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Hall, Jeff G.
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Argue, Brad T.
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Lyamichev, Victor
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Kaiser, Michael
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                                                          Conservative
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                                                                     6.9%;
                                                                                                                                                                                                                                                                                                                             Lisa C.
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                                                                       Score 16.6;
Pred. No. 3
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Pred. No. 3
                                                          Mismatches
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RESULT 38 US-10-310-914A-970522

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RESULT 40
US-11-101-244-1493132/c
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US-11-083-784-1493132/c
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US-11-083-784-1493132
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
                                                          GENERAL INFORMATION:
                                                                      Sequence 1493132, Application US/11101244
Publication No. US20050246794A1
                                                                                                                                                                                                                                                                                           Query Match
Best Local
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SOFTWARE: Proprietary
SEQ ID NO 1493132
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                APPLICANT: Dharmacon, APPLICANT: Khvorova,
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
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TYPE: RNA
ORGANISM: Human
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SOFTWARE: PatentIn version 3.3
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APPLICANT: Khvorova, Anastasia
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Reynolds,
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Pred. No. 4
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Pred. No. 4.
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3 SEQ ID NO 970523 LENGTH: 20
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US-11-101-244-1493132
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 853027
                                                                                                                                                                           Sequence 853027, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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SEQ ID NO 1493132
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
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PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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ORGANISM: Human
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Pred. No. 41
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Pred. No. 43;
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RESULT 45
US-10-310-914A-1111010
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US-10-310-914A-998415
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US-10-310-914A-560231
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 988415
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local S
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APPLICANT: Shiler, Kvuzet
TITLE OF INVENTION: Bioinformatically detectable group
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
TILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                     LENGTH: 22
TYPE: RNA
ORGANISM: Human
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TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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Pred. No. 3
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Pred. No. 37
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Pred. No. 3
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                                 APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CCUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1256042
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200.CPUS91
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1111010
                                                                                                                                                                                                                                                          Sequence 1256042, Application US/10310914A Publication No. US20060003322A1
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LENGTH: 23
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CURRENT APPLICATION NUMBER: US/10/310,914À
CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
LENGTH: 23
TYPE: RNA
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Pred. No. 35;
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Pred. No. 3:
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RESULT 48
US-10-310-914A-126098/C
; Sequence 126098, Application US/10310914A
; Publication No. US20060003322A1
RESULT 50
US-10-310-914A-306631/c
; Sequence 306631, Application US/10310914A
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US-10-310-914A-204775
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US-10-310-914A-1256042
                                                                                                                                                                                                                           ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-204775
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SEQ ID NO 204775
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILLNG DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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TYPE: RNA
ORGANISM: Human
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17; Conservative
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l Similarity 71.4%;
15; Conservative
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85.7%;
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Pred. No. 41;
3; Mismatches
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Pred. No. 4:
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Pred. No. 3
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                                                                                                                                                                                         Length 21;
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Sequence 1148315, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kruzat
TITLE OF INVENTION: Bioinformatically detecta
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087,0200 CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CUURENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1148315
LENGTH: 21
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Sequence 565231, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 00607.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 565231
FILENCTH: 21
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US-10-310-914A-1148315
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LENGTH: 21
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ORGANISM: Human
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ORGANISM: Human
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Pred. No. 41;
7; Mismatches
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Pred. No. 4
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OTHER INFORMATION: Description of Artificial Sequence: PCR Primer; OTHER INFORMATION: Sequence
US-09-965-422-121
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                                                                                                            SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 121
LENGTH: 22
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                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60%
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,286
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/236,284
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
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CURRENT FILING DATE: 2001-09-27
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APPLICANT: Tchernev, Velizar T
TITLE OF INVENTION: No. US20030216545Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21401-132
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APPLICANT: Casman, Stacie
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                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A APPLICATION NUMBER: 60/237,581
FILING DATE: 2000-10-03
APPLICATION NUMBER: 60/238,735
FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/263,691 FILING DATE: 2001-01-24
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/262,498 FILING DATE: 2001-01-18
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/262,156
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/260,338
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-10-16
APPLICATION NUMBER: 60/260,019
FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/240,736
                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/266,109
                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-19
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/263,133
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-
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Vernet, Corine
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MacDougall, John R
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Shenoy, Suresh G
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o. US20030216545A1
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Pred. No. 4:
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                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Sequence US-10-005-041A-187
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US-10-005-041A-187
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                                                                                                                                                                                                              SEQ ID NO 187
LENGTH: 22
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Best Local Similarity
Matches 18; Conserv
                                                          Matches
                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                     FILE REFERENCE: 21402-215
CURRENT APPLICATION NUMBER: US/10/005,041A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/251,459
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 60/259,007
                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 205
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gunther, Erik
APPLICANT: Gerlach, Valerie
FITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-215
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                                                                                                                                                                   FEATURE:
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                          133 TCTCTTTGGAGCACCTCTCAC 153
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                                                          18;
2 TCTCTTTAGAGCCCCTTTCAC 22
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Ellerman, Karen
Stone, David J
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MacDougall, John R
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Mayotte, Jane E
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Burgess, Catherine E
Shimkets, Richard A
Spytek, Kimberly A
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Ballinger, Robert A
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5. US20030232331A1
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                                                          Conservative
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85.7%;
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                                                                       Score 16.2;
Pred. No. 3
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Pred. No. 39;
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RESULT 55
US-10-085-198-526
; Sequence 526, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
; FILE REPERENCE: 21402-279

CURRENT APPLICATION NUMBER: US/10/085,198

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APPLICANT: Galdzicka, Marzena
APPLICANT: Galdzicka, Marzena
ITITE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
ITITE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
ITITE OF INVENTION: NUCLEIC ACID SEQUENCES
FILE REFERENCE: 07917-238001
CURRENT APPLICATION NUMBER: US/10/913,280
CURRENT FILING DATE: 2004-08-06
PRIOR APPLICATION NUMBER: US 60/493,238
PRIOR FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US 60/568,958
PRIOR FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 920
SOFTWARE: FASUSEQ FOR Windows Version 4.0
SEQ ID NO 144
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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US-10-913-280-144
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide primer
US-10-085-198-526
                                                                                                                                                   US-10-913-280-144
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PRIOR FILLING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/286,096
PRIOR FILLING DATE: 2001-04-21
PRIOR APPLICATION NUMBER: 60/299,695
PRIOR FILLING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/315,614
PRIOR FILLING DATE: 2001-08-29
PRIOR FILLING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/272,405
PRIOR FILLING DATE: 2001-08-29
PRIOR FILLING DATE: 2001-08-29
PRIOR FILLING DATE: 2001-08-29
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 526
LENGTH: 22
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                                                                                   Match 6.7%;
Local Similarity 85.7%;
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APPLICATION NUMBER: 60/311,981
FILING DATE: 2001-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/312,858
FILING DATE: 2001-08-16
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126 GTTTCCATCTCTTTGGAGCAC 146
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Similarity 85.7%;
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                                                                                      Score 16.2;
Pred. No. 3
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Pred. No. 39;
                                                               Mismatches
                                                                                        39,
                                                                                                         DB 1;
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; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-401
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; ORGANISM: Homo Sapiens
US-10-708-204-668
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US-10-708-204-1098/c
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Sequence 1098, Application US/10708204
Publication No. US20050222399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
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CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 401
LENGTH: 22
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 668
LENGTH: 22
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Publication No. US20
GENERAL INFORMATION:
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Publication No. US20050222399A1
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Best Local Similarity
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLECTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE /
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                           52 CCAGCTGCTGCCTCACCTGCT 72
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US-10-708-204-1976
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US-10-708-204-1209/c
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; ORGANISM: Homo Sapiens
US-10-708-204-1098
                                                          Best Loc
Matches
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CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: Patentin version 3.2
SEQ ID NO 1976
LENGTH: 22
TYPE: RNA
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TITLE OF INVENTION: BIGINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 1209
LENGTH: 22
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GENERAL INFORMATION:
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SOFTWARE: PatentIn version
SEQ ID NO 1098
LENGTH: 22
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Best Local Similarity
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TITLE OF INVENTION: BIOINFORMATICALLY
TITLE OF INVENTION: OLIGONUCLEOTIDES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 55033
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ORGANISM: Homo Sapiens
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; ORGANISM: Homo Sapiens
US-10-708-204-1991
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US-10-708-204-2334/c
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TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-2118
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US-10-708-204-1991/c
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US-10-708-204-2118/c
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TITLE OF INVENTION: BIOINFORMATICALLY DETECT
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOC:
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 5503
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: Patentin version 3.2
                                                                       Sequence 2334, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY
TITLE OF INVENTION: OLICONUCLEOTIDES
TITLE OF INVENTION: THEREOF
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CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2118
LENGTH: 22
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Publication No. US20050222399A1
GENERAL INFORMATION:
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Publication No. US20050222399A1
GENERAL INFORMATION:
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LENGTH: 22
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Best Local :
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Best Local Similarity
Matches 18; Conserv
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 55033
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
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Pred. No. 3
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Pred. No. 39;
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ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
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US-10-310-914A-222541/c; Sequence 222541, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION:
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US-10-708-204-2487
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US-10-708-204-2487/c
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CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: Patentin version 3.2
SEQ ID NO 2487
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Publication No. US20050222399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
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LENGTH: 22
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                                                                                            Query Match
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
NUMBER OF SEQ ID NOS: 1388402
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                                                                                                                                           TYPE: RNA
ORGANISM: Human
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                              46 ACCTCCCCAGCTGCTGCCTCA 66
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Pred. No. 39;
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Pred. No. 39;
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ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
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US-10-310-914A-1084017/c | Sequence 1084017, Application US/10310914A
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Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 853475, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200,CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 853475
LENGTH: 22
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Best Local S
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SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 653245
LENGTH: 22
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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ORGANISM: Human
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Pred. No. 39;
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Pred. No. 39;
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RESULT 71
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                                                                                                                              US-10-310-914A-1084916
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1084916
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Sequence 1084916, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 1084697
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Best Local Similarity
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                                                                                                                                           TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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ORGANISM: Human
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Pred. No. 39
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Pred. No. 3:
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RESULT 73
US-10-310-914A-1215686/c
US-10-10-914A-1215686, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                           RESULT 74
US-10-310-914A-1217123/c
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
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TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
                                 FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                           APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
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SOFTWARE: PatentIn version 3.3 EQ ID NO 1217123
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ORGANISM: Human
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Pred. No. 39;
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APPLICANT: Shiler, Kruzat
TITLE OF INVENTION: Beinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1263320
                                                                                                                                                                   SEQ ID NO 1287830
LENGTH: 22
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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TYPE: RNA
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ORGANISM: Human
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GACTGGAAGATCCACCTCCCC
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                                                                           Score 16.2;
Pred. No. 39;
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Pred. No. 3
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Pred. No. 39;
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RESULT 77

FILE REFERENCE: 06087.0200.CPUS01

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CURRENT APPLICATION NUMBER: US/10/913,280
CURRENT FILING DATE: 2004-08-06
PRIOR APPLICATION NUMBER: US 60/493,238
PRIOR FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US 60/568,958
PRIOR FILING DATE: 2004-05-07
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US-10-310-914A-126107/c
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOCTWARE: Patentin version 3.3
SEQ ID NO 126107
LENGTH: 23
TABLE OF NUMBER OF SEQ ID NOS: 1388402
SOCTWARE: Patentin version 3.3
SEQ ID NO 126107
                                                                                                                                                    Sequence 445725, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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Matches
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APPLICANT: Ginns, E
APPLICANT: Galdzic
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Galdzicka, Marzena
TITLE OF INVENTION: SYSTEMS AND METHODS FOR
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
FILE REFERENCE: 07917-238001
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18; Conserv
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Pred. No. 37;
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Pred. No. 37;
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US-11-083-784-1311431/c
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US-10-310-914A-1335478
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/602,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1311431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1335478, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 445725
LENGTH: 23
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APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anas
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Best Local
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                                                                                                                                                                         FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1311431, Application US/11083784 Publication No. US20050245475A1
                                                                                                                                                                                                                             APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
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TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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Reynolds, Angela
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Pred. No. 37;
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Pred. No. 3
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; ORGANISM: Homo sapiens
US-11-083-784-1311431
                                                                                                                                                                                                                                                                                                                                                                US-11-101-244-1311431/c
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US-11-083-784-1488626
                                                                                                                                                                                                                                                                                                       Sequence 1311431, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
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Publication No. U
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                                               CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
                                                                                                                                                        APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional
FILE REFERENCE: 13499US
                                                                                                                                                                                                                              APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anas
APPLICANT: Reynolds, Ange
APPLICANT: Leake, Devin
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 19
TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/426,137 PRIOR FILING DATE: 2002-11-14
SOFTWARE: Proprietary
EQ ID NO 1311431
                                NUMBER OF SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1591911
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.0%;
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Reynolds, Angela
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Reynolds, Angela
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Pred. No. 47;
3; Mismatches
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47;
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US-10-310-914A-178568/c
Sequence 178568, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-101-244-1488626
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                                                                US-10-310-914A-178568
                                                                             NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 178568
LENGTH: 19
TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1488626
   Matches
                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Best Local !
                               Query Match
                                                                                                                                                                        APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CUSS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13495US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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 17; Conserv
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Reynolds, Angela
Leake, Devin
   Conservative
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ilarity 100.0%;
Conservative (
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9 Score 15.8; D
Pred. No. 50;
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Pred. No. 47;
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47;
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RESULT 88
US-10-310-914A-851035/c
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; ORGANISM: Human
US-10-310-914A-370776
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US-10-310-914A-178650/c
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Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes at the control of the contr
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                     Sequence 851035, Application US/10310914A
Publication No. US20060003322A1
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SEQ ID NO 370776
LENGTH: 19
APPLICANT: Bentwich,
APPLICANT: Shiler, K
TITLE OF INVENTION: B
TITLE OF INVENTION:
                                                                                                                                        GENERAL INFORMATION:
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
NUMBER OF SEQ ID NOS: 1388403
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-10-310-914A-178650
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17; Conserv
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                                   Bioinformatically detectable group
                                                                       Kvuzat
       uses thereof
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Pred. No. 50;
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Pred. No. 50;
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                                   of novel regulatory genes
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RESULT 89
US-10-310-914A-1115160/c
; Sequence 1115160, Application US/10310914A
; Publication No. US20060003322A1
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; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-851035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-310-914A-1115160
                                                    PILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1384402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1115160
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TYPE: RNA
ORGANISM: Human
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CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
EQ ID NO 207366
                                                                                                                                                                                                                                            APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 89.
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Reynolds, Angela
Leake, Devin
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Pred. No. 50
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Pred. No. 50
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; TYPE: RNA; Homo sapiens; ORGANISM: Homo sapiens US-11-083-784-207502
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US-11-083-784-675126
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
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US-11-083-784-207502
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-207366
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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SOFTWARE: Proprietary
SEQ ID NO 207502
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Best Local Similarity 68.4%;
Matches 13; Conservative
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APPLICANT:
APPLICANT:
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Best Local :
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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APPLICANT: Khvorova,
APPLICANT: Reynolds,
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
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Local Similarity 68.4%;
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Reynolds, Angela
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Reynolds, Angela
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US20050245475A1
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Pred. No. 50;
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Pred. No. 5
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-19-14
NUMBER OF SEQ ID NOS: 1591911
SOPTWARE: Proprietary
SEQ ID NO 1246640
LENGTH: 19
TYPE: RNA
APPLICANT: Dharmacon, Inc.

APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: US/10/714,333
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US-11-083-784-675126
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US-11-083-784-1246640
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SOFTWARE: Proprietary
SEQ ID NO 675126
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Publication No. US20050245475A1
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Best Local
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IPPLICANT: Marshall, William
IPPLICANT: Scaringe, Stephen
IPPLICANT: Stephen
IPPLICANT STATE OF INVENTION: Functional and Hyperfunctional sirNA
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Similarity 68.4%;
L3; Conservative
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US20050245475A1
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Pred. No. 50;
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; ORGANISM: Homo sapiens
US-11-083-784-1358279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-11-101-244-207366
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Publication No. US20050246794A1
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SOFTWARE: Proprietary
SEQ ID NO 207366
LENGTH: 19
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PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1358279
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Best Local (
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CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
                                                                              APPLICANT: Marshall, William APPLICANT: Scaringe, Stephen TITLE OF INVENTION: Functional and Hyperfunctional siRNA FILE REFERENCE: 13499US
                                                                                                                                                      APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
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APPLICANT: Khvorova,
APPLICANT: Reynolds,
APPLICANT: Leake, Dev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
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Local Similarity 89.5%;
nes 17; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
13; Conserv
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Pred. No. 50
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Pred. No. 50;
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; ORGANISM: Homo sapiens
US-11-101-244-675126
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US-11-101-244-207502
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                                                                                                                                                                                                           Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT. TO
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Best Local Similarity
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SEQ ID NO 207502
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FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/502,050 PRIOR FILING DATE: 2003-09-10 PRIOR APPLICATION NUMBER: 60/426,137 PRIOR FILING DATE: 2002-11-14 NUMBER OF SEQ ID NOS: 1591911 SOFTWARE: Proprietary
                                                                                        APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
APPLICANT: Neuronal Sirna
                                                                                                                                                                                     APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anas
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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CURRENT FILING DATE: 2005-04-07
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APPLICANT: Khvorova, Ana
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Reynolds, Angela
Leake, Devin
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Pred. No. 5
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Pred. No. 50;
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US-10-310-914A-178569/c
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                                                        NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 178569
LENGTH: 20
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TYPE: RNA
ORGANISM: Human
3-10-310-914A-178569
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Publication No. US20050246794A1
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APPLICANT: MARSHALL, WILLIAM
APPLICANT: Scaringe, Stephen
TITLE OP INVENTION: Functional and Hyperfunctional
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
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                                                                                                                           APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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NUMBER OF SEQ ID NOS:
SOFTWARE: Proprietary
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NUMBER OF SEQ ID NOS: 1591911
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TYPE: RNA
ORGANISM: Homo sapiens
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Pred. No. 50;
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Pred. No. 5
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RESULT 103

US-10-647-918-7690

; Sequence 7690, Application US/10847918

; Publication No. US20050119210A1

; GENERAL INFORMATION:
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US-10-310-914A-1204303
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1139581
LENGTH: 20
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Matches
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Best Local Similarity
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Best Local Similarity
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-10-310-914A-1139581
                                                                                                                                                                                                                                                                                                                              APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                     ENGTH: 20
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llarity 73.7%;
Conservative
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Pred. No. 4
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Pred. No. 4
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Pred. No. 47;
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US-10-847-918-7692/c
US-10-847-918-7692/c
Sequence 7692, Application US/10847918
Publication No. US20050119210A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: He, Xiaobing
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Slonim, Donna
APPLICANT: Howen, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
                                                                                                                                                                                        RESULT 105
US-10-847-918-8050
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US-10-847-918-7690
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 7692
LENGTH.
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APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: PAtentin version 3.2
SEQ ID NO 7690
LENGTH: 21
TWORE: NAM
                                                                                                                                Sequence 8050, Application US/10847918 Publication No. US20050119210A1 GENERAL INFORMATION:
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Best Local
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APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
                                                                                           APPLICANT: Wyeth APPLICANT: Be,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wyeth
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17; Conserv
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                                                                                           Be, Xiaobing
                                                                             Liu,
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Pred. No. 4
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US-10-831-997-768/c
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; ORGANISM: Homo sapiens
US-10-847-918-8050
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APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US(10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 8052
LENGTH: 21
TYPE: RNA
ORGANISM: RNA: antisense strand
                                                                                                                                                                                 APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michel
APPLICANT: Ireland, James &
APPLICANT: Bolk, Stacey
APPLICANT: Daley, George Q
                                                                                                                                                                                                                                                                                       Sequence 768, Application US/10831997 Publication No. US20050244834A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 8050
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APPLICANT: McCarthy, Jeanette J.

TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/10/831,997
CURRENT FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: US/09/657,472
PRIOR PILING DATE: 2000-09-07
PRIOR PILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
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Local Similarity 89.5%;
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Ireland, James S.
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89.5%; Pred. No. 49
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Pred. No. 49
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US-10-310-914A-227677
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US-10-310-914A-227677
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US-10-310-914A-117008
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                                                                                                 SEQ ID NO 227677
LENGTH: 21
TYPE: RNA
ORGANISM: Human
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200,CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 117008
LENGTH: 21
TYPE: RNA
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APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3
Query Match 6.5%;
Best Local Similarity 57.9%;
Matches 11; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 768
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PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
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Local Similarity 81.0%;
les 17; Conservative
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73.7%;
    Score 15.8; D
Pred. No. 45;
6; Mismatches
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Pred. No. 49
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Pred. No. 45
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                                       DB 1;
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                                       Length 21;
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RESULT 110
US-10-310-914A-593921/c
US-10-310-914A-593921/c
Sequence 593921, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 593921
LENGTH: 21
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APPLICANT: Schrwich, Schrift Strike of Invention: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 800173
LENGTH: 21
TYPE: RNA
ORGANISM: Human
US-10-310-914A-800173
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US-10-708-204-288/c
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US-10-310-914A-593921
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Matches
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLECTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 800173, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
                                                                                           Sequence 288, Application US/10708204
Publication No. US20050222399A1
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Best Local :
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17; Conserv
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Pred. No. 45;
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Sequence 16067, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:
   APPLICANT: Bentwich, Isaac
   APPLICANT: Shiler, Kvuzat
   TITLE OF INVENTION: Bioinformatically detectal
   TITLE OF INVENTION: uses thereof
   FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A
   CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1188402
   SOFTWARE: PatentIn version 3.3
   SEQ ID NO 160067

JENGTH: 22
   TYPE: RNA
   ORGANISM: Human
   US-10-310-914A-160067
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; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-288
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US-10-708-204-2661
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US-10-708-204-2661/c
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Publication No. US20050222399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLECTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE,
TITLE OF INVENTION: THEREOF
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CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2661
LENGTH: 22
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CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOPTWARE: PatentIn version 3.2
SEQ ID NO 288
LENGTH: 22
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                 Local Similarity
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nes 17; Conserv
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Score 15.8; D. Pred. No. 43; 5; Mismatches
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Pred. No. 43;
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Pred. No. 43;
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US-10-310-914A-978748/c
; Sequence 978748, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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US-10-310-914A-802509
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 978748
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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TYPE: RNA
ORGANISM: Human
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TYPE: RNA
ORGANISM: Human
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Local Similarity 57.9%;
es 11; Conservative
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Pred. No. 43
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Pred. No. 4:
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US-10-310-914A-419337/c
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US-10-310-914A-45234
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                                                                                                                                             NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 419337
LENGTH: 22
                                                                                                                                                                                                                                                                                                                               Sequence 419337, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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                                Matches
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CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1115299
LENGTH: 22
                                                               Query Match
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Best Local Similarity
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APPLICANT: Shiler, Kruzat
APPLICANT: Shiler, Kruzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
                                                                                                               TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Human
                              Local Similarity 81.8 es 18; Conservative
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52 CCAGCTGCTGCCTCACCTGCTT 73
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                                              Score 15.6;
Pred. No. 4
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Pred. No. 4
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Pred. No. 4
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US-10-310-914A-877383/c

Sequence 877383, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof

FILE REFERENCE: 6087,0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT STING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 877383
                                                                                                            RESULT 122
US-10-910-914A-993524/c
; Sequence 993524, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 955140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 955140, Application US/10310914A Publication No. US20060003322A1
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TYPE: RNA
ORGANISM: Human
                APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Human
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Pred. No. 4
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable greater of the property 
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; Sequence 1326011, Application US/10310914A
; Publication No. US20060003322A1
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; ORGANISM: Human
US-10-310-914A-993524
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                                                                                                                             US-10-310-914A-1326011
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID 0.1326011
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SOFTWARE: PatentIn version
SEQ ID NO 993524
LENGTH: 22
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TYPE: RNA
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ORGANISM: Human
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l Similarity
18; Conserv
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RESULT 1
US-11-217-529-49117
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Maximum Match 100%
Listing first 26 summaries
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US-10-11-321-421-262
US-10-12-1339-1303
US-10-424-339-1303
US-10-424-339-1484
US-11-217-936-1113
US-11-217-936-1141
US-11-255-139A-6889
US-11-255-139A-6889
US-11-255-139A-6889
US-11-27-689-17
US-11-27-689-17
US-11-27-936-1347
US-11-285-139A-4949
US-11-293-697-4928
US-11-361-627-55
US-11-361-627-55
US-11-361-627-55
US-11-524-432-606
US-11-524-432-606
US-11-525-139A-5820
US-11-525-139A-5820
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US-11-525-139A-4513
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                                                  ALIGNMENTS
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(without alignments)
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Sequence 262, App
Sequence 736, App
Sequence 1303, Ap
Sequence 5004, Ap
Sequence 1113, Ap
Sequence 1113, Ap
Sequence 1114, Ap
Sequence 6418, Ap
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4928, Ap
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1347, Ap
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                                    Sequence 736, Application US/10511937 Publication No. US20060088836A1 GENERAL INFORMATION:
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 APPLICANT:
                       APPLICANT: EXPRESSION DIAGNOSTICS, INC.
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Wohlgemuth, Fry, Kirk
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US-10-511-937-736/c
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SOFTWARE: Patentin version 3.1
SEQ ID NO 262
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.3
SEQ ID NO 49117
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKANURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49117, Application US/11217529
Publication No. US20060099612A1
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASNA GONDI
FILE REFERENCE: TX-1-C2-1
CURRENT APPLICATION NUMBER: US/11/321,421
CURRENT FILING DATE: 2005-12-29
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 09/94,825
PRIOR APPLICATION NUMBER: 09/94,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1997-12-19
                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic Primer
                                                                                                                                                    Local Similarity
mes 17; Conserv
                                                                                                  189 TGTCTGTTAGGGTTGTCTAG 208
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ASHIKARI, TOSHIHIKO
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o. US20060115496A1
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Pred. No. 1.
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Woodward, Robert

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; ORGANISM: Homo sapiens
US-10-511-937-736
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                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US 03/02510
PRIOR FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: PCT/US 03/05346
PRIOR APPLICATION NUMBER: PCT/US 03/05346
PRIOR PRILING DATE: 2003-02-20
PRIOR FILLING DATE: 2003-02-20
PRIOR PRILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILLING DATE: 2002-02-20
PRIOR PRILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILLING DATE: 2002-03-11
PRIOR FILLING DATE: 2002-03-11
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Best Local S
Matches 15
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 736
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APPLICANT: Chowrira, Bharat
APPLICANT: Polisky, Barry
TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP:
TITLE OF INVENTION: Expression or Expression of Genes Involved
TITLE OF INVENTION: Using Short Interfering Nucleic Acid (sina)
FILE REFERENCE: 400/113 (MBHB03-38)
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CURRENT FILING DATE: 2003-04-25
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PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
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SOFTWARE:
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                                     OR FILING DATE: 2002-08-29
OR APPLICATION NUMBER: US 60/408,378
OR FILING DATE: 2002-09-05
OR APPLICATION NUMBER: US 60/409,293
OR FILING DATE: 2002-09-09
OR APPLICATION NUMBER: US 60/440,129
OR APPLICATION NUMBER: US 60/440,129
OR FILING DATE: 2003-01-15
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Local Similarity 93.8%;
                                                                                                                                                                                              APPLICATION NUMBER: US 60/386,782
FILING DATE: 2002-06-06
APPLICATION NUMBER: US 60/406,784
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PatentIn version
                     SEQ ID NOS: 1714
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Haeberli, Peter
Chowrira, Bharat
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Beigelman, Leonid
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Pred. No. 5.2;
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APPLICANT: POLISKY, BARTY
TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
FITTLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase
FILE OF INVENTION: Using Short Interfering Nucleic Acid (sina)
FILE REFERENCE: 400/113 (MEHBOJ-388)
CURRENT APPLICATION NUMBER: US/10/424,339
CURRENT PILING DATE: 2003-04-25
PRIOR FILING DATE: 2003-01-25
PRIOR APPLICATION NUMBER: PCT/US 03/02510
PRIOR APPLICATION NUMBER: PCT/US 03/05346
PRIOR APPLICATION NUMBER: PCT/US 03/05346
PRIOR APPLICATION NUMBER: PCT/US 03/05028
PRIOR FILING DATE: 2003-02-20
PRIOR FILING DATE: 2003-02-20
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR APPLICATION NUMBER: US 60/366,782
PRIOR APPLICATION NUMBER: US 60/366,782
PRIOR APPLICATION NUMBER: US 60/366,782
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR APPLICATION NUMBER: US 60/406,378
PRIO
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SOFTWARE: PatentIn version
SEQ ID NO 1484
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TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Artificial Sequence
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  GCCCTCAACGCCTCGTTCC 1
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Beigelman, Leoni
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Chowrira, Bharat
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                                                                                                                                        Score 14.2;
Pred. No. 5
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Pred. No. 5
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                                                                                                                          US-11-217-936-1582/c
                                                                                                                                                   RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized
US-11-293-697-5004
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US-11-293-697-5004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jadhab, Vasant
APPLICANT: Carroll, Joseph
APPLICANT: Stria Therapeutics, Inc.
APPLICANT: Stria Therapeutics, Inc.
APPLICANT: Stria Therapeutics, Inc.
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
TITLE OF INVENTION: ($INA)
FILE REFERENCE: 05-727 (400/271)
CURRENT APPLICATION NUMBER: US/11/217,936
CURRENT FILING DATE: 2005-09-01
NUMBER OF SEQ ID NOS: 5036
SOFTWARE: Patentin version 3.3
SEQ ID NO 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5004
                                                                                    Sequence 1582, Application US/11217936 Publication No. US20060148743A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1113, Application US/11217936 Publication No. US20060148743A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Jadhab, Vasant
APPLICANT: Carroll, Joseph
APPLICANT: Sirna Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
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ORGANISM: Artificial Sequence
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Pred. No. 5.
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Pred. No. 5
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APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in
TITLE OF INVENTION: density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/11/370,584
CURRENT FILING DATE: 2006-03-08
PRIOR APPLICATION NUMBER: US/10/349,143
PRIOR FILING DATE: 2003-01-21
                                                                                                                                                                                                                                                            US-11-370-584-6418/c
                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: QPCR primer US-11-221-332-141
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PRIOR FILING DATE: 2003-05-07
NUMBER OF SEQ ID NOS: 298
SOFTWARE: PatentIn version 3.0
SEQ ID NO 141
LENGTH: 20
                                                                                                                                                                                             Sequence 6418, Application US/11370584 Publication No. US20060177863A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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Best Local
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TITLE OF INVENTION: Enzymes invovled in apoptosis
FILE REFERIOCS: 8912/2042
CURRENT APPLICATION NUMBER: US/11/221,332
CURRENT FILING DATE: 2005-09-07
PRIOR APPLICATION NUMBER: PCT/GB2004/00957
PRIOR FILING DATE: 2004-03-05
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FILE REFERENCE: 05-727 (400/271)
CURRENT APPLICATION NUMBER: US/11/217,936
CURRENT FILING DATE: 2005-09-01
NUMBER OF SEQ ID NOS: 5036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial
FEATURE:
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Pred. No. 5.
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NUMBER OF SEQ ID NOS: 8014

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 6888

LENGTH: 17

TYPE: RNA
ORGANISM: Homo sapiens
US-11-255-139A-6888
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; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1999-04-21
; PRIOR PILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1990-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6418
; SEQ ID NO 6418
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US-11-255-139A-6889/c
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US-11-370-584-6418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6888, Application US/11255139A Publication No. US20060154271A1 GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/11/255,139A
CURRENT FILING DATE: 2005-10-20
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: Patentin version 3.0
SEQ ID NO 6899
LENGTH: 17
                                                                                                                                                                                                                                               Sequence 6889, Application US/11255139A
Publication No. US20060154271A1
                                                                                                                                                                                                                                GENERAL INFORMATION
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Best Local
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APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MeHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/11/255,139A
CURRENT FILING DATE: 2005-10-20
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NAME/KEY: primer_bind
LOCATION: 1..19
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15; Conserv
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Similarity 93.3%;
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Pred. No. 8.9;
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US-11-327-689-17/c
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Publication No. US20060177854A1
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ORGANISM: Homo sapiens
                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/497,957

FILING DATE: 04-FEB-2000

APPLICATION NUMBER: US/08/834,497

FILING DATE: 04-APR-1997

APPLICATION NUMBER: US 08/652,265

FILING DATE: 23-MAY-196

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912

PILING DATE: 04-APR-1996

APPLICATION NUMBER: US 08/630,912

PILING DATE: 04-APR-1996

APPLICATION NUMBER: US 08/630,912

PILING DATE: 04-APR-1996
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Local Similarity 93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows 95
SOPTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS NUMBER OF SEQUENCES: 76
                                                       FEATURE:
                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                 MOLECULE TYPE: DNA
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                                                                                                LENGTH: 18 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                           NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/11/327,689
FILING DATE: 05-Jan-2006
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                             TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
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OTHER INFORMATION: /mod_base= OTHER
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                                      NAME/KEY:
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Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
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Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
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                                    modified_base
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Pred. No. 8
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APPLICANT: Joshab, Vasant
APPLICANT: Carroll, Joseph
APPLICANT: Sirna Therapeutics, Inc.
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of
TITLE OF INVENTION: (HDAC) Gene Expression Using Short Inte
TITLE OF INVENTION: (siNA)
FILE REFERENCE: 05-727 (400/271)
CURRENT APPLICATION NUMBER: US/11/217,936
CURRENT APPLICATION NUMBER: US/11/217,936
CURRENT FILING DATE: 2005-09-01
NUMBER OF SEQ ID NOS: 5036
SOFTWARE: PatentIn version 3.3
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
TITLE OF INVENTION: RAY Interference Mediated Inhibition Of Histone Deacetylase
TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
TITLE OF INVENTION: (six)
FILE REFERENCE: 05-727 (400/271)
CURRENT APPLICATION NUMBER: US/11/217,936
CURRENT FILING DATE: 2005-09-01
NUMBER OF SEQ ID NOS: 5036
SOFTWARE: Patentin version 3.3
SEQ ID NO 1347
                                                                                                                                                                                                                                                                                                     Sequence 1816, Application US/11217936 Publication No. US20060148743A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                           SEQ ID NO 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic
ORGANISM: Artificial Sequence
                                     ENGTH: 19
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Local Similarity 93.3%;
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ion No. US20060148743A1
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Pred. No. 7.
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Pred. No. 8
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                                                                                                                                                                                      of Histone
Interfering
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Nucleic Acid
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TITLE OF INVENTION: Method and nucleic acids for TITLE OF INVENTION: proliferative disorders FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
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US-10-517-441-1250/c
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; OTHER INFORMATION: Synthetic
US-11-217-936-1816
                                                                                                                                                          US-11-184-215-43/c
                                                                                                                                                                              RESULT 17
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Matches
                                                                                                      Sequence 43, Application US/11184215 Publication No. US20060122790A1 GENERAL INFORMATION:
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SEQ ID NO 1250
LENGTH: 18
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APPLICANT: Fowler, Craig A.
APPLICANT: Mehra, Vinod C.
APPLICANT: Mehra, Vinod C.
APPLICANT: ROSSO, Thomas L.
TITLE OF INVENTION: OLIGANUCLEOTIDE ORDERING SYSTEM
FILE REFERENCE: ILLINC.050A
CURRENT APPLICATION NUMBER: US/11/184,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
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                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Local Similarity 93.3%;
es 14; Conservativo
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MODEL, Fabian
NIMMRICH, Inko
RUJAN, Tamas
SCHMITT, Armin
SCHMITT, Manfred
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MAIER, Sabine
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ilarity 83.3%;
Conservative
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Pred. No. 9
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Pred. No. 7.9;
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CURRENT FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: 60/634,164
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized US-11-293-697-4928
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; ORGANISM: Homo sapiens
US-11-255-139A-4949
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US-11-255-139A-4949
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US-11-184-215-43
                                                                                                            PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4928
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4949, Application US/11255139A Publication No. US20060154271A1 GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    Sequence 4928, Application US/11293697 Publication No. US20060105376A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McSwiggen, James
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/11/255,139A
CURRENT FILING DATE: 2005-10-20
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                 TITLE OF INVENTION: Novel full length cDNA FILE REFERENCE: H1-A0106 CURRENT PEPLICATION NUMBER: US/11/293,697 CURRENT FILING DATE: 2005-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sirna Therapeutics, Inc. APPLICANT: McSwiggen, James
                                                   LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 17
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Pred. No. 11,
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                                                                                                          US-11-327-689-49
                               Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTSEQ for Windows Vert
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/327,689
FILING DATE: 05-Jan-2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                         MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
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36 TGGGAGCTCCACCT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/497,957
FILING DATE: 04-FSB-2000
APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
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                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                      TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
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No. US20060177854A1
                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/630,912 FILING DATE: 04-APR-1996
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Ruddy, David
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Feder, John N.
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                                 0; Mismatches
                                                  Score 12.4; 1
Pred. No. 13;
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Pred. No. 10;
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                                                                     Length 17;
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TGGGTGCTCCACCT 14

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MOLECULE TYPE: DNA (genomic)
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SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-11-327-689-50
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                                                                                                  Query Match
Best Local Similarity
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                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOPTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                     36 TGGGAGCTCCACCT 49
                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/497,957
FILING DATE: 04-FEB-2000
APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/11/327,689
FILING DATE: 05-Jan-2006
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                      LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
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STATE: New York
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                                                                                 Conservative
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Ruddy, David
Tsuchihashi, Zenta
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Feder, John N.
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                                                                                                5.1%;
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                                                                            Score 12.4; Depred. No. 13; O; Mismatches
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                                                                                                                    DB 1; Length 17;
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                                                                              Gaps
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RESULT 22

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; SEQ ID NO 55
; LENGTH: 17
; TYPE: DNA
; ORCANISM: Homo sapiens
US-11-361-627-55
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US-10-524-432-606
; Sequence 606, App
; Publication No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 23
US-11-255-139A-5820/c
; Sequence 5820, Application US/11255139A
; Publication No. US20060154271A1
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; Sequence 55, Application US/11361627
; Publication No. US20060199208A1
GENERAL INFORMATION:
APPLICANT: Genzyme Corporation
APPLICANT: The Johns Hopkins University
TITLE OF INVENTION: BRAIN ENDOTHELIAL EXPRESSION PATTERNS
FILE REFERENCE: 003482.00010
CURRENT APPLICATION NUMBER: US/10/524,432
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: US 60/403,390
PRIOR FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5820
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Best Local Similarity 92.9%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: McSwiggen, James
ITILE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relater
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/11/255,139A
CURRENT FILING DATE: 2005-10-20
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/343,298
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 104
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CURRENT APPLICATION NUMBER: US/11/361,627
CURRENT FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: US/10/272,461
PRIOR FILING DATE: 2002-10-16
PRIOR FILING DATE: 2002-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bingham, Jonathan
TITLE OF INVENTION: METHODS AND SYSTEMS FOR POLYNUCLEOTIDE DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Srinivasan, Subha APPLICANT: Bingham, Jonatha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                 39 GAGCTCCACCTCCC 52
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 13;
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Pred. No. 13;
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GENERAL INCOMPANE, KEVIN R.

APPLICANT: SOWERS, KEVIN R.

APPLICANT: FAGERVOID, SONJA K.

APPLICANT: MATTS, JOY E. M.

APPLICANT: MAY, HAROLD D.

APPLICANT: MAY, HAROLD D.

TITLE OF INVENTION: GENE PROBES FOR THE SELECTIVE DETECTION OF MICROORGANISMS THAT TITLE OF INVENTION: REDUCTIVELY DECHLORINATE POLYCHLORINATED BIPHENYL COMPOUNDS

FILE REFERENCE: 4115-206

CURRENT APPLICATION NUMBER: US/11/190,801

CURRENT APPLICATION NUMBER: 60/591,514

PRIOR APPLICATION NUMBER: 60/591,514

PRIOR FILING DATE: 2004-07-27

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.3

SEQ ID NO 1

LENGTH: 17

TYPE: DNA

ORGANISM: Artificial Sequence
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; PRIOR FILLING DATE: 2003-04-01
; NUMBER OF SEQ ID NOS: 869
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 606
; SEQ ID NO 606
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-524-432-606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 26
US-11-255-139A-4513
US-11-255-139A-4513, Application US/11255139A; Sequence 4513, Application US/11255139A; Publication No. US20060154271A1
; GENERAL INFORMATION;
; GENERAL INFORMATION;
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US-11-190-801-1/c
JS-11-190-801-1/c
JS
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-4513
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                                                                                                                                                                APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
PILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/11/255,139A
CURRENT FILING DATE: 2005-10-20
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
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Search completed: October Job time: 0.001 secs

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2006, 15:38:59

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Patent: WO 2005075685-A 1578 18-AUG-2005; NESTEC S.A. (CH)
                                                Canis familiaris
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia; Canidae;
                                                                                                            CS150458.1 GI:74270448
                                                                                     Canis familiaris (dog)
                      Middleton, R.P.
                                             Canie.
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(without alignments)
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ACCESSION: AR279129
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                                                                                                                                Spytek, K.A., Casman, S., Padigaru, M., Dickson, K., Verr
Spaderna, S.K., Shenoy, S., Gerlach, V., Ellerman, K., &
Macdougall, J.R., Smithson, G., Li, L., Malyankar, U.M.,
Gunther, B. and Tchernev, V.T.
G-protein coupled receptors
Patent: WO 0226985-A 121 04-APR-2002;
Curagen Corporation (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9615"
                                                               organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
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/note="Description of Artificial Sequence: oligonucleotide
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Matches 18; Conserv
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                                                           18;
                                                                                                                                                                                                     Li,L., Ballinger,R.A., Padigaru,M., Kekuda,R., Colman,S.D., Spytek,K.A., Casman,S.J., Vernet,C.A., Shenoy,S.G., Gusev,V., Malyankar,U.M., Edinger,S., Gerlach,V., Smithson,G., Stone,D.J., Sciore,P., Macdougall,J.R., Gunther,E., Peyman,J.A., Ellerman,K., Gangolli,E.A. and Millet,I.
G-protein coupled receptors and nucleic acids encoding same Patent: WO 02059313-A 539 01-AUG-2002;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
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                 TCTCTTTGGAGCACCTCTCAC 153
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                                                                                                               /organism="synthetic construct"
/mol type="unassigned DNA"
/mol type="unassigned DNA"
/db xref="teaxon:32630"
/note="PCR Primer Sequence"
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/mol type="unassigned DNA"
/mol xef="taxon:32630"
/noTe="PCR Primer Sequence"
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AX095590/c
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AR529565
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Single nucleotide polymorphisms in genes Patent: WO 0118250-A 768 15-MAR-2001; WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) Pharmaceuticals, Inc. (US)
Expression systems using DD173031 DD173031.1 GI:83967286 WO 2005054467-A/31.
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Patent: US 6727063-A 768 27-ARR-2004;
Millennium Pharmaceuticals, Inc. and Whitehead Institute
Biomedical Research; Cambridge, MA
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Lander, E.S., Cargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and
McCarthy, J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                DD173031
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="genomic !
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                                    systems using
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Pred. No. 3.5;
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AR704960
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OS Artificial
PN W0 2005054467-A/31
PD 16-JUN-2005
PF 03-DEC-2004 W0 2004JP01800
PF 03-DEC-2003 JP 200 3-40520
PI hiroyuki tsunoda, kiyoshi i
CC Description of Artificial
CC Description of Artificial
CC Sequence
FH Key Location/C
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Unknown.
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Sequence 23 from patent US 6929912.
AR704960 22 PP 12 PP 
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Tsunoda, H. and Habu, K.
Expression systems using mammalian beta-Actin promoter
Patent: WO 2005054467-A 31 16-JUN-2005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 22)
Guida,M., Hall,J., Petros,W.P., Vredenburgh,J.J.,
Marks,J.R.
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03-DEC-2003 JP 200 3-405269
hiroyuki tsunoda,kiyoshi habu
Description of Artificial Sequence : Artificially Synthesized
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/mol_type="genomic DNA"
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Milhausen, M.J.
Methods for the detection of encysted Patent: US 6514694-A 262 04-FEB-2003;
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Hayden, M.R., Brooks-Wiison, A.R. and Pimstone, S.N.

Process for identifying modulators of ABC1 activity

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Senon Genetics, Inc.; Burnaby;
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ALIGNMENTS

RESULT 1

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US-09-702-251-85

Sequence 85, Application US/09702251

Patent No. 6372492

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Lex M. Cowsert

TITLE OF INVENTION: ANTISENSE MODULATION OF

FILE REFERENCE: RTS-0199

CURRENT APPLICATION NUMBER: US/09/702,251

CURRENT FILING DATE: 2000-10-30
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  RESULT 2
   US-08-765-340-30
   JS-08-765-340-30
  Sequence 30, Appl
Patent No. 615009
SEQ ID NO 85
  Matches
   Query Match
   APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 145146/94
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 311130/94
FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
ANAME: CERMININ 157115
                  NUMBER OF SEQ ID NOS:
   TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS:
   GENERAL INFORMATION:
  TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic
   ZIF: 1712
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, SOFTWARE: #1.30 (EPO) CURRENT APPLICATION DATA:
   NAME: SERUNIAN, LESLIE
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 14!
TELECOMMUNICATION INFORMATION:
   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
   APPLICANT: MATSUDA, Y.,
APPLICANT: KONDO, S.
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
TITLE OF INVENTION: COMPOUND
  ADDRESSEE:
STREET: 3
   STRANDEDNESS:
  TYPE: nucleic acid
   Local
   COUNTRY:
   147 CCCTTCTCCTTCTGCCAT 164
  al Similarity 94.4%;
17; Conservation
  10154
  NEW YORK
  CCCTCCTCCTTCTGCCAT 20
   Application US/08765340
  UCHIDA, K.,
UCHIDA, T.,
TANAKA, Y.,
MATSUDA, Y.,
   345 PARK AVENUE
   USA
  MORGAN & FINNEGAN, L.L.P
   single
  ANTISENSE MODULATION OF TALIN EXPRESSION
  185
  0;
   Score 16.4;
Pred. No. 1
  1452-4005
  Mismatches
  DNA
  Version
  10;
  DB 1;
  Length 20;
  Indels
  0,
  Gaps
  0
```

```
GENERAL INFORMATION:
APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
TITLE OF INVENTION: No. 6767720el cDNAs encoding catenin-binding proteins with
TITLE OF INVENTION: function in signalling and/or gene regulation
FILE REFERENCE: 2676-4415US
CURRENT APPLICATION NUMBER: US/09/574,779B
CURRENT FILING DATE: 200-05-19
PRIOR APPLICATION NUMBER: 99201543.8
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 88
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
Query Match
Best Local Similarity
Thes 17; Conserve
  묽
   Ş
   밁
  Ş
  ; OTHER INFORMATION: Antisense Oligonucleotide US-09-593-711A-63
   ; OTHER INFORMATION: Antisense Oligonucleotide US-09-702-251-85
  US-09-593-711A-63
  ; OTHER INFORMATION: Description of Artificial Sequence: US-09-574-779B-88
  US-09-574-779B-88/c
   CURRENT APPLICATION NUMBER: US/09/593,711A
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 244
SEQ ID NO 63
LENGTH: 20
TYPE: DNA
   Sequence 63, Application US/09593711A Patent No. 6271030 GENERAL INFORMATION:
  Sequence 88, Application US/09574779B Patent No. 6767720
  Query Match
Best Local
   Matches
  Query Match
  Matches
   APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
  FILE REFERENCE:
  TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
  FEATURE:
   ORGANISM: Artificial Sequence
  LENGTH: 20
  Local Similarity hes 16; Conserv
  105 TCTCATTCTCCTGCTC 120
   182 GACTTCACAAGAAGCAA 198
  17 GACTTCACAAGAGGCAA
  1 Similarity
16; Conserv
                 Conservative
   Conservative
  Conservative
   RTS-0118
   94.1%;
                            6.4%;
85.0%;
  100.0%;
  6.8%; Score 16;
100.0%; Pred. No.
   18
               Score 15.2; D
Pred. No. 16;
O; Mismatches
   0;
  0
               0
   Score 15.4;
Pred. No. 1
   Mismatches
  Mismatches
  15;
   12
   ВВ
  DB 1; Length 20;
   1;
  0;
  Length 20;
  Length 20;
                 Indels
   Indels
  Indels
   primer FVR1479F
               0
   0
  0;
   Gaps
               0
  0
  0
```

```
GENERAL INCOMPANDAMENTAL PROJUCTION IN APPLICANT: WRIGHT, Jim A.

APPLICANT: LEE, Yoon S.

TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE

TITLE OF INVENTION: SQUENCES AND METHODS OF USING SAME TO MODULATE CELL

TITLE OF INVENTION: GROWTH

FILE REFERENCE: 032396-046

CURRENT FILING DATE: 1999-04-22

EARLIER APPLICATION NUMBER: US 60/082,791

EARLIER APPLICATION NUMBER: US 60/082,791

EARLIER FILING DATE: 1998-04-23

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PATENTIN Ver. 2.0

FEQ ID NO

ORGANISM: Human

US-09-295-593-9

A 4%: Score 15.2; DB 1; Length 20;
US-09-484-629B-28/c
Sequence 28, Application US/09484629B
; Patent No. 6998472
; GENERAL INFORMATION:
  밁
   ई
  RESULT 6
US-09-295-593-9/c
  유
   ঠ
  RESULT 5
US-09-593-711A-180
  밁
  RESULT 7
   ; OTHER INFORMATION: Antisense Oligonucleotide US-09-593-711A-180
   CURRENT APPLICATION NUMBER: US/09/593,711A
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 244
SEQ ID NO 180
LENGTH: 20
Type: ....
  Query Match
Best Local Similarity
Matches 17; Conserv
  Best Local Similarity 85.0 Matches 17; Conservative
  Sequence 9, Application US/09295593 Patent No. 6417169
   Sequence 180, Application US/09593711A Patent No. 6271030
  Query Match
   APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butl
  APPLICANT:
  ORGANISM: Artificial Sequence FEATURE:
   TYPE: DNA
  INFORMATION:
   136 ACACCTGCTCCCCTTCTCC 155
   98 GGCCCCCTCTCATTCTCCTG 117
  GAGACACCTGCTCCCCCTTC 152
  GGCCCCCGCTCTTTCTCCCG 1
  GCGACAGCTGCTCCACCTTC 20
  ACAGCTGCTCCACCTTCTTC 20
  Jacqueline Wyatt
  Conservative
   6.4%;
85.0%;
   ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
   Butler
  0; Mismatches
   Score 15.2;
Pred. No. 16
  Mismatches
  DB
  ۳
  Length 20;
  Indels
  0;
  <u>.</u>
   Gaps
  Gaps
  0,
  0;
```

```
; APPLICANT: Medical Research Council
TITLE OF INVENTION: Obesity gene
FILE REFERENCE: 18396/1140
CURRENT APPLICATION NUMBER: US/09/484,629B
CURRENT FILING DATE: 2000-01-18
FRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
NUMBER OF SEO ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
LENGTH: 21
  밁
  RESULT 8
  ; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: synthetic primer
US-09-484-629B-28
   US-08-741-406-10/c
   CURRENT APPLICATION NUMBER: US/0P/0F

CURRING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V6

CURRINT APPLICATION DATA:

APPLICATION NUMBER: US/0P/-

FILING DATE:
CLASSIFICATOR
   Patent No. 5721118
GENERAL INFORMATION:
  Sequence 10, Application US/08741406 Patent No. 5721118
  Matches
   Query Match
Best Local :
  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/550
FILING DATE: 31-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
   TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
  FEATURE:
OTHER INFORMATION: synthetic primer FEATURE:
   TYPE: DNA
ORGANISM: Artificial
   REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
  SEQUENCE CHARACTERISTICS
   TITLE OF INVENTION: Mammalian Artific
   APPLICANT:
  NUMBER OF SEQUENCES:
TOPOLOGY:
                  STRANDEDNESS:
  CITY: San Diego
   ENGTH:
  139 CCTGCTCCCCTTCTCTTC 158
  20 cerecreceserecree 1
  1 Similarity
17; Conserv
                            nucleic acid
   California
  United States
   Scheffler,
  Conservative
                 single
   6.4%;
85.0%;
  Mammalian Artificial Chromosomes
  US 08/550,717
   Immo E.
  0,
   P-G
  Score 15.2; D
Pred. No. 15;
0; Mismatches
  Version #1.25
  DB 1; Length 21;
  Indels
  <u>,</u>
  Gaps
```

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178 CAGGGACTTCACAAG 192

Matches Query Match

15;

Conservative

0

Mismatches

0

0

Gaps

0

Local

Similarity

6.4%; Score 15; 100.0%; Pred. No.

DB 1; 17;

Length 20; Indels

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문
   밁
  US-09-517-467B-252
  RESULT 10
  US-09-024-472-10/c
              GENERAL INFORMATION:
APPLICANT: Ian Popoff
APPLICANT: Ian Popoff
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION
FILE REFERENCE: RTS-0150
  Query Match
Best Local Similarity 100.
Matches 15; Conservative
  Sequence 10, App...
  Sequence 252, Application US/09517467B Patent No. 6451602
   TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
   GENERAL INFORMATION:
APPLICANT: Scheff
CURRENT APPLICATION NUMBER: US/09/517,4678
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,472
   SEQUENCE CHARACTERISTICS:
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
   APPLICATION NUMBER: US 08/550,717
FILING DATE: 31-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2317
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE:
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
   NUMBER OF SEQUENCES: 1
  TITLE OF INVENTION:
  LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   CLASSIFICATION:
  STREET: 4370 La
CITY: San Diego
   TOPOLOGY:
  FILING DATE
   COUNTRY:
   ADDRESSEE:
  178 CAGGGACTTCACAAG 192
  16 CAGGGACTTCACAAG 2
   16 CAGGGACTTCACAAG
   California
  Application US/09024472
  E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite
   United States
  Scheffler,
   linear
   Floppy disk
   6.4%; Score 15;
100.0%; Pred. No.
tive 0; Mismatcl
  Mammalian Artific
Methods of Using
  Immo E.
   US/08/741,406
   10:
  Artificial Chromosomes and
   Mismatches
  Same
  DB 1; Length 20; 17;
   0
   Indels
   0
  Gaps
   0
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   á
   US-09-076-259-2
  ; OTHER INFORMATION: Antisense Oligonucleotide US-09-517-467B-252
   US-09-076-259-2/c
  CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/517,467
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 345
SEQ ID NO 252
LENGTH: 20
               Query Match
Best Local Similarity
  Patent No. 6548245
GENERAL INFORMATION:
APPLICANT: Lilly,
   Sequence 2, Application US/09076259
  Matches
   Matches
  Query Match
   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/046,720
APPLICATION UNMBER: 60/046,720
FILING DATE: 16-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7104
TELECOMUNICATION INFORMATION:
TELECHONE: 617-720-3500
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
   APPLICANT:
  ORGANISM: Artificial Sequence FEATURE:
  TYPE: DNA
   SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076 250
FILING DATE.
  APPLICANT: Drazen, Jeffrey M.
TITLE OF INVENTION: METHODS FOR DIAGNOSIS, PREDICTION
TITLE OF INVENTION: AND TREATMENT OF ASTEMA AND OTHER INFLAMMATORY CONDITIONS
TITLE OF INVENTION: BASED ON ECTAXIN CODING SEQUENCE POLYMORPHISM
NUMBER OF SEQUENCES: 6
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARDER TOTALE
  TOPOLOGY: 1
   ADDRESSEE: Wolf, Gre
   STRANDEDNESS:
  TYPE: nucleic acid
   COUNTRY: U.S.A. ZIP: 02210-2211
  STATE: MA
   CITY: Boston
   Local
   TELEFAX:
   41 TGCCATCCCCTTGGTGAT 58
  16;
   Similarity
  recearecerregreer 18
  600 Atlantic Avenue
   617-720-2441
6.3%;
ilarity 88.9%;
Conservative
  Luster,
  Conservative
   single
   Craig M
  6.3%;
   Greenfield & Sacks, P.C
  Andrew D.
   2
 0
               Score 14.8;
Pred. No. 18;
  0;
  Score 14.8;
Pred. No. 1
   Mismatches
  Mismatches
                                 BB
  DB 1;
                                1.
   Length 20;
                              Length 20;
 Indels
 0
  0
 Gaps
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 0
  0
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; TOPOLOGY: linear; MOLECULE TYPE: Other; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-413-255-2
  RESULT 12
US-10-413-255-2/c
   US-08-117-952-294/c
   RESULT 13
  밁
   밁
  Sequence 294, Application US/08117952 Patent No. 5851760
   Sequence 2, Application US/10413255
Patent No. 6949637
GENERAL INFORMATION:
  Matches
  Query Match
   GENERAL INFORMATION:
  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
  OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/413,255

FILING DATE: 14-Apr-2003

CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259

APPLICATION NUMBER: 09/076,259
   Local
  COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
   NAME: Trevisan, Maria A.
REGISTRATION NUMBER: 48,207
REFERENCE/DOCKET NUMBER: B00801.70282.US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
   TITLE OF INVENTION: METHODS FOR DIAGNOSIS, PREDICTION
AND TREATMENT OF ASTHMA AND OTHER INFLAMMATORY CONDITIONS
BASED ON ECTAXIN CODING SEQUENCE POLYMORPHISM
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, G
  APPLICANT: Lilly,
   NUMBER OF SEQUENCES:
  20 CGTGAGAGGTGGTGGTTT 3
  70 CGTGAGAGCTGGTTGTTT 87
  l Similarity
16; Conserv
  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
  CITY: Boston
STATE: MA
   TELEFAX: 617-720-2441
  STREET: 600 Atlantic Avenue
   LENGTH: 20 base pairs
  Conservative
  Luster, Andrew D.
Drazen, Jeffrey M.
   6.3%;
  Craig
  Greenfield & Sacks, P.C.
  0
  Score 14.8; DB 1; Length 20; Pred. No. 18;
   Mismatches
   Ν.
  0
   Gaps
  0
```

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밁
   S
   ; ANTI-SENSE:
US-08-117-952-294
   US-09-825-923-6
   Query Match
Best Local Similarity
Matches 16; Conserv
   Sequence 6, Application US/09825923 Patent No. 6696556 GENERAL INFORMATION:
APPLICANT: Nyyss"nen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Kauhanen, Jussi
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/99/825,923
CURRENT FILING DATE: 2001-04-05
  APPLICANT:
  APPLICANT:
   APPLICANT:
   TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO:
  APPLICANT: Snapir, Amir
   APPLICANT:
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
PILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,15
   MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-BOSE #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
  SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
  ZIP: 90071
COMPUTER READABLE FORM:
  TELECOMMUNICATION INFORMATION: TELEPHONE: 619-546-4737
   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
  CITY: Los Angeles
  REFERENCE/DOCKET NUMBER:
   MEDIUM TYPE:
   ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 South Flower Street, Suite 2000
  STRANDEDNESS:
  TELEPHONE:
   COUNTRY:
   18
   74 AGAGCTGGTTGTTGAAA 91
   nucleic acid
  Koulu, Markku
Pesonen, Ullamari
Scheinin, Mika
Salonen, Jükka T
Tuomainen, Tomi-Pekka
Lakka, Timo A
   AAAGCTGGTTTTTTGAAA 1
   Heinonen, Paula
Alhopuro, Pia
  Karvonen, Matti
   USA
  Conservative
   linear
  ŏ
   Floppy disk
   Oligonucleotide
   6.3%;
   US 08/078,471
   31,192
  <u>,</u>
   P41 9423
   Score 14.8;
Pred. No. 1
  Mismatches
   DB 1;
   #1.25
  2
   Length 21;
  Indels
  0;
  Gaps
```

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```
RESULT 16
US-09-056-285A-41
; Sequence 41, Application US/09056285A
; Patent No. 6403307
; GENERAL INFORMATION:
   밁
   á
   ; OTHER INFORMATION: Description of Artificial Sequence: PCR primer pair 1; directed ; OTHER INFORMATION: to Homo sapiens US-10-077-870-6
  RESULT 15
  맑
  8
  US-10-077-870-6
  US-09-825-923-6
   APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR PILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 6
  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 19
TYPE: DNA
   Query Match
Best Local Similarity
   GENERAL INFORMATION:
   Sequence 6, Application US/10077870 Patent No. 7029849
   Query Match
Best Local (
   Matches
   Matches
  PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
  TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: PCR primer OTHER INFORMATION: pair
  FEATURE:
  ORGANISM: Artificial Sequence
   Local Similarity 93.8%;
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
  Pingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
   APPLICANT: Stone, Edw
Sheffield,
   143
  143 CTCCCCCTTCTCCTTC 158
   15;
   15; Conservative
   CTCCCCCTCCTCCTTC 19
  CTCCCCCTTCTCCTTC 158
  crececercerecite 19
  STATE: MA
  CITY: Boston
   Conservative
   Alward, Wallace L.M.
   6.1%; Score 14.4; 93.8%; Pred. No. 2:
   Edwin M.
eld, Val C.
  HOAG & ELIOT LLP
   0
   0
   Score 14.4;
Pred. No. 2;
  Mismatches
   Mismatches
  DB 1;
   В
   1,
   ۲.
   Length 19;
   Length 19;
   Indels
   Indels
   0
   0
   Gaps
   Gaps
   0
   0
```

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S
  US-09-952-464A-41
   RESULT 17
   В
  US-09-056-285A-41
  US-09-952-464A-41
   PRIOR APPLICATION NUMBER: 09/461,542
PRIOR FILING DATE: 1999-12-15
PRIOR PELICATION NUMBER: 09/366,952
PRIOR FILING DATE: 1999-08-04
PRIOR APPLICATION NUMBER: 09/056,285
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 08/822,999
PRIOR FILING DATE: 1997-03-21
  NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 20
  GENERAL INFORMATION:
  Matches
                    Best Local
                                    Query Match
  Sequence 41,
   Matches
   Query Match
  Patent No. 69561
   FILE REFERENCE: 21087.0017U11
CURRENT APPLICATION NUMBER: US/09/952,464A
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/473,273
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
  APPLICANT: Alward, Wallace L.M.
APPLICANT: Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
  APPLICANT: Stone, Edwin M. APPLICANT: Sheffield, Val C.
  FEATURE: OTHER INFORMATION: Description of Artificial Sequence; No. 6956103e OTHER INFORMATION: Synthetic construct
  TYPE: DNA ORGANISM: Artificial Sequence
  INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
  LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer".
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
   Local Similarity
mes 15; Conserv
   CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY_AGENT INFORMATION:
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
   149 CTTCTCCTTCTGCCAT 164
Similarity
   CATCTCCTTCTGCCAT 18
   NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
  Application US/09952464A
   Conservative
Conservative
                  6.1%;
   6.1%;
93.8%;
   <u>.</u>
  <u>,</u>
   Score 14.4;
Pred. No. 21;
                  Score 14.4;
Pred. No. 21;
   Mismatches
  Mismatches
                                      DB 1;
   Version #1.30
   BB
   ۲.
                                    Length 20;
   Length 20;
  Indels
   Indels
   0,
  <u>,</u>
Gaps
   Gaps
  0
   0
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149 CTTCTCCTTCTGCCAT 164

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CURRENT APPLICATION NUMBER: US/08/850,993; CURRENT FILING DATE: 1997-05-05; EARLIER APPLICATION NUMBER: 0539/96; EARLIER FILING DATE: 1996-05-06; NUMBER OF SEQ ID NOS: 25; SOPTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 10; SEQ ID NO 10; LENGTH: 20; TYPE: DNA 10 ORGANISM: human
밁
                              ঠ
   US-08-850-993-10/c
  밁
  ঠ
  ; FEATURE:
; NAME/KEY: primer_bind
LOCATION: 1..19
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-8732 for SEQ 2136, US-09-422-978-10001
   밁
   US-09-422-978-10001/c
  CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-3
EARLIER FILING DATE: 1998-11-3
EARLIER FILING DATE: 1998-04-21
  Query Match
Best Local Similarity 84.2
16; Conservative
  Matches
   Query Match
Best Local (
  SEQ ID NO 10001
  GENERAL INFORMATION:
  Patent No.
  GENERAL INFORMATION:
   Patent No. 653775
  APPLICANT: Andersen, Carsten
APPLICANT: Pedersen, Oluf B.
TITLE OF INVENTION: Mutant cDNA Encoding The p85alpha
TITLE OF INVENTION: Subunit Of Phosphatidylinositol 3
FILE REFERENCE: 4802 200-US
   APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
   APPLICANT: Hansen, Torben
   NUMBER OF SEQ ID NOS: 11796
   ORGANISM: Homo Sapiens
  TYPE: DNA
   ENGTH: 19
  209 CATGCTTCTTGTTCT 227
  10, Application US/08850993
5. 5955277
                                 77
  19 CTTACTTCTTGTTGTCT 1
  10001,
20
   Similarity
                                 GCTGGTTGTTTGAAAGAGC 95
  Conservative
  Application US/09422978
   6.0%;
  6.0%;
  0
  0
  Score 14.2;
Pred. No. 23;
   Score 14.2;
Pred. No. 2
   Mismatches
  Migmatches
   멂
  DB 1; Length 19;
   7;
   Length 20;
  Indels
  0
  0
   Gaps
  Gaps
  0
   ä
  0
   complen
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RESULT 21
US-09-283-011-35/c
  g
   á
  RESULT 20
US-09-392-350-35/c
  US-09-392-350-35
   Sequence 35, Application US/09392350
Patent No. 6133032
GENERAL INFORMATION:
APPLICANT: Brett p. Monia
APPLICANT: Lex M. Cowsert
   Sequence 35, Application US/09283011 Patent No. 6207401
   Query Match
Best Local :
   SEQ ID NO 35
LENGTH: 20
   Matches
   Patent No.
APPLICATION NUMBER: 09/012,135
FILING DATE: January 22, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 6207401ember 25,
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
  OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FASTSEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/283,011 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
  CURRENT APPLICATION NUMBER: US/09/392,350 CURRENT FILING DATE: 1999-09-08
   TITLE OF INVENTION: ANTISENSE MODULATION OF PI3 KINASE P110 BETA EXPRESSION FILE REFERENCE: RTS-0075
  GENERAL INFORMATION:
   NUMBER OF SEQ ID NOS: 47
   ORGANISM: Artificial Sequence FEATURE:
  OTHER INFORMATION: Antisense Oligonucleotide
   TYPE: DNA
   APPLICANT: Plowman, Grego
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGN
TITLE OF INVENTION: AND/(
  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
  CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES:
  STREET: Suite 4700
CITY: Los Angeles
STATE: California
  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
   COMPUTER:
   COUNTRY:
   Match 6.0%;
Local Similarity 84.2%;
  19
   64 AGTTCACGTGAGAGCTGGT 82
  90071-2066
  AGTICATGICAGGGCTGGT 1
   Conservative
   IBM Compatible
   AND/OR
   Gregory
   DIAGNOSIS AND TREATMENT OF AND/OR AUR-2 RELATED DISORD
   0
   Score 14.2;
Pred. No. 23;
   1.44 Mb
   Mismatches
   25,
  DB 1;
   ω
••
  Length 20;
   Indels
   0;
   Gaps
```

in complemer

```
Sequence 11320, Application US/09422978

Patent No. 6537751

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ila
CURRENT NELICATION: Biallelic markers for use in
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1998-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER APPLICATION DATE: 1998-04-21
  FILE REFERENCE: RTS-0118
CURRENT APPLICATION NUMBER: US/09/593,711A
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 244
SEQ ID NO 62
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
   밁
   RESULT 23
US-09-422-978-11320
   문
   ঠ
   RESULT 22
US-09-593-711A-62
  S
  OTHER INFORMATION: Antisense Oligonucleotide
US-09-593-711A-62
   GENERAL INFORMATION:
Brett P. Monia
APPLICANT: Madeline M. Butle
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION:
TOTAL
  Best Loc
Matches
  NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 11320
LENGTH: 20
   Sequence 62, Application US/09593711A Patent No. 6271030
  Query Match
Best Local Similarity
  Matches
  Query Match 6.0%;
Best Local Similarity 84.2%;
  SEQUENCE CHARACTERISTICS
                    TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
  LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  TELEX:
   138 ACCTGCTCCCCCTTCTCCT 156
  182 GACTTCACAAGAAGCAAAT 200
   20
  16;
   GTCTTCACAGGAGGCAAAT 2
   AGCTGCTCCACCTTCTTCT 19
  67-3510
  Conservative
  Conservative
  linear
  6.0%;
   ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
   Butler
  35:
  0
  0; Mismatches
  Score 14.2;
Pred. No. 23;
  Score 14.2;
Pred. No. 2:
  Mismatches
  DB 1;
  DB 1;
   ä
  u
••
   constructing a high density...
  Length 20;
  Length 20;
  Indels
  Indels
  0,
  Gaps
  Gaps
  0
  0
```

```
Query Match
Best Local Similarity
Thes 16; Conserve
   ; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-4207 for SEQ 3455, US-09-422-978-11320
  밁
   밁
  Ş
  RESULT 25
US-09-012-135A-35/c
   á
  ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-033-936-35
   GENERAL INFORMATION:
APPLICANT: YOSHIDA, I
APPLICANT: HANAOXA, I
APPLICANT: HANAOXA, I
APPLICANT: OSHIMURA,
APPLICANT: ISHIDA, II
  RESULT 24
US-09-033-936-35/c
  APPLICANT: ISHIDA, ISAO
TITLE OF INVENTION: CHIMERIC ANIMAL AND METHOD FOR PRODUCING THE
FILE REFERENCE: 081356/0114
CURRENT APPLICATION NUMBER: US/09/033,936
CURRENT FILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
LENGTH: 20
TYPE: DNA
Artificial Course.
   Sequence 35, Application US/09012135A Patent No. 6716575
  Sequence 35, Application US/09033936 Patent No. 6632976
  Matches
   Query Match
  GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORD
   ORGANISM: Artificial Sequence FEATURE:
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
   NUMBER OF SEQUENCES:
CURRENT APPLICATION DATA:
              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
  CITY: Los Angeles
STATE: California
  Local Similarity
les 16; Conserv
  ZIP: 90071-2066
  COUNTRY:
   136 ACACCTGCTCCCCCTTCTC 154
  104 CTCTCATTCTCCTGCTCCC 122
  20
   N
   CTCTCCATCTCCTACTCCC 20
   OSHIMURA, MITSUO
   U.S.A.
   Conservative
  Conservative
   KAZUNORI
   6.0%;
  6.0%;
   KAZUMA
   HITOSHI
   39
  0;
   .
,
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Pred. No. 23;
  Score 14.2;
Pred. No. 23;
   1.44 Mb
  Mismatches
   В
  DB 1; Length 20,
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  Indels
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  0
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ş
  US-09-784-332-35/c
  밁
  US-09-012-135A-35
   Query Match
Best Local Similarity 84.2
   Sequence 35, Application Patent No. 6841579
GENERAL INFORMATION:
   TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   FILING DATE: January 9, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 6716575ember 25, 1:
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
  TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
   ATTORNEY/AGENT INFORMATION
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
COMPUTER: IBM COMPATIBLE.

COMPUTER: IBM COMPATIBLE.

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/784,332

FILING DATE: 16-Feb-2001

CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: 09/283,011

FILING DATE: «Unknown»

APPLICATION NUMBER: 09/012,135

FILING DATE: January 22, 198

APPLICATION NUMBER: 09/012,788

  TELEPHONE: (213) 955-0440
   STRANDEDNESS:
TOPOLOGY: 11r
  TYPE: nucleic acid
  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
   APPLICATION NUMBER: 09/005,268
   APPLICATION NUMBER: US/09/012,135A
  COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5"
  NUMBER OF SEQUENCES:
   TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
AND/OR AUR-2 RELATED DISORDERS
   APPLICANT: Plowman, Gregory
Mossie, Kevin
   CORRESPONDENCE ADDRESS:
  182 GACTTCACAAGAAGCAAAT 200
  20 GTCTTCACAGGAGGCAAAT 2
   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
  CITY: Los Angeles
STATE: California
   Application US/09784332
   linear
   January 22, 1998
   single
  6.0%;
  storage
  Diskette, 1.44 Mb
   ; Score 14.2; D;
; Pred. No. 23;
0; Mismatches
  1996
   DB 1; Length 20;
   Indels
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   Gaps
   0
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RESULT 27
US-08-765-340-29
  COMPUTER READABLE FORM:

MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 145146/94
FILING DATE: 27-UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 311130/94
FILING DATE: 27-UN-1994
PRIOR APPLICATION NUMBER: JP 31130/94
FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
   Matches
   Query Match 6.0%; Score 14.2; Best Local Similarity 84.2%; Pred. No. 23;
  Patent No.
  GENERAL INFORMATION:
   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
   APPLICANT: UCHIDA, K.,
APPLICANT: UCHIDA, T.,
APPLICANT: TANAKA, Y.,
APPLICANT: MATSUDA, Y.,
APPLICANT: MONDO, S.,
APPLICANT: KONDO, S.,
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
TITLE OF INVENTION: COMPOUND
NUMBER OF SEQUENCES: 185
TELEFAX: (212) 751-6849 FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
   CORRESPONDENCE ADDRESS:
  STATE: NEW YORK
  COUNTRY: U. ZIP: 10154
   ADDRESSEE:
STREET: 34
   FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
  SEQUENCE DESCRIPTION: SEQ ID NO: 35:
  TELEPHONE: (213) 489-1600
  29, 50092
11, 6150092
   182 GACTTCACAAGAAGCAAAT 200
  20 GTCTTCACAGGAGGCAAAT 2
   16;
   LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
   NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
  TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
  Application US/08765340
   E: MORGAN & FINNEGAN, L.L.P.
345 PARK AVENUE
  USA
   Conservative
  PatentIn Release #1.0, Version
   0; Mismatches
   DB 1;
   Length 20;
   Indels
   <u>.</u>
   Gaps
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```
S
   RESULT 28
US-08-373-124A-178
   Query Match 5.9
Best Local Similarity 100.
Matches 14; Conservative
Query Match
  COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.
SOCTWARE: WOR'D PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,124
FILING DATE: January 13, 1995
PRIOR APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: PEDUARY 7, 1994
APPLICATION NUMBER: 07/937,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WARDLURG, Richard
BEGISTRATION RUMBER: 32,327
   GENERAL INFORMATION:
   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
  TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
  REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
  APPLICANT:
   CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES:
   APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
   TELLEFAX: 12-
TELEFAX: 67-3510
   LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   TELEPHONE: (213) 955-0440
   STREET:
  STRANDEDNESS: single
  COUNTRY:
  ADDRESSEE:
  152 CTCCTTCTGCCATG 165
   90071
  Los Angeles
: California
   Suite 4700
   E: Lyon & Lyon
633 West Fifth Street
  Application US/08373124A
  Draper, Kenneth
McSwiggen, James
   U.S.A.
   Stinchcomb, Dan T.
  linear
  5.9%;
5.8%; Score 13.8;
   US/08/373,124A
   0; Mismatches
  Score 14; DB 1; Pred. No. 24;
   209/035
  DOS 5.0
  1.44 Mb
DB 1;
   0; Indels
  Length 20
Length 17;
   0,
   Gaps
   0
```

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밁
문
                            Ś
  TELEFAX: 1427
TELEX: 67-3510
INFORWATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
TYPE: nucleic scid
   US-08-373-124A-180
  US-08-373-124A-180
  Patent No.
   Sequence
  Best Local Similarity 52.9
Matches 9; Conservative
   Matches
  Query Match
  FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
   GENERAL INFORMATION:
   FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,46
  SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
  NUMBER OF SEQUENCES: 2
  Local Similarity hes 9; Conserv
   TELEPHONE: (213) 955-0440
  TOPOLOGY: lir
  FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
   OPERATING SYSTEM:
   COUNTRY: U.S.A.
ZIP: 90071
   CITY: Los Angeles
STATE: California
   ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
   APPLICATION NUMBER: US/08/373,124A
   140 CTGCTCCCCTTCTCT 156
                            143 CTCCCCCTTCTCTTCT 159
  1 CUCCUCCUCCUUCUCCU 17
   Application US/08373124A
   McSwiggen, James
Jarvis, Thale
   Conservative
   linear
  IBM Compatible
  METHODS AND COMPOSITIONS FOR TREATMENT OF RESTENOSIS AND CANCER USING RIBOZYMES
   Kenneth
   5.8%;
  IBM P.C.
  52.9%;
  08/245,466
  209/035
  6
  6,
  Pred. No. 31;
6; Mismatches
  Score 13.8;
Pred. No. 31;
  DOS 5.0
   Mismatches
  DB 1; Length 17;
  <u>ب</u>
   Indels
  ;
  0;
  Gaps
  0
  0
```

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ZIP: 90071

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: GOTAGE

COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,628

FILING DATE: 05-MAY-1995

CLASSIFICATION DATA:

APPLICATION UMBER: 08/373,124

FILING DATE: January 13, 1995

APPLICATION NUMBER: 08/245,466

PILING DATE: May 18, 1994

APPLICATION DATE: May 18, 1994
   RESULT 31
US-08-435-628-180
   밁
   Ś
  US-08-435-628-178
   US-08-435-628-178
Sequence 180, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
   Query Match 5.8%;
Best Local Similarity 52.9%;
Matches 9; Conservative
  Patent No.
  TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
   FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
   GENERAL INFOR
APPLICANT:
   APPLICANT: Draper, Neuron.

APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: CANCER USING RIBOZYMES
TITLE OF INVENTION: CANCER USING RIBOZYMES
  SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   NAME: Warburg, Richard REGISTRATION NUMBER: 32,327 REGERENCE/DOCKET NUMBER: 209/035 TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
   ELECUPACE: (213)
  STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Anno 1
   TOPOLOGY:
   140 CTGCTCCCCCTTCTCT 156
  178, Application US/08435628
o. 5817796
  INFORMATION:
   1 cuccuccuccuucuccu 17
  Los Angeles
: California
  U.S.A.
   linear
  955-0440
   Score 13.8;
Pred. No. 31
   Mismatches
   DB 1; Length 17;
   0;
   0,
```

```
Query Match
Best Local Similarity
Thes 9; Conserve
   밁
   Ş
RESULT 32
US-08-311-486C-1151
   US-08-435-628-180
  APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18,1994
APPLICATION NUMBER: 08/192,943
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/986,422
FILING DATE: August 26, 1992
APPLICATION NUMBER: 07/966,422
APTORNEY/AGENT INFORMATION:
NAME: Watburg, Richard
REGISTRATION NUMBER: 32,327
REGERENCY/DOCKET NUMBER: 32,327
  TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
   OPERATING SYSTEM: IBM P.C. DOS SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
   TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Comparible
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
   APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
   TOPOLOGY: 11
  REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 20
   COUNTRY:
   TELEFAX:
   143 CTCCCCCTTCTCCTTCT 159
   1 cuccuccouccuccu 17
   9007:
  nucleic acid
   (213) 955-0440
  Conservative
   linear
   single
  52.98;
  6,
  Score 13.8;
Pred. No. 31;
  Mismatches
  DB 1;
  Length 17;
  Indels .
  0
  Ö
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Sequence 1151, Application US/08311486C Patent No. 5811300

GENERAL INFORMATION:

APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kenneth Draper
APPLICANT: Mevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF

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밁
   S
   US-09-422-978-4193/c
  US-08-311-486C-1151
  Sequence 4193, Application US/09422978 Patent No. 6537751
   Matches
  Best Local Similarity
   Query Match
                               GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallalic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-04-21
  APPLICATION NUMBER: US/08/311,480
FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including a
PRIOR APPLICATION DATA: including a
PRIOR APPLICATION DATA: described b
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 193
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: DECEMBER: 07/981,849
ATTORNEY/AGENT INFORMATION:
NUMBER OF SEQ ID NOS
EQ ID NO 4193
  TELEX: 67-3510
NFORMATION FOR SEQ ID NO:
   SEQUENCE CHARACTERISTICS
  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
   TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
  CURRENT APPLICATION DATA
   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
   NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
   OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
   LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   COMPUTER:
  TELEFAX:
  ADDRESSEE:
  ENGTH:
   13;
   91 AGAGCCTGGCCCCCTCT 107
  90071-2066
  Los Angeles
California
   AGAGCCAGCCCCCCUCU 17
   E: Lyon & Lyon
633 West Fifth
  Suite 4700
  (213)
   Conservative
   linear
   IBM Compatible
  955-0440
  5.8%;
76.5%;
  US/08/311,486C
per 23, 1994
  including application described below:
   Street
   2;
  Score 13.8;
Pred. No. 29;
   209/166
  SOG
  1.44
   Mismatches
  ₹
   DB 1;
   2
   Length 18;
   Indels
   0,
  two
   Gaps
   0
```

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Query Match
Best Local Similarity
Tatches 15; Conserve
                           5
   밁
  Ś
   ; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13878 for SEQ 259,
US-09-422-978-4193
밁
  ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) PCT-US95-04094-3
   RESULT 34
PCT-US95-04094-3
  Sequence 3, Application PC/TUS9504094 GENERAL INFORMATION:
  Matches
   Query Match
  TELEFAX: (703) 836-202: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 18 base pairs
  TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
   APPLICANT: ALMS, William
APPLICANT: WHITE, Barbara
TITLE OF INVENTION: HUMAN INTERLEUKIN VARIANTS GENERATED
TITLE OF INVENTION: ALTERNATIVE SPLICING
NUMBER OF SEQUENCES: 22
CORRESPONDENCE: 22
   REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: FC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
   CORRESPONDENCE ADDRESS:
  STRANDEDNESS: 81
   LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  COUNTRY: United States ZIP: 22313-1404
  Local
  FILING DATE:
  STREET: P.O. Box CITY: Alexandria
   APPLICATION NUMBER:
   CLASSIFICATION:
  TELEPHONE:
  NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113
  ADDRESSEE:
                              113 TCCTGCTCCCACTCTTG 129
  110 Trerecrecreceaere 126
   17 TTCTCCTAATCCCACTC 1
  l Similarity
15; Conserv
  Virginia
TCCTGCTCCAACTCCTG 17
   P.O. Box 1404
   (703) 836-2021
  Conservative
  Conservative
  Burns, Doane, Swecker & Mathis
  (703)
   06-APR-1994
  5.8%;
88.2%;
  836-6620
   5.8%;
  US 08/224,010
   PCT/US95/04094
  Score 13.8; D
Pred. No. 29;
0; Mismatches
  <u>,</u>
  0
   Score 13.8;
Pred. No. 29;
  Mismatches
   DB 1;
   DB
   ۲.
   Length 18;
   Length 18
  Indels
  0
  0;
  Gaps
  Gaps
  0
  0
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RESULT 35 US-08-502-185-9/c ; Sequence 9, Application US/08502185

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RESULT 36
US-08-398-945-9/c
   밁
   გ
   US-08-502-185-9
   Sequence 9, Application US/08398945
Patent No. 5639872
  Matches 15;
  Query Match
   GENERAL INFORMATION:
  REFERENCE/DOCKET NUMBER: HY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1301
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
   SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,185
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   APPLICANT: Robinson, Gregory S.
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
  MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
  APPLICANT: Robinson, Gregory S.
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
   MEDIUM TYPE: Floppy
   NUMBER OF SEQUENCES: 5
  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
  STREET:
STREET:
ATTY: Boston
Massac
   CORRESPONDENCE ADDRESS
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
   NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
  COUNTRY: USA
ZIP: 02109
   Local Similarity
   FILING DATE:
  CITY: Boston
   DDRESSEE:
  DDRESSEE:
   213 CTTCTTGTTCTGC 229
  INFORMATION:
   02109
   5639736
  Massachusetts
   Massachusetts
  E: Lappin & Kusmer
200 State Street
   3: Lappin & Kusmer
200 State Street
  Conservative
   CDNA
  88.2%;
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  HYZ-031CPDV1
  Score 13.8;
Pred. No. 2
  DB 1;
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; TOPOLOGY: linear
; MOLECULE TYPE: CDN
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-398-945-9
; HYPOTHETICAL:
; ANTI-SENSE: 1
US-08-501-779-9
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US-08-501-779-9/c
  5.8%;
Best Local Similarity 88.2%;
Matches 15; Conservative
  Patent No. 5661135
GENERAL INFORMATION:
APPLICANT: Robins
  Sequence 9, Application US/08501779 Patent No. 5661135
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,779
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031CPDV2
  TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO:
  TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE:
  MOLECULE TYPE:
  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
  NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
   SEQUENCE CHARACTERISTICS:
   TELECOMMUNICATION INFORMATION:
   REFERENCE/DOCKET NUMBER: HY
TELECOMMUNICATION INFORMATION:
  TITLE OF INVENTION:
   STREET: STREET: Soston
   STRANDEDNESS: single TOPOLOGY: linear
   NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
  TELEPHONE:
  COUNTRY:
  STRANDEDNESS:
   TYPE: nucleic acid
   TELEPHONE: 617-330-1300
  ENGTH:
  213 cricircircicicico 229
  19 CGTCTTGTTCTGTGTGC 3
   nucleic acid
   Massachusetts
  19 base pairs
                     ŏ
  Robinson,
  linear
                                    ö
   CDNA
   CDNA
   single
  Oligonucleotides
   Gregory S.
Human VEGF-Specific
   9
  0;
   HYZ-031CIP
   Score 13.8;
Pred. No. 2
  Mismatches
  DB 1;
  Length 19;
  Indels
  0;
  Gaps
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0;

Query Match Best Local Similarity

> Score 13.8; Pred. No. 27;

DB 1;

Length 19;

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RESULT 39
US-08-378-860-9/c
   밁
   밁
  US-08-501-713-9/c
   US-08-501-713-9
GENERAL INFORMATION:
APPLICANT: Robinson,
APPLICANT: Smith, Lo:
APPLICANT: SINTENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
  Sequence 9, Application US/08501713
Patent No. 5710136
GENERAL INFORMATION:
   Sequence 9, Application US/08378860 Patent No. 5731294
   Matches
   Matches
  Query Match
  TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
  APPLICANT: Robinson, Gregory S.
APPLICANT: Smith, Lois E.H.
TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: Newpascularization Using
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
  NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
   ANTI-SENSE: NO
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,713
FILING DATE:
  HYPOTHETICAL:
   MOLECULE TYPE:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  COUNTRY: UL.
  Match 5.8%;
Local Similarity 88.2%;
   STRANDEDNESS: si
TOPOLOGY: linear
  STATE: Massachusetts
   TYPE: nucleic acid
   213 CTTCTTGTTCTGTCTGC 229
   213 CTTCTTGTTCTGTCTGC 229
   19
   15;
   19
   15;
   Boston
   cercricirciererec 3
   cerciferrererec 3
   Conservative
   Robinson, Gregory S. Smith, Lois E.H.
   USA
   Conservative
   ŏ
  CDNA
   single
                Neovascularization Using VEGF-Specific
   Oligonucleotides
  Inhibition of
   0,
   0
   Score 13.8;
Pred. No. 2
  HYZ-031DV2
   Mismatches
   Mismatches
  DB 1;
   2
   Length 19;
   Indels
   Indels
   0
   0,
   Gaps
   Gaps
   0
   0
  뭕
  Ş
  US-08-378-860-9
  APPLICANT:
```

```
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEPAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
  Query Match
Best Local Similarity
Matches 15; Conserv
   Sequence 9, Application US/08501626
Patent No. 5801156
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,626
FILING DATE:
CLASSIFICATION: 435
   -08-501-626-9/c
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/378,860
FILING DATE:
   GENERAL INFORMATION:
APPLICANT: Robins
   TITLE OF INVENTION: Neovascularization
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
  MOLECULE TYPE: CD
   TITLE OF INVENTION:
TITLE OF INVENTION:
  HYPOTHETICAL:
ANTI-SENSE: 1
  ATTORNEY/AGENT INFORMATION: NAME: Kerner, Ann-Louise
   NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
ATTORNEY/AGENT INFORMATION:
  STREET: 200 S
CITY: Boston
STATE: Massac
  COUNTRY: USA
ZIP: 02109
  STRANDEDNESS: single TOPOLOGY: linear
  TYPE: nucleic acid
   STREET: 200 (
CITY: Boston
  CLASSIFICATION:
   COUNTRY: USA
   213 CTTCTTGTTCTGTCTGC 229
   19 dererrerrerere 3
  Massachusetts
   Massachusetts
   Robinson, Gregory S. Smith, Lois E.H.
   Conservative
   ĕ
  CDNA
  Ann-Louise
  5.8%;
  Inhibition of
   US/08/378,860
   <u>.</u>
  HYZ-031
   Score 13.8;
Pred. No. 27;
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US-08-501-356-9/c
   ; ANTI-SENSE: NO US-08-501-626-9
  RESULT 41
   Sequence 9, Applic Patent No. 5814620
  Matches
  Query Match
Best Local Similarity
  TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
   TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 9:
  ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
  GENERAL INFORMATION:
  SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,356
  COMPUTER READABLE FORM:
ANTI-SENSE:
              MOLECULE TYPE: C
   TITLE OF INVENTION: Inhibition of INTENTION: Neovascularization Using TITLE OF INVENTION: VEGF-Specific TITLE OF INVENTION: Oligonucleotides
   APPLICANT:
  MOLECULE TYPE: CI
  SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
  TELEPHONE: 617-330-1300
   CORRESPONDENCE ADDRESS
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  FILING DATE:
   COUNTRY: USA
ZIP: 02109
  STREET:
   TOPOLOGY: linear
  CLASSIFICATION:
   REFERENCE/DOCKET NUMBER:
  STRANDEDNESS:
   TYPE: nucleic acid
  ADDRESSEE:
   STRANDEDNESS:
  TYPE: nucleic acid
   REGISTRATION NUMBER:
   213 CTTCTTGTTCTGTCTGC 229
  15;
  19 CGTCTTGTTCTGTGC 3
   Boston
  Kerner, Ann-Louise
  Massachusetts
   Application US/08501356
  3: Lappin & Kusmer
200 State Street
   Smith, Lois E.H.
  Robinson, Gregory S.
  Conservative
 ö
   linear
                             CDNA
   CDNA
  single
  single
   5.8%;
  33,523
   HYZ-031DV3
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   Score 13.8;
Pred. No. 27
   HYZ-031DV4
  DB 1;
  Length 19;
  Indels
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Query Match

5.8%; Score 13.8;

DB 1;

Length 19;

```
Ş
  В
   밁
  Patent No. 6455304

Patent No. 6455304

GENERAL INFORMATION: Weigel, Paul H.

APPLICANT: Weigel, Paul L.

DeAngelis, Paul L.
  RESULT 43
US-09-146-893-6
  US-08-270-581-6
  RESULT 42
US-08-270-581-6
  Sequence 6, Apr--
Sequence 6, Apr--
No. 5856168
   Matches
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  Best Local Similarity
  COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,581
FILING DATE:
  TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO:
   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
  TOPOLOGY: 11
MOLECULE TYPE:
   SEQUENCE CHARACTERISTICS:
  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
  APPLICANT: Weigel, Paul H.
APPLICANT: DeAngelis, Paul L.
APPLICANT: Papaconstantinou,
   APPLICANT: Papaconstantinou, John IITLE OF INVENTION: Hyaluronate Sy IITLE OF INVENTION: Thereof
  Local Similarity
   CITY: Houston
STATE: TX
   STRANDEDNESS:
   ENGTH:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                NUMBER OF SEQUENCES:
  TITLE OF INVENTION: Hyaluronate Synthase Gene and Uses Thereof
  · 213 CTTCTTGTTCTGTCTGC 229
   19 CGTCTTGTTCTGTGTGC 3
  32 ATGGTTTAGTGCCATCC 48
  INFORMATION:
  2 ATGGCTTAGTGCCATTC 18
  nucleic acid
  Application US/08270581
   Conservative
   713-789-2679
  Conservative
  DNA (genomic)
  single
   5.8%;
  Hyaluronate Synthase Gene and Uses
  88.2%;
   5
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   UTSG:161\PAR
  Pred. No. 27;
0; Mismatches
  Score 13.8;
Pred. No. 2
   Mismatches
  John
   Version #1.25
  DB 1;
  2;
  Length 19;
   Indels
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  0;
   Gaps
   0
  0,
```

```
GENERAL INFORMATION:

APPLICANT: MEIGEL, PAUL E.

APPLICANT: DEANGELIS, PAUL L.

APPLICANT: DEANGELIS, PAUL L.

APPLICANT: DEANGELIS, PAUL L.

APPLICANT: DEANGELIS, PAUL L.

FITTLE OF INVENTION: HYALURONATE SYNTHASE GENES AND USES THEREOF

FILE REFERENCE: 35541.073

CURRENT APPLICATION NUMBER: US/10/117,795

CURRENT FILING DATE: 2002-04-03

PRIOR APPLICATION NUMBER: 09/559,793

PRIOR APPLICATION NUMBER: 09/559,793

PRIOR APPLICATION DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PATENTIN VETSION 3.1

SEQ ID NO 8
   ; OTHER INFORMATION: OLIGONUCLECTIDE PROBE US-10-117-795-8
  US-10-117-795-8
   밁
  Ś
  US-09-146-893-6
   Query Match 5.8%;
Best Local Similarity 88.2%;
Matches 15; Conservative
   Sequence 8, Application US/10117795 Patent No. 6852514
  Matches
  Query Match
Best Local Similarity
  TYPE: DNA
  ORGANISM: ARTIFICIAL SEQUENCE FEATURE:
  TELEPHONE: 713-787-1400
TELEPAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
   ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   APPLICATION NUMBER: 08/270,581
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSG:161\PAR
TELECOMMUNICATION INFORMATION:
   SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,893
FILING DATE: 03-Sep-1998
CLASSIFICATION: -UTIKNOWN>
PRIOR APPLICATION DATA:
   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO:
  32 ATGGTTTAGTGCCATCC 48
32 ATGGTTTAGTGCCATCC 48
  15;
  19
   N
   ATGGCTTAGTGCCATTC 18
  LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  STREET: P. O. CITY: Houston
  Conservative
  5.8%;
  0
   Score 13.8;
Pred. No. 27;
  Score 13.8;
Pred. No. 27;
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  Mismatches
   9
  DB 1;
   띪
   1;
  2;
  2
  Length 19;
   Length 19;
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   Indels
   #1.25
  0
   0
   Gaps
  Gaps
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PRIOR APPLICATION NUMBER: 09/146,893
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 8
LENGTH: 19
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
FEATURE:
  Query Match
Best Local Similarity
"Thes 15; Conserva
   Query Match
Best Local Similarity
Watches 15; Conserva
   밁
  밁
  Ś
  RESULT 45
US-10-124-222-8
                                 S
  ; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE US-11-024-426-8
   US-11-024-426-8
   ; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE US-10-124-222-8
   APPLICANT: PAPACONSTÂNTINOU, JOHN
TITLE OF INVENTION: HYALIRONATE SYNTHASE GENES ANI
FILE REFERENCE: 35541.069
CURRENT APPLICATION NUMBER: US/10/124,222
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 09/146,893
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
   밁
  Sequence 8, Application US/10124222
Patent No. 685502
GENERAL INFORMATION:
APPLICANT: WEIGEL, PAUL E.
APPLICANT: DEANGELIS, PAUL L.
   GENERAL INFORMATION:
   Sequence 8, Application US/11024426 Patent No. 7026159
  SEQ ID NO 8
   APPLICANT: WEIGEL, PAUL E.
APPLICANT: DEANGELIS, PAUL L.
APPLICANT: DEANGELIS, PAUL L.
APPLICANT: DAPACONSTANTINOU, JOHN
TITLE OF INVENTION: HYALURONATE SYNTHASE GENES
FILE REFERENCE: 35541.069
CURRENT APPLICATION NUMBER: US/11/024,426
CURRENT FILING DATE: 2004-12-30
CURRENT FILING DATE: 2004-12-30
   TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
  32 ATGGTTTAGTGCCATCC 48
                                     32 ATGGTTTAGTGCCATCC 48
   N
  2 ATGGCTTAGTGCCATTC 18
AIGGCTTAGTGCCATTC 18
   ATGGCTTAGTGCCATTC 18
   Conservative
   Conservative
  5.8%;
   5.8%; Score 13.8;
88.2%; Pred. No. 27;
   0
   0
  Score 13.8;
Pred. No. 2
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  AND USES THEREOF
   2
   Length 19
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   Gaps
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RESULT 47 US-10-156-306B-6881/c US-10-156-306B-6881, Application US/10156306B ; Patent No. 7022828

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RESULT 49
US-09-358-972-204/c
  밁
  8
  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306B-6882
  US-10-156-306B-6882/c
   몽
   ફ
   RESULT 48
  Best Loc
Matches
  Sequence 204, Application US/09358972 Patent No. 6235480
   SOFTWARE: PatentIn version 3.0 SEQ ID NO 6882
  Patent No. 7022828
GENERAL INFORMATION:
   Sequence
   SOFTWARE: PatentIn version 3.0
SEQ ID NO 6881
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
S-10-156-306B-6881
   Matches
  Query Match
Best Local Similarity
   APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MBH801-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306B
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8014
SOFTWARF. Data.
   GENERAL INFORMATION:
   Query Match
   APPLICANT: C
   APPLICANT: Shultz, John W
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
   APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
  APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwijgen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: M8HB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306B
CURRENT FILING DATE: 2002-05-28
  APPLICANT: Olson, Ryan J. APPLICANT: Wood, Keith W.
  APPLICANT: Hartnett, James R.
   NUMBER OF SEQ ID NOS: 8014
  ENGTH:
   Local
E OF INVENTION: Nucleic Acid Detection REFERENCE: Pro-103 6868/75528
  INFORMATION:
  148 CCTTCTCCTTCTGCC 162
   148 CCTTCTCCTTCTGCC 162
  15
   16
   14;
   Similarity
   ccrecrecrierece 2
                                   Welch,
   Application US/10156306B
   Conservative
  Conservative
   Trent
                             Roy
   5.7%; Score 13.4;
93.3%; Pred. No. 35
  5.7%; Score 13.4;
93.3%; Pred. No. 35
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   Mismatches
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   В
   B
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  1; Length 17;
   Length 17;
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  or Conditions Relate
  Gaps
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밁
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  δ
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  US-09-406-064-70
   SOFTWARE: Pate
SOFTWARE: Pate
; SEQ ID NO 70
FONCTH: 18
  US-09-406-064-70/c
  RESULT 50
   APPLICANT: Shultz, John W
APPLICANT: Lewis, Martin K.
APPLICANT: Leippe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B
   Matches
  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 204
LENGTH: 18
  Query Match
  Best Local Similarity
Matches 14; Conser
   Query Match
  TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
FILE REFERENCE: PRO-107.0 (6866/75532)
CURRENT APPLICATION NUMBER: US/09/406,064
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: 09/358,972
EARLIER FILING DATE: 1999-07-21
EARLIER FILING DATE: 1999-07-21
EARLIER FILING DATE: 1999-02-16
EARLIER FILING DATE: 1999-02-16
EARLIER FILING DATE: 1998-03-13
  CURRENT APPLICATION NUMBER: US/09/358,972
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
   NUMBER OF SEQ ID NOS: 99
   EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
  APPLICANT: Andrews, Christine APPLICANT: Hartnett, James R.
   EARLIER APPLICATION NUMBER: 09/042,287
   APPLICANT: Wood, Keith V. APPLICANT: Welch, Roy
  APPLICANT: Gu,
   OTHER INFORMATION: Description of Artificial Sequence: CAH reverse OTHER INFORMATION: probe
  TYPE: DNA
  ORGANISM: Artificial Sequence
  ORGANISM: Artificial Sequence FEATURE:
   TYPE: DNA
   FEATURE:
   Local Similarity
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17
   70, Application US/09406064
). 6270973
   17
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  TTGGTGATGAGTGAG
   Conservative
  Conservative
  Trent
  5.78;
   5.7%;
  65
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  0,
  Score 13.4; I
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0; Mismatches
  Score 13.4;
Pred. No. 3
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  DB
   B
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US-09-430-615-40/c

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APPLICANT: Olson, Ryan J
APPLICANT: Welch, Roy
TITLE OF INVENTION: Improved Nucleic Acid Detection
FILE REFERENCE: Improved Nucleic Acid Detection
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: 09/358,972
EARLIER FILING DATE: 1999-07-21
SARLIER FILING DATE: 1999-03-18
FARLIER FILING DATE: 1998-03-18
SARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 45
LENGTH: 18
  RESULT 52
US-09-406-065-45/c
   밁
   ঠ
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; OTHER INFORMATION: Description of Artificial Sequence:CAH reverse
; OTHER INFORMATION: probe
US-09-430-615-40
  APPLICANT: Leippé, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B
APPLICANT: Andrews, Christine A
APPLICANT: Harthett, James R
   Sequence 40, Application US/09430615 Patent No. 6277578
  SEQ ID NO 40
LENGTH: 18
  Matches
  Query Match
   Sequence 45, Application US/09406065
Patent No. 6312902
   Patent No.
   PRIOR APPLICATION NUMBER: 09/042,287
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver. 2.0
  CURRENT APPLICATION NUMBER: US/09/430,615
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/358,972
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: 09/252,436
PRIOR APPLICATION NUMBER: 09/252,436
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
   APPLICANT:
  APPLICANT: Shultz, John W
APPLICANT: Lewis, Martin K.
  FILE REFERENCE:
  APPLICANT:
  APPLICANT:
  APPLICANT: Shultz, John William TITLE OF INVENTION: Method for J
  APPLICANT:
   APPLICANT: Gu,
   TYPE: DNA ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
   Local
   INFORMATION:
   INFORMATION:
   17
   51 TTGGTGATGAGTGAG 65
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Similarity 93.3%;
   Mandrekar, Michelle
Andrews, Christine Ann
   Welch, Roy
   Hartnett, James Robert
  Lewis, Martin K.
  Conservative
   Trent
  Donna
  Method for Amplified Nucleic
  0,
   Score 13.4;
Pred. No. 3:
  Mismatches
  DB 1;
  1;
  Acid Detection
  Length 18;
  Indels
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  Gaps
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APPLICANT: Byrne, Jennifer A.
APPLICANT: Basset, Paul
ITITLE OF INVENTION: Members of the D52 Gene Fai
FILE REFERENCE: 1183.0210001
CURRENT APPLICATION NUMBER: US/09/250,611
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 48
LENGTH: 18
  ; OTHER INFORMATION: Description US-09-250-609-48
  ; FEATURE:
; OTHER INFORMATION: Description
; OTHER INFORMATION: probe
US-09-406-065-45
밁
                       á
   밁
   문
  S
   US-09-250-611-48
  US-09-250-611-48
  US-09-250-609-48
   RESULT 53
  CURRENT APPLICATION NUMBER: US/09/250,609A
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 48
   Sequence 48, Applicate Patent No. 6458943 GENERAL INFORMATION:
   Query Match
Best Local S
   GENERAL INFORMATION:
  Sequence 48, Application US/09250611
Patent No. 6528283
  Query Match
Best Local Similarity
  Matches
  Matches
   Query Match
  APPLICANT: Byrne, Jennifer A.
TITLE OF INVENTION: Members of the D52 Gene
FILE REFERENCE: 1383.0210002
   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
  LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
   OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
  FEATURE:
   Local
  51 TTGGTGATGAGTGAG 65
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  51 TTGGTGATGAGTGAG 65
                            51 TTGGTGATGAGTGAG
  14;
 N
   2 TIGGIGATGACTGAG 16
  Similarity
  Similarity
   TTGGGGATGAGTGAG
   Application US/09250609A
  Conservative
  Conservative
  Conservative
  93.3%;
  5.7%;
93.3%;
   5.7%;
93.3%;
                            65
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  0
   Score
Pred.
  Score 13.4;
Pred. No. 3
  Score 13.4;
Pred. No. 33;
  of Artificial Sequence: PCR Primer
  of Artificial Sequence: CAH reverse
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  Mismatches
  13.4;
No. 33;
   DB
   BG
   BG
   1;
   1;
   Length 18
  Length 18;
  Indels
  Indels
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  0
  0
   Gaps
  Gaps
  Gaps
  0
  0
  0
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S
  US-09-422-978-11764
   US-09-422-978-11764
   CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
   PRIOR APPLICATION NUMBER: 09/042,287
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 70
  SEQ ID NO 11764
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
  Query Match
Best Local :
   Sequence 11764, Appl Patent No. 6537751 GENERAL INFORMATION:
  -09-788-847-70/c
   Matches
  FILE REFERENCE: PRO-107.0 (6868/75532)
CURRENT APPLICATION NUMBER: US/09/788,847
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/406,064
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
  APPLICANT:
  APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use
FILE REFERENCE: GENSET.020CP1
  PRIOR APPLICATION NUMBER: 09/252,436
PRIOR FILING DATE: 1999-02-18
   APPLICANT: Welch, ROY
TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
  ENERAL INFORMATION:
  APPLICANT:
   APPLICANT:
  APPLICANT:
  NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: downstream amplification primer 99-889 for SEQ 3899, in complemer
   PPLICANT:
  PPLICANT:
   PPLICANT:
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: probe
   ORGANISM: Artificial Sequence
   LENGTH: 18
TYPE: DNA
   PPLICANT:
  Local Similarity
  113 TCCTGCTCCCACTCT 127
   70,
   14; Conservative
   Mandrekar, Michelle
Kephart, Daniel
Rhodes, Richard B
  Andrews, Christine A. Hartnett, James R.
   Application US/09788847
   Wood, Keith V.
   eippe, Donna
  Jewis, Martin K.
  Application US/09422978
   Trent
  93.3%;
   0
  Score 13.4;
Pred. No. 33;
   Mismatches
   BB
  in constructing a high density...
   <u>;</u>
   Length 18;
  Indels
  0
  Gaps
  0
```

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밁
   US-09-255-912-14
   US-09-790-417-204
  밁
   Ś
   US-09-788-847-70
  US-09-790-417-204/c
   SEQ ID NO 14
LENGTH: 18
  PRIOR APPLICATION NUMBER: 09/042,287
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 204
   Patent No. 6037142
GENERAL INFORMATION:
  Sequence 14, Application US/09255912 Patent No. 6037142
   Best Local Similarity
Matches 14; Conserv
  Query, Match
Best Local Similarity
   Query Match
  Matches
   FILE REFERENCE: RTS-0044
CURRENT APPLICATION NUMBER: US/09/255,912
CURRENT FILING DATE: 1999-02-23
  APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
   FILE REFERENCE: Pro-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/790,417
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/358,972
PRIOR FILING DATE: 1999-07-21
PRIOR FILING DATE: 1999-07-21
   Patent No.
  NUMBER OF SEQ ID NOS: 47
   APPLICANT:
  APPLICANT: Shultz, APPLICANT: Lewis,
  APPLICANT:
   OTHER INFORMATION: Description of Artificial Sequence: CAH reverse OTHER INFORMATION: probe
   TYPE: DNA
ORGANISM: Artificial Sequence
   APPLICANT
ORGANISM: Artificial Sequence FEATURE:
                              TYPE: DNA
   PPLICANT:
   FEATURE:
  ENGTH: 18
  INFORMATION:
   17
   51 TTGGTGATGAGTGAG
  204, Application US/09790417
  17
  51 TTGGTGATGAGTGAG 65
   INVENTION: Nucleic Acid Detection RENCE: Pro-103 6868/75528
  Olson, Ryan J. Wood, Keith W. Welch, Roy
   TTGGGGATGAGTGAG
   Kephart, Daniei
Rhodes, Richard B.
  Mandrekar, Michelle
  Andrews, Christine
Hartnett, James R.
  Lewis, Martin K.
   Conservative
   Conservative
   Trent
   John W
   Donna
   5.7%;
93.3%;
  93.3%;
   65
   <u>,</u>
   Þ
  Score 13.4;
Pred. No. 3
  Score 13.4;
Pred. No. 3:
   Mismatches
   Mismatches
   ВB
   DB 1;
   1;
   Length 18;
   Indels
   0
   0
   Gaps
   Gaps
```

```
; OTHER INFORMATION: Antisense Oligonucleotide US-09-255-912-14
밁
  RESULT 59
US-08-413-740A-162
   밁
                        Ş
  ; HYPOTHETICAL: 1
; ANTI-SENSE: NO
US-08-413-740A-162
  Query Match
Best Local Similarity
Matches 15; Conserv
   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,740A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION UNMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
  Sequence 162, Application US/08413740A Patent No. 6171859
  Matches
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   TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  GENERAL INFORMATION:
  ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  TOPOLIVE: OF MOLECULE TYPE: OF
  ATTORNEY/AGENT INFORMATION:
   NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 21.
TELECOMMUNICATION INFORMATION:
   STREET: 1020
CTTY: Washington
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon &
  NUMBER OF SEQUENCES:
  TITLE OF INVENTION: TITLE OF INVENTION:
   APPLICANT:
  Local
  STRANDEDNESS:
   TELEPHONE:
  ENGTH:
                             106
  104 CTCTCATTCTCCTGCTCC 121
   1 crerecrececciócice 18
  . Similarity
  nucleic acid
                             CTCATTCTCCTGCTCCCA 123
  1025 Connecticut Avenue, N.W
  (202)
  MILLER, SCOTT W.
   Conservative
  USA
   HERRNSTADT,
  Conservative
  PARKER, WILLI
DAVIS, ROBERT
  linear
  Kenyon & Kenyon
  (202)
  other nucleic acid
   double
   429-1776
  5.6%;
  Defects
   WILLIAM D.
   5.6%;
   Diagnosis, Therapy and Cellular and Animal Models for Diseases Associated With Mitochondrial
   CORINNA
   162:
  Score 13.2; D
Pred. No. 35;
0; Mismatches
   2105/7
  0; Mismatches
  Score 13.2;
Pred. No. 35;
   DB 1;
   DB 1;
   ω
--
   Length 18;
   Length 18;
   Indels
  Indels
  0
  ۰,
  Gaps
  Gaps
  0
   0
```

```
Sequence 7274, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for FILE REFERENCE: GENSET.020CP1
  US-08-413-740A-164
  RESULT 60
  US-09-422-978-7274/c
  RESULT 61
  US-08-413-740A-164
  Sequence 164, Application US/08413740A Patent No. 6171859
   Matches
   Query Match
   APPLICATION NUMBER: US/08//
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US:
APPLICATION NUMBER: PCT/US:
APPLICATION NUMBER: 08/413,
EILING DATE: 30-MAR-1995
APPLICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  GENERAL INFORMATION:
   INFORMATION FOR SEQ ID NO:
   APPLICANT:
APPLICANT:
APPLICANT:
  COUNTRY: USA
ZIP: 20036-5405
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  HYPOTHETICAL: 1
  TOPOLOGY: li
  SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
   TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 429-1776
  CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES:
   TITLE OF INVENTION:
   NAME: Bonham, David B.
REGISTRATION NUMBER: 34:
REFERENCE/DOCKET NUMBER:
   Local
  STRANDEDNESS: double
  ADDRESSEE:
   106 CTCATTCTCCTGCTCCCA 123
   15; Conservative
  H: 18 base pairs
  Washington
   CTCCTACTCCTGCTCGCA 18
  ង
  PARKER, WILLIAM PARKER, ROBERT
  1025 Connecticut Avenue, N.W.
   (202)
  linear
  Kenyon & Kenyon
  ð
  other nucleic
   429-0796
   5.6%;
   Diagnosis, Then
Animal Models 1
Defects
   ADT, CORINNA WILLIAM D.
   SCOTT W.
  08/413,740
  PCT/US95/04063
   US/08/413,740A
  34297
   2105/7
   Score 13.2; D
Pred. No. 35;
0; Mismatches
   <u>.</u>
                   markers for use in constructing a high density...
  acid
   Therapy and Cellular and els for Diseases Associated With Mitochondrial
   В
   1; Length 18;
   Indels
   0,
   0
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RESULT 62
US-09-448-312-162
   융
   Sequence 162, Applicat Patent No. 6867197 GENERAL INFORMATION:
  Best
  NUMBER OF SEQ ID NOS:
SEQ ID NO 7274
   Matches
  Query Match
   CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
   CURRENT APPLICATION NUMBER: US/09/422,978
   ORGANISM: Homo Sapiens
  FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
   LENGTH: 18
TYPE: DNA
                      INFORMATION
  OTHER INFORMATION: upstream amplification primer 99-3391 for SEQ 3340
  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/413,740

FILING DATE: «Unknown»

APPLICATION UNMBER: PCT/US95/04063

FILING DATE: 30-MAR-1995

APPLICATION NUMBER: 08/413,740

FILING DATE: 30-MAR-1995

APPLICATION NUMBER: 08/413,740

FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bonham, David B.

REGISTRATION NUMBER: 34297

REFERENCE/DOCKET NUMBER: 2105/7

TELECOMMUNICATION:

   Local
   COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  CURRENT APPLICATION DATA:
SEQUENCE
  CORRESPONDENCE ADDRESS
   TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated With Mitochondrial
   APPLICANT: HERRNSTADT, CORINNA
   NUMBER OF SEQUENCES:
   18
  25 CTCATGAATGGTTTAGTG 42
   15;
  Similarity 83.3%;
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
   APPLICATION NUMBER: US/09/448,312 FILING DATE: 23-No. 6867197-1999 CLASSIFICATION: (Unknown)
  CITY: Washington
                    TELEFAX: (202) 4
N FOR SEQ ID NO:
  ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue,
  Application US/09448312
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CHARACTERISTICS
  DAVIS,
  PARKER,
  ROBERT
   SCOTT W.
  WILLIAM D.
                                      429-0796
   Defects
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   Score 13.2;
Pred. No. 35;
   Mismatches
  BB
  1;
  Length 18;
   Indels
   ô
   Gaps
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RESULT 63
US-09-448-312-164
   밁
  ş
; SEQUENCE DESCRIPTION: US-09-448-312-164
  US-09-448-312-162
   Sequence 164, Applicat Patent No. 6867197 GENERAL INFORMATION:
  Query Match
Best Local Similarity
Matches 15; Conserv
  TELEFAX: (202) 42
INFORMATION FOR SEQ ID NO:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION NUMBER: US/09/448,312
APPLICATION NUMBER: US/09/448,312
FILING DATE: 23-No. 6867197-1999
   APPLICATION NUMBER: 08/413,740
FILING DATE: <UNKNOWNS
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
                                  ANTI-SENSE: NO
   SEQUENCE CHARACTERISTICS:
   TELECOMMUNICATION INFORMATION:
  PRIOR APPLICATION DATA:
   NUMBER OF SEQUENCES: 206
   TITLE OF INVENTION: Diagnosis, The Animal Models
   APPLICANT: HERRNSTADT, CORINNA
   SEQUENCE DESCRIPTION: SEQ ID NO: 162:
  ANTI-SENSE: NO
   HYPOTHETICAL: NO
  TOPOLOGY: linear MOLECULE TYPE: other nucleic
  106 CTCATTCTCCTGCTCCCA 123
   1 CTCCTACTCCTGCTCGCA 18
  NAME: Bonham, David B.
REGISTRATION NUMBER: 3429
REFERENCE/DOCKET NUMBER:
   TYPE: nucleic acid
  CITY: Washington
STATE: DC
   CLASSIFICATION: <Unknown>
  TYPE: nucleic acid
STRANDEDNESS: double
  TELEPHONE: (202) 429-1776
  STRANDEDNESS: double
  LENGTH: 18 base pairs
   Application US/09448312
  Conservative
  20036-5405
   PARKER, WILLIA
DAVIS, ROBERT
MILLER, SCOTT
  USA
   5.6%;
  SCOTT W.
   WILLIAM D.
  429-0796
   Defects
                 SEQ ID NO: 164:
  0;
   Score 13.2;
Pred. No. 3
  Mismatches
  acid
   Therapy and Cellular and
els for Diseases Associated With Mitochondrial
   Version #1.30
  ÐB
  ۲
  ω
'
  Length 18;
  Indels
  0
  Gaps
  0
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RESULT 65
PCT-US95-04063-162
  ફ
   밁
  밁
  US-09-769-787-365/c
   RESULT 64
  US-09-769-787-365
  Sequence 162, Application PC/TUS9504063 GENERAL INFORMATION:
  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 365
LENGTH: 18
  Query Match
Best Local Similarity
Matches 15; Conserv
  Patent No. 6936252
GENERAL INFORMATION:
   Matches
  Best Local Similarity
   Query Match
   Sequence 365,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION:
   PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
  APPLICANT: Microbial Technics Limited APPLICANT: Gilbert, Christophe FG APPLICANT: Hansbro, Philip M TITLE OF INVENTION: Proteins
  NUMBER OF SEQ ID NOS: 388
   CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
   APPLICANT: PARKER, WILLIAM D. APPLICANT: DAVIS, ROBERT APPLICANT: MILLER, SCOTT W. TITLE OF INVENTION: Diagnosis, TITLE OF INVENTION: Animal Moderation of INVENTION: Defects
   FILE REFERENCE: PWC/P21129WO
  TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
   OTHER INFORMATION: Description of Artificial Sequence: Primer
   STREET: 1027
CITY: Washington
  CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES:
   APPLICANT:
   ADDRESSEE:
   106 CTCATTCTCCTGCTCCCA 123
  18
  10 CATGGGGGCAGATCCCTC 27
   15; Conservative
  20036-5405
   CTCCTACTCCTGCTCGCA 18
   E: Kenyon & Kenyon
1025 Connecticut Avenue, N.W.
   Application US/09769787
  USA
  Conservative
   HERRNSTADT, CORINNA
  PatentIn Release #1.0, Version #1.30
  5.6%;
83.3%;
   5.6%;
  Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated With Mitochondrial
                                     PCT/US95/04063
   0
  0; Mismatches
  Score 13.2;
Pred. No. 35;
   Score 13.2;
Pred. No. 3
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  35
   DB 1;
   DB 1;
   Length 18;
   Length 18;
   Indels
  Indels
  <u>,</u>
   0
  Gaps
   Gaps
  0
   0
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   RESULT 66
PCT-US95-04063-164
   PCT-US95-04063-162
   Sequence 164, Applica GENERAL INFORMATION:
  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
AREGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1376
TELEPHONE: (202) 429-1376
  Matches
   Query Match
  TELEFAX: (202) 429-0796 INFORMATION FOR SEQ ID NO:
   TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
  APPLICANT:
APPLICANT:
   APPLICANT: MILLER, TITLE OF INVENTION:
  ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
  ANTI-SENSE:
  MOLECULE TYPE:
HYPOTHETICAL:
   REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
  ATTORNEY/AGENT INFORMATION:
   TITLE OF INVENTION:
  5.6%;
Local Similarity 83.3%;
nes 15; Conservative
   COUNTRY:
   CITY: Washington
  TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
  NAME: Bonham, David REGISTRATION NUMBER:
   TOPOLOGY:
   TYPE: nucleic acid
   ADDRESSEE:
  STRANDEDNESS:
  TELEPHONE:
  106 CTCATTCTCCTGCTCCCA 123
   μ
  CTCCTACTCCTGCTCGCA 18
  ង
   E: Kenyon & Kenyon
1025 Connecticut Avenue, N.W.
  Application PC/TUS9504063
  USA
   MILLER, SCOTT W.
  ö
  DAVIS, ROBERT
   HERRNSTADT, CORINNA
   linear
                NO
   ĕ
   (202) 429-1776
   other nucleic acid
                                 other nucleic acid
   double
   double
   David B.
   WILLIAM D.
   Defects
  Diagnosis, Therapy and Cellular and Animal Models for Diseases Associated With Mitochondrial
  206
   34297
  0
  2105/7
  Score 13.2;
Pred. No. 35;
  Mismatches
   DB 1;
   Length 18;
  Indels
  <u>.</u>
  Gaps
  0
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Matches

15;

Conservative

Score 13.2; 1 Pred. No. 35; 0; Mismatches

Indels

0

Gaps

0

Query Match Best Local Similarity

5.6%; 83.3%;

DB 1; Length 18;

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RESULT 68
US-08-311-760A-385
; Sequence 385, Application US/08311760A
; Patent No. 5599706
   묽
   श
  US-08-311-760A-343
   밁
  5
   Best Loc
Matches
  Query Match
  Patent No.
   TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
  COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PASETSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,760A
FILING DATE: September 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
  NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
   SEQUENCE CHARACTERISTICS:
  APPLICANT: Newton, Roger S.
APPLICANT: Randyarack, Randy
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: PLASMA LIFOPROTEIN (a) [LF(a)]
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
TITLE OF INVENTION:
   APPLICANT:
APPLICANT:
   FILING DATE:
ATTORNEY/AGENT INFORMATION:
   STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
   CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES:
   COMPUTER: IBM Com
OPERATING SYSTEM:
   ADDRESSEE:
   Local
   106 CTCATTCTCCTGCTCCCA 123
  INFORMATION:
   41 recearcecerreere se
  l Similarity
  90071
   1 CTCCTACTCCTGCTCGCA 18
  5599706
   udackaccccuuddud 16
  Suite 4700
   E: Lyon & Lyon
633 West Fifth Street
   Application US/08311760A
   (213) 955-0440
   5.4%; Score 12.8; Ilarity 62.5%; Pred. No. 46; Conservative 4; Mismatches
   Stinchcomb, Dan T.
McSwiggen, James
   392
   208/155
  DB 1; Length 16;
   (LP(a) BY
  0
  0
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밁
   US-08-486-421-24/c
   RESULT 69
   US-08-311-760A-385
  Sequence 24, Application US/08486421 Patent No. 5672479
  Matches
  Patent No.
  Query Match
Best Local
  GENERAL INFORMATION:
   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
   COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS:
SOFTMARE: FASISEO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,7/
FILING DATE: September 23, 1994
PRIOR APPLICATION DATA:
  GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: McSwiggen, James

APPLICANT: Newton, Roger S.

APPLICANT: Newton, Roger S.

APPLICANT: Ramharack, Randy

TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES

TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)]

TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN

TITLE OF INVENTION:
  ATTORNEY/AGENT INFORMATION:
NAME: Wazburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
  APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
  NUMBER OF SEQUENCES:
  TELEFAX: 121.
TELEFAX: 67-3510
TELEFAX: 67-3510
   CITY: New York
STATE: New York
           COUNTRY: U.S.A.
ZIP: 10036-2711
   LENGTH: 16 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
   APPLICATION NUMBER: FILING DATE:
  Match 5.4%;
Local Similarity 62.5%;
  TELEPHONE: (213) 489-160
TELEFAX: (213) 955-0440
   STREET:
   ADDRESSEE:
   COUNTRY:
  41 TGCCATCCCCTTGGTG 56
  10;
   1 végéAgécéceuvégye 16
   90071
   New York
   1155 Avenue of the Americas
   U.S.A.
  Conservative
   Pennie & Edmonds
  51
  US/08/311,760A
  4
  Score 12.8;
Pred. No. 4
  208/155
  DOS 5.0
  Mismatches
  46
  DB 1;
  C LEVELS OF
  Length 16;
  Indels
  0
  Gaps
```

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  밁
   US-08-470-911-24/c
   US-08-486-421-24
   Sequence 24, Application US/08470911
Patent No. 5756684
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAUYA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-990
TELEPHONE: (212) 790-990
TELEPAX: 66141 DERNITE
TELEPAX: 66141 DERNITE
  Query Match
Best Local
   Matches
   GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION US/08/486,421
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
   TOPOLOGY: un
   REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
   STREET: 1155 Aven
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
  SEQUENCE CHARACTERISTICS
  TELEFAX: (212, TELEFAX: 66141 PENNIE
   STRANDEDNESS: single
   MEDIUM TYPE:
COMPUTER: IF
   ADDRESSEE:
  ENGTH:
   147 CCCTTCTCTTCTGCC 162
   14;
  16
  Similarity
   1: 16 base pairs
  cccrrcrcccrcrccc 1
                                     66141 PENNIE
   1155 Avenue of the Americas
   Conservative
   unknown
   IBM PC compatible YSTEM: PC-DOS/MS-DOS
   Pennie & Edmonds
   Floppy disk
   DNA (genomic)
  5.4%; Score 12.8;
87.5%; Pred. No. 40
  24:
   0
   Mismatches
  DB 1;
   2,
  Length 16;
   Indels
   0,
   Gaps
   0
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-470-911-24
         5
  밁
  US-08-173-489C-168
   US-08-173-489C-168
   Sequence 168, Application US/08173489C Patent No. 5861244
   Matches
   Query Match
Best Local :
   Query Match 5.4%; Score 12.8; Best Local Similarity 87.5%; Pred. No. 46; Matches 14; Conservative 0; Mismatches
   Patent No.
  ZIP: 10021.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage

COMPUTER: IBM PC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2

SOFTWARE: Wordperfect Version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,489C
  TELBEAX: (attorney) (212) 2.
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 bases
  GENERAL INFORMATION:
   FILING DALL.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
APPLICATION NUMBER: 29 OCT 1992
TOTATION:
   FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,17
REFERENCE/DOCKET NUMBER: U
   NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSE: PROFILE DIAGNOSTIC SCIENCES, INC.
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK.
  PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO:
   HYPOTHETICAL: yes
   MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate ayw sequence region in Seq ID No. 5861244167
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
   APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
   APPLICANT:
  ANTI-SENSE:
  TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
   147 CCCTTCTCCTTCTGCC 162
144 TCCCCCTTCTCCTTCT 159
  16 CCCTTCTCCCTCTCCC 1
   l Similarity 87.1
   NEW YORK
  USA
  no
  WANG,
   , C. -G.
URN, A. G.
   5.4%;
87.5%;
  26,179
   U9518-6
   ٥,
   Score 12.8;
Pred. No. 4
   Mismatches
   Mismatches
   168 :FROM 1 TO
  명
  멂
  1;
  Length 16;
  Length 16;
   Indels
   Indels
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   <u>,</u>
   Gaps
   Gaps
   0
   0,
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RESULT 73
US-08-774-310-343
   밁
   US-08-486-809-24
  US-08-486-809-24/c
  Sequence 24, Applicat Patent No. 5869622 GENERAL INFORMATION:
   Sequence 343,
  Matches 14; Conservative
   Query Match
  TELEFAX: (212) 869-974:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-909
TELEFAX: (212) 869-9741/8864
   TOPOLOGY: ur
MOLECULE TYPE:
   SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,809
FILING DATE: 07-7UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  APPLICANT: NewFor, Roger S.
APPLICANT: Rembarack, Randy
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
TITLE OF INVENTION:
   APPLICANT:
   CORRESPONDENCE ADDRESS
   NUMBER OF SEQUENCES:
  APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
                                       NUMBER OF SEQUENCES: 392
  y Match 5.4%; Score 12.8; Local Similarity 87.5%; Pred. No. 4
   TYPE: nucleic acid
STRANDEDNESS: single
   ZIP: 10036-2711
   CITY: New York
   COUNTRY:
  ADDRESSEE:
   ö.
  147 CCCTTCTCCTTCTGCC 162
  INFORMATION:
   43, Application US/08774310
5877022
  New York
  Application US/08486809
  16 base pairs
   E: Pennie & Edmonds
1155 Avenue of the Americas
  Stinchcomb, Daniel T. McSwiggen, James
   unknown
E: DNA (genomic)
ADDRESS:
Lyon & Lyon
  0;
  Mismatches
   DB 1;
   Length 16;
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  Gaps
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RESULT 74
US-08-774-310-385
   US-08-774-310-343
   Sequence 385, App.
  Matches
  Query Match
   TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
   GENERAL INFORMATION:
  APPLICANT: Ramharack TITLE OF INVENTION:  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
   APPLICATION NUMBER: US/08/774,3
FILLING DATE: December 23, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,760
PILLING DATE: September 23, 1994
ATTORNEY/AGENT INFORMATION:
  SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,310
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESQ Version 1.5
CURRENT APPLICATION DATA:
   SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
  APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McSwiggen, James
   TELEPHONE: (213) 489-1600
   APPLICANT:
   COUNTRY: U
   ALUKESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
   NAME: Warburg, Richard REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
  Match 5.4%;
Local Similarity 62.5%;
   TOPOLOGY:
  STRANDEDNESS:
  OPERATING SYSTEM:
   TELEFAX:
  41 recearcecerreere 56
   ET: Suite 4700
: Los Angeles
E: California
  10;
  1 UGGCAGCCCCUUGGUG 16
  90071
  nucleic acid
   Los Angeles
  California
   Application US/08774310
  633 West Fifth Street
   U.S.A.
   (213) 955-0440
   U.S.A.
  Conservative
   Ramharack,
   linear
   IBM Compatible
  single
  Roger S.
  RIBOZYME TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF PLASMA LIPOPROTEIN (a) [LP(a)] BY INHIBITING APOLIPOPROTEIN
  392
   IBM P.C. DOS 5.0
   32,327
  4.
  Score 12.8;
Pred. No. 4
  223/229
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   ₹
  DB 1;
  Length 16;
  0;
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0;

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   US-08-774-310-385
   Sequence 9, Application US/08290978A Patent No. 5624834
  Matches
  Query Match
  08-290-978A-9
  TELEFAX: (202) 887-07/
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
  GENERAL INFORMATI
APPLICANT: KUS
   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
   ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0044.00
TELECOMMUNICATION INFORMATION:
  APPLICATION NUMBER: 08/311,760 FILING DATE: September 23, 1994 ATTORNEY/AGENT INFORMATION:
                           SEQUENCE CHARACTERISTICS
LENGTH: 17 base pairs
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
  APPLICATION NUMBER: FILING DATE: Decembe PRIOR APPLICATION DATA:
   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
   TELEPHONE: (213) 489-1600
  NUMBER OF SEQUENCES: 1
   TITLE OF INVENTION: CLONING AND EXPRESSION OF THE TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS NUMBER OF SEQUENCES: 15
  APPLICANT:
   TELEPHONE: (202) 887-0763
  APPLICATION NUMBER: US/08/290,978A FILING DATE: 17-OCT-1994 CLASSIFICATION: 435
  Local Similarity
  COUNTRY:
   STREET:
  TYPE: nucleic acid
   TELEPHONE: (213) 955-0440
STRANDEDNESS:
  ZIP: 20006-1812
  TOPOLOGY: 1i
  REFERENCE/DOCKET NUMBER:
  NAME: Warburg, Richard
REGISTRATION NUMBER: 3
  ADDRESSEE:
   41 TGCCATCCCCTTGGTG 56
  10;
  1 UGGCAGCCCCUUGGUG 16
   Washington
  67-3510
  2000 Pennsylvania Avenue N.W.
  ROLIN, CLAUS
  Conservative
   USA
   VAN OOYEN,
  KESTER, HERMANUS C.M.
  linear
  KUSTERS-VAN SOMEREN, MARGO
  MORRISON & FOERSTER
   (202) 887-1500
   December 23, 1996
  single
   JACOB
  5.4%; Score 12.8;
62.5%; Pred. No. 46
   US/08/774,310
   ALBERT J.J.
  4
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US-08-290-978A-9
US-08-373-124A-176
  US-08-373-124A-176
   Query Match
Best Local 9
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GENERAL INFORMATION:
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  HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: pgaX NcoI antisense
                         SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   APPLICATION NUMBER: 07/936,422 FILING DATE: August 26, 1992 ATTORNEY AGENT INFORMATION:
  COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/:
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
   TELEPHONE: (213) 489-1600
   FILING DATE: January 13, 1995 PRIOR APPLICATION DATA:
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   MOLECULE TYPE:
   CORRESPONDENCE ADDRESS:
   TITLE OF INVENTION:
  TELEFAX: 12-1
TELEFAX: 67-3510
   NAME: Warburg, Richard REGISTRATION NUMBER: 32. REFERENCE/DOCKET NUMBER:
   APPLICATION NUMBER: 08/245,466 FILING DATE: May 18, 1994 APPLICATION NUMBER: 08/192,943
   CITY: Los Angeles
STATE: California
   ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
   PILING DATE: February 7,
APPLICATION NUMBER: 07/9
  ZIP: 9007
  COUNTRY:
   TOPOLOGY:
                TOPOLOGY:
   FILING DATE:
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   39 AGTGCCATCCCTTGG 54
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   Similarity
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   McSwiggen, James
   (213) 955-0440
   U.S.A.
  Jarvie,
   Draper,
  Conservative
  Stinchcomb, Dan T
               linear
   December 7,
  DNA
  METHODS AND COMPOSITIONS FOR TREATMENT OF RESTENOSIS AND CANCER USING RIBOZYMES
  Thale
   Kenneth
   (genomic)
   5.4%; Score 12.8;
87.5%; Pred. No. 43;
  07/987,132
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Query Match

5.4%;

Score 12.8;

DB 1;

Length 17;

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  US-08-373-124A-182
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  Query Match
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   Sequence 182, Application US/08373124A
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
   GENERAL INFORMATION:
  NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
   SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
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FILING DATE: May 18, 1994
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
  TITLE OF INVENTION:
   APPLICANT: McSwiggen, James
TITLE OF INVENTION: METERS
TITLE OF INVENTION: METERS
THE OF INVENTION: METERS
   APPLICANT:
  CORRESPONDENCE ADDRESS
   NUMBER OF SEQUENCES:
   STREET: 633 West Fifth Street
STREET: 630 West Fifth Street
STREET: Suite 4700
   LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  TELEPHONE: (213) 955-0440
   COMPUTER: IBM CON
OPERATING SYSTEM:
   ocal
  144 TCCCCCTTCTCCTTCT 159
                                144 TCCCCCTTCTCCTTCT 159
  ET: Suite 4700
: Los Angeles
E: California
   2 uccuccuccuccuucu 17
  Similarity
8; Conserv
  INVENTION: METHODS AND COMPOSITIONS FOR INVENTION: TREATMENT OF RESTENOSIS AND INVENTION: CANCER USING RIBOZYMES
uccuccuucuccuccu 16
   U.S.A.
  5.4%;
llarity 50.0%;
Conservative
  SS: single
linear
  Stinchcomb, Dan T.
  IBM Compatible
   IBM P.C. DOS 5.0
   2627
  Pred. No. 43;
  Score 12.8; DB 1; Length 17; Pred. No. 43; 6; Mismatches 2; Indels
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  Gaps
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RESULT 78

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망
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   Query Match
Best Local Similarity
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US-08-435-628-176
   US-08-373-124A-184
  US-08-373-124A-184
  Patent No.
  Sequence 184, Application US/08373124A
   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
   FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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  CORRESPONDENCE ADDRESS
   TITLE OF INVENTION:
  TITLE OF INVENTION:
   TELEFAX: 1--
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  UMBER OF SEQUENCES:
   ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
   TYPE: nucleic acid
STRANDEDNESS: sing
  APPLICATION NUMBER:
  ZIP: 90071
   OPERATING SYSTEM:
   106 CTCATTCTCCTGCTCC 121
   1 CUCCUUCUCCUCCUCC 16
  /6, Application US/08435628 5817796
  Warburg, Richard
   Los Angeles
: California
                            Stinchcomb, Dan T. Draper, Kenneth McSwiggen, James
   (213) 955-0440
   U.S.A.
   Stinchcomb, Dan
Draper, Kenneth
  Conservative
  Jarvis, Thale
   McSwiggen,
   IBM Compatible
   single
  50.0%;
  CANCER USING RIBOZYMES
Thale
METHODS AND COMPOSITIONS FOR
   IBM P.C. DOS 5.0
   METHODS AND COMPOSITIONS FOR TREATMENT OF RESTENOSIS AND
  US/08/373,124A
   James
  6,
  Score 12.8;
Pred. No. 4
   209/035
  Mismatches
  DB 1;
  Length 17;
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  Gaps
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US-08-435-628-182
   US-08-435-628-176
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  Sequence 182,
  GENERAL INFORMATION:
APPLICANT: Stinche
APPLICANT: Draper,
  FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
   SOFTMARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/43
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
  atent No.
  SEQUENCE CHARACTERISTICS:
  APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: MCSWiggen, James
APPLICANT: MCSWiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
  NAME: Warburg, Richard REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 209 TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
   TITLE OF INVENTION:
  TELEPHONE: (213) 955-0440
  ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
   TOPOLOGY: 1i
  CITY: Los Angeles
STATE: California
   APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
  OPERATING SYSTEM:
  COUNTRY:
  ENGTH:
   144 TCCCCCTTCTCTTCT 159
   2 uccuccuccuccucu 17
  82, Application US/08435628
5817796
  90071
  nucleic acid
  67-3510
3: Lyon & Lyon
633 West Fifth Street
  U.S.A.
   linear
  IBM Compatible
   single
   TREATMENT OF RESTENOSIS AND CANCER USING RIBOZYMES
  IBM P.C.
  2627
   US/08/435,628
  209/035
  DOS 5.0
   Mismatches
   DB 1;
   2;
   Length 17;
   Indels
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   Gaps
   0
   밁
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   US-08-435-628-184
  US-08-435-628-182
  Query Match
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                                    COUNTRY:
                      90071
   Suite 4700
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TELEFAX: (213,
TELEFAX: (213,
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
  Sequence 184, Application US/08435628 Patent No. 5817796 GENERAL INFORMATION:
  Best Local Similarity
Matches 8; Conserv
  FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: AUGUST 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
PILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
PILING DATE: May 18, 1994
APPLICATION NUMBER: 08/92,943
APPLICATION NUMBER: 08/92,943
  APPLICANT: Stinchcomb
APPLICANT: Draper, Ke
APPLICANT: McSwidgen,
APPLICANT: Jarvis, Th
TITLE OF INVENTION: M
TITLE OF INVENTION: C
  OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
  CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
   APPLICATION NUMBER: FILING DATE: 05-MAY CLASSIFICATION: 514
   FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
   144 TCCCCCTTCTCCTTCT 159
  1 UCCUCCUUCUCCUCCU 16
   Los Angeles
California
  McSwiggen, James
Jarvis, Thale
   Draper, Kenneth
                                  U.S.A.
  Stinchcomb, Dan T.
  Conservative
   05-MAY-1995
  50.0%;
  METHODS AND COMPOSITIONS FOR TREATMENT OF RESTENOSIS AND CANCER USING RIBOZYMES 2627.
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   182:
  6
  Score 12.8;
Pred. No. 4
  Mismatches
   DB 1; Length 17;
  <u>,</u>
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Gaps

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밁
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   US-08-435-628-184
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
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FILING DATE: January 13, 1995
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FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,32
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
   APPLICANT:
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APPLICANT:
              ZIP: 20066-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  TITLE OF INVENTION: CITITLE OF INVENTION: EXNUMBER OF SEQUENCES: 1
  NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
  CURRENT APPLICATION DATA:
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   PRIOR APPLICATION DATA:
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  MEDIUM TYPE:
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COMPUTER: IE
   ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Avenue N.W. CITY: Washington STATE: DC
  OPERATING SYSTEM:
SOFTWARE: Word Pe
   COUNTRY:
   APPLICATION NUMBER:
  106 CTCATTCTCCTGCTCC 121
   1 cuccuucuccuccucc 16
  Application US/08780869
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   ROLIN, CLAUS
  KUSTERS-VAN SOMEREN, MARGO
MULLER, YVONNE
KESTER, HERMANUS C.M.
VISSER, JACOB
VAN OYEN, ALBERT J.J.
  USA
  Word Perfect 5.1
   IBM Compatible
   05-MAY-1995
  CLONING AND EXPRESSION OF THE EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS
   5.4%; Score 12.8;
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US-09-827-998-467/c
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  GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDhMORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
  SOFTWARE: Acomica Sequence Listing Engine Patent No. 6656700
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   TELEPHONE: (202) 887-15
TELEPAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
   TYPE: DNA ORGANISM: Homo sapiens
   LENGTH: 17
  TOPOLOGY: linear
MOLECULE TYPE: DNA
MOLECULE TYPE: NO
  ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: pgax NcoI antisense
  HYPOTHETICAL: NO ANTI-SENSE: YES
  SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
  REGISTRATION NUMBER: 29,959
REFERENCE/FOCKET NUMBER: 46:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
   APPLICATION NUMBER: US 08/290,978 FILING DATE: 17-OCT-1994 ATTORNEY/AGENT INFORMATION:
  PRIOR APPLICATION DATA:
  5.4%;
Local Similarity 87.5%;
es 14; Conservation
   CLASSIFICATION:
  STRANDEDNESS: 811
TOPOLOGY: linear
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   AGTGCCATCTCCATGG 16
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87.5%; Pred. No. 43;
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Sequence 467, Application US/09827998 Patent No. 6656700 GENERAL INFORMATION:

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NUMBER OF SEO ID NOS: 1881
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
  FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
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  NUMBER OF SEQ ID NOS:
  CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
   APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
  APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
  APPLICANT:
   APPLICANT:
   APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN
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Local Similarity 87.5%;
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FILING DATE: 2000-09-27
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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PENN, Sharron G.
HANZEL, David K.
   Application data removed -
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  Score 12.8; D
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   DB 1;
   File Wrapper or PALM
  ٠.
در
   Length 17;
  Indels
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문
  S
 밁
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US-09-866-108A-201/c
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-25
  Remaining Prior Application NUMBER OF SEQ ID NOS: 15755
  PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR FILING DATE: 2001-01-30
   APPLICANT: GU, Yizhong APPLICANT: JI, Yongga
   TYPE: DNA
ORGANISM: Homo sapiens
   PRICANT: CHEN, Wensheng
PRICANT: SHANNON, MARK
ITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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   APPLICATION NUMBER: PCT/US01/00668
   APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
   APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
   FILING DATE:
   APPLICATION NUMBER: PCT/US01/00667
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  109 ATTCTCCTGCTCCCAC 124
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   17 AATCTTCTGCTCCCAC
   14;
  Similarity
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PENN, Sharron G.
HANZEL, David K.
AATCTTCTGCTCCCAC
   ICATION NUMBER: PCT/US01/00665
   RANK, David R.
   Application US/09866108A
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  Conservative
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   2001-01-30
  2001-01-30
   2001-01-30
   2001-01-30
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87.5%;
   5.4%;
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   0;
  0
  Score 12.8;
Pred. No. 4:
   Score 12.8;
Pred. No. 43;
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   Mismatches
  See
   DB
   DΒ
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   Length 17
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US-09-866-108A-2940/c

Sequence 2940, Application US/09866108A Patent No. 6686188

GENERAL

NERAL INFORMATION: APPLICANT: GU, Yizhong APPLICANT: JI, Yonggang APPLICANT: PENN, Sharron

<u>۾</u>

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US-09-866-108A-2941/c
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US-09-866-108A-2940
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  SEQ ID NO 2940
  FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
  PRIOR APPLICATION NUMBER: US 60/207,456
   APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
  SOFTWARE: Aeomica Sequence Listing Engine
  PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
  PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
  CURRENT APPLICATION NUMBER: US/09/866,108A
   APPLICANT: GU, Yizhong
  APPLICANT: SHANNON, MAXK
ITTLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
  PPLICANT:
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  APPLICATION NUMBER: GB 24263.6
                   APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
   FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
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FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
  FILING DATE: 2001-01-30
   APPLICATION NUMBER: PCT/US01/00663
  FILING DATE: 2001-01-30
  FILING DATE: 2001-01-30
   APPLICATION NUMBER: PCT/US01/00665
  FILING DATE: 2001-01-30
   FILING DATE: 2001-01-30
   APPLICATION NUMBER: PCT/US01/00668
   APPLICATION NUMBER: PCT/US01/00669
  APPLICATION NUMBER: PCT/US01/00667
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>. 6686188
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  17 TGATGAGTGAGACCAC 2
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  2001-05-25
  2001-05-25
  Score 12.8;
Pred. No. 4:
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  PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR FILING DATE: 2001-01-30
   PRIOR APPLICATION NUMBER: PCT/US01/00668 PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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  APPLICANT: GU, Yizhong APPLICANT: JI, Yongga
   SOFTWARE:
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
   PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
  APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYSSIN-LIKE GENE EXPRESSED
  APPLICANT:
   APPLICANT:
   PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 2001-01-30
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   FILING DATE: 2001-01-30
   APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
  INFORMATION:
  10395, Application US/09866108A
o. 6686188
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  55 TGATGAGTGAGTTCAC 70
  14;
  6686188
   Aeomica Sequence
   HANZEL, David K.
  CHEN, Wensheng
  Conservative
   AEOMICA-T
   Yonggang
  PCT/US01/00664
   Listing Engine
   Score 12.8;
Pred. No. 43
  Mismatches
  See File Wrapper or PALM.
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   ВB
   1:
  IN HUMAN HEART AND MUSCLE
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US-09-404-912-310
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US-09-866-108A-10396
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CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PRIOR DATE: 2001-01-30

PRIOR PRIOR DATE: 2001-01-30
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GENERAL INFORMATION:
   SOFTWARE: Aeomica Sequence Listing Engine Patent No. 6686188
SEQ ID NO 10396
  Matches
  APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: John Landers
APPLICANT: David Houseman
  Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 15755
  APPLICANT: RANK, David R.
APPLICANT: CHAP, Mensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
   APPLICANT:
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   APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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  CTCATCCTCCGGCTCC 17
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  CTCATCCTCCGGCTCC 16
  Application US/09404912
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  Application US/09866108A
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; TYPE: DNA
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US-09-404-912-310
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  TITLE OF INVENTION: Methods and Products Related to TITLE OF INVENTION: Genotyping and DNA Analysis FILE REFERENCE: M0656/7045(HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/404,912
CURRENT FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: US 60/101,757
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22283
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 691
  문
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  US-09-404-912-558
   US-10-156-306B-3650/c
  RESULT 93
  ; ORGANISM: Homo Sapiens
US-09-404-912-558
  RESULT 92
Sequence 3650, Application US/10156306B
Patent No. 7022828
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relater
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
   SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 558
LENGTH: 17
  GENERAL INFORMATION:
APPLICANT: John Landers
APPLICANT: David Houseman
APPLICANT: Barbara Jordan
APPLICANT: Alain Charest
  Sequence 558, Application US/09404912 Patent No. 6703228
  NUMBER OF SEQ ID NOS: 691
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 310
LENGTH: 17
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  TITLE OF INVENTION: Methods and Products Related TITLE OF INVENTION: Genotyping and DNA Analysis FILE REFERENCE: M0656/7045(HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/404,912

CURRENT FILING DATE: 1990-09-24

PRIOR APPLICATION NUMBER: US 60/101,757

PRIOR FILING DATE: 1998-09-25

PRIOR APPLICATION NUMBER: ECT/US99/22283

PRIOR FILING DATE: 1999-09-24
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   APPLICANT:
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  209 CATECTTCTTGTTCTG 224
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14; Conserv
   1 CATTOTTCTTTTTCTG 16
  N
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   Alain Charest
   Barbara Jordan
   5.4%;
ilarity 87.5%;
Conservative
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  Score 12.8;
Pred. No. 43;
  Score 12.8;
Pred. No. 43;
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   DB
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FILE REFERENCE: MBHB01-664-A (400/050)

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US-10-156-306B-3650
밁
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  US-08-684-672-27/c
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Matches
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  APPLICATION NUMBER: US/08/684,672
FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,997
FILING DATE: 27-APR-1993
ATTORNEY/AGENT INFORMATION:
   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  CURRENT APPLICATION NUMBER: US/10/156,306B CURRENT FILING DATE: 2002-05-28
  REGISTRATION NUMBER: 32,747
REFERENCE/DOCKET NUMBER: 03/
TELECOMMUNICATION INFORMATION: (703) 836-6620
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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   STRANDEDNESS: 81
TOPOLOGY: linear
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   TYPE: nucleic acid
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   CITY: Alexandria
  STREET:
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   16 GCTCCGCCTTCTCGTT 1
   14;
   22313-1404
   7, Application US/08684672
5700926
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   18 base pairs
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P.O. Box 1404
  United States
   (703)
  de la CHAPELLE, Albert
SRIVASTAVA, Anand Kumar
   Conservative
   SCHLESSINGER, David
   DNA (genomic)
   single
   836-2021
10: 27:
  MOLECULAR CLONING OF THE ANHIDROTIC ECTODERMAL DYSPLASIA GENE
   5.4%; Score 12.8;
87.5%; Pred. No. 41
   DOANE, SWECKER & MATHIS, L.L.P
  Brian P.
  0
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Pred. No. 4
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; OTHER INFORMATION: AntiBense Oligonucleotide US-09-161-244-51
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Patent No. 60v--
Patent INFORMATION:
   Sequence 51, App. No. 600481
  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
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Best Local Similarity 87.5%;
   Sequence 26, Applica
Patent No. 5891671
GENERAL INFORMATION:
  Matches
  APPLICANT: Bennett, C. Frank
APPLICANT: Cowsert, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION (
FILE REFERENCE: RTS-0007
CURRENT APPLICATION NUMBER: US/09/161,244
CURRENT FILING DATE: 1998-09-25
   TITLE OF INVENTION: METHOD FOR CLEAVING CHIMERIC ENZYME USING PROCESSING TITLE OF INVENTION: ENZYME FILE REFERENCE: 001560-294
CURRENT APPLICATION NUMBER: US/08/811,028C
CURRENT FILING DATE: 1987-03-04
EARLIER APPLICATION NUMBER: JP 8-70906
EARLIER FILING DATE: 1996-03-04
  NUMBER OF SEQ ID NOS: 54
  APPLICANT: SUZUKI, APPLICANT: MAGOTA, APPLICANT: MASUDA,
   ORGANISM: Artificial Sequence FEATURE:
  TYPE: DNA
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   TYPE: DNA
  OTHER INFORMATION: Description of Artificial Sequence:primer S12
  208 CCATGCTTCTTGTTCT 223
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  14;
                           AGATCCCTCATGAATG 34
AGATCCCTCACAAATG 16
   Application US/08811028C
   Application US/09161244
  Conservative
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  , Koji
, Toyofumi
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87.5%;
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Pred. No. 4
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Pred. No. 4:
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RESULT 97 US-09-091-219-19

Sequence 19, Application US/09091219
Patent No. 6171592
GENERAL INFORMATION:

APPLICANT: STUDDERT, Michael J. APPLICANT: CRABB, Brendan S. APPLICANT: FENG, Li

```
APPLICANT: Bennett, C. Frank
APPLICANT: Cowsert, Lex M
TITLE OF INVESTION: Antisense Modulation of CD40 Exp
FILE REFERENCE: RTS-0002
CURRENT FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 67
SEQ ID NO 67
SEQ TO N
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US-09-071-433-67
  US-09-071-433-67/c
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Patent NO. 6492173
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN DZ EXPRESSION
FILE REFERENCE: RTS-0275
CURRENT APPLICATION UNMERE: US/09/920,760
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 89
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LENGTH: 18
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SOFTWARE: Patentin Ver. 2.0
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CURRENT APPLICATION NUMBER: US/09/091,219
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: PCT/AU96/00815
EARLIER FILING DATE: 1996-12-18
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EARLIER FILING DATE: 1995-12-18
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  AAGAGACACCTGCTTC 18
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CURRENT FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/091,219

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN7201

PRIOR FILING DATE: EARLIER FILING DATE: 1995-12-18

NUMBER OF SEQ ID NOS: 25

SOPTWARE: PATENTIN Ver. 2.0

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LENGTH: 18

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APPLICANT: STUDDERT, Michael J.
APPLICANT: CRABB, Exendan S.
APPLICANT: FENG, Li
  Query Match
Best Local Similarity
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Patent No. 6531136
  TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS FILE REFERENCE: 040268/0151
  115
  131 ATGAGACACCTGCTCC
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  3 AAGAGACACCTGCTTC 18
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   Application US/09660541
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87.5%;
 2
2006, 15:37:36
   146
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Search completed: October Job time: 0.001 secs

Copyright

GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.

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Minimum
Maximum
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Maximum Match 100%
Listing first 98 summaries
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  Perfect score:
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   length: 0
length: 2000000000
  IDENTITY_NUC
Gapop 10.0 , Gapext 0.5
   Match
   US-10-642-946-6_3002-3237
236
   Query
   October 2,
   98 seqs, 2026 residues
   tgtctgggtcatgggggcag.....ttgttctgtctgcaaaactg 236
   Length
    2006, 15:45:39 ;
   멂
  AAV33949
ACL41022
ACL40867
                 AED05615
AED05615
ABX97349
ADN62252
ABN89272
  ABL45056
ABK96689
ABK96692
  AED05620
AED05617
ABZ22095
AD051553
ACL40112
ACL400870
ACL40870
ACL40870
ACL40873
ACL40873
ACL40873
ACL40873
ACL56405
ACC36405
ACC36405
ACC36450
ACC36450
  AED05616
AED05619
   ACL40869
AEC02687
AAH37262
AEC36449
AEC36402
  Ħ
  AED05618
   SUMMARIES
  ; Search time 0.001 Seconds (without alignments) 956.272 Million cell updates/sec
   N. Geneseg
  196
  ABCC4 SIRNA SENSE
C20orf103 SIRNA an
Oligonucleotide 1-
VEGF/VEGFR2 multif
VEGF/VEGFR2 multif
   Short interfering Polyanionic polyme Human serine/threo ABCC4 siRNA sense C20orf103 target o
   VEGF/VEGFR2 multif
VEGF/VEGFR2 multif
Short interfering
Short interfering
Short interfering
Short interfering
   Short
Short
   C20orf103 siRNA an
Human IgE short in
SNP specific lower
  Gibbon interleukin
C20orf103 siRNA an
C20orf103 target o
   Human
  PCR primer used to
Human chromosome 1
  Description
                                 Human
   Interleukin-3 (IL-Interleukin-3 (IL-
t interfering
t interfering
n NOV-associat
n NOV40a RTQ-P
n Talin antise
n talin phosph
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|   |          |         |          |          |          |          |           |                |          |          |          |          |            |          |          |          |          |          |            |              |          |          |            |              |         |          |             |          |                |         |           |          |               |                 |          |         |            | •        |         |          |            |            |          |         |            |          |            |         |                |          |            |          |          |
|---|----------|---------|----------|----------|----------|----------|-----------|----------------|----------|----------|----------|----------|------------|----------|----------|----------|----------|----------|------------|--------------|----------|----------|------------|--------------|---------|----------|-------------|----------|----------------|---------|-----------|----------|---------------|-----------------|----------|---------|------------|----------|---------|----------|------------|------------|----------|---------|------------|----------|------------|---------|----------------|----------|------------|----------|----------|
|   | (        | 2 0     | Ω        |          |          |          |           |                |          | O.       | ი ი      | 3        | C          | n        | ი        |          | n i      | n c      | <b>а</b> О |              |          | ď        | כ          |              | Ω       | Ω        | O (         | ດເ       | a              | O       | Ω         |          | ი ი           | , U             | n        |         | •          | 3 0      | O       | O        | ດເ         | o 0        | Ω        | (       | Ω          |          |            | c       | n              | •        | <u>ი</u> ი | )        | a        |
|   | 98       | 9 6     | 95       | 94       | 93       | 9 1      | פַ פַ     | 9              | 88       | 87       | 86       | N 1      | P 0        | 82       | 81       | 80       | 79       | 78       | 36         | 75           | 74       | 73       | 75         | 70           | 69      | 8        | 67          | თ (      | ນ <del>ຖ</del> | 54      | 62        | 61       | 9 6           | л (л<br>6 (с    | 57       | 56      | ភ (<br>ភ ( | <b>ე</b> | 52      | 51       | 2 1        | 4 4<br>3 0 | 47       | 46      | 4 4<br>5 0 | 43       | 42         | 4 4     | 9              | 38       | 37<br>37   | 3 3      | 34       |
|   | ٠ 4.     | ء. د    | 4.       | 4.       | 4.       | ٠.       | ٠.        |                | 4.       | ٠.       | . 4.     | ٠, 4     | 4.4        | 4.       | 4.       | 4.       | 4.       | 14.8     | 1 5        | 5            | 5        |          | лυ         | າຸຕ          | 5       | 5        | S           | 5        | <b>л</b> и     | лŗ      | ī         | 5.       | 5             | лυ              | ຸ່ນ      | 15.2    | <u>ب</u>   | лv       | ຸ່ນ     | 5        | <b>σ</b> . | n u        | 5        | 5       | 15.4       | · 5      | 5 .        |         | · .            | 5        | 15.8       | 'n       |          |
|   |          | •       | ٠        | •        |          |          | ٠         | •              | •        | •        |          | •        | •          | •        | ٠        | •        |          |          |            |              | 6.       | o (      | •          | •            | ٠       | ٥.       | 6           |          |                | ησ      | ٠         | •        | <u>ه</u> :    | n σ             | ٠,٥      |         | <u>ه</u> . | •        | •       | •        |            | •          | •        |         |            | ٠        |            |         | •              |          | <u>.</u>   | •        | <b>6</b> |
|   |          |         |          |          |          |          |           | ω              |          |          |          |          |            |          |          |          |          |          |            | 42           |          |          | 4          |              | 4.      | 44       | 44          |          | 44             | × 45    |           | 4        | , z           | <b>1</b> 4.42   | - 42     | 44      | . 44       | 4 4      |         |          |            |            |          |         |            |          | σ.         |         |                |          |            | 100      | _        |
|   | 2 5      | 3 5     | 22       | 21       | 21       | 2 1      | 3 6       | 22             | 21       | 21       | 20       | 200      | 2 0        | 20       | 20       | 20       | 19       | 19       | 9 0        | 21           | 21       | 21       | 2 1        | 2 22         | 21      | 21       | 21          | 21       | 2 0            | 3 6     | 20        | 20       | 20            | 0 0             | 20       | 20      | 0 0        | 0 0      | 20      | 20       | 20         | ) C        | 20       | 17      | 17         | 77       | 22         | 21      | 122            | 21       | 21         | 20       | 20       |
|   | μ,       |         | ۰,       | ۲        | - 1      | ٠,       | ۔ د       | ۰,             | 1-4      | Н.       | 4 مو     | 4 د      | <b>-</b> 4 | ب.       | ۰,       | _        | ן בן     |          | 4 بـ       | _            | ۲        | μ,       | - ب        | بر د         | <u></u> | -        | <b>1</b> -4 | 4 سر     | <b>-</b>       | - ب     | . р       | 1        | μ,            |                 | - р      | ۲       | μ,         | <b>-</b> | - μ     | <b>–</b> | <b>-</b> - |            | . р      | μ;      | <b></b>    | - ب      | <b>~</b> + |         | . р            | <b>-</b> | <b></b>    | ــر د    |          |
|   | AEC02566 | ACL4087 | ADU26863 | AAS43674 | AAS43676 | AAS43673 | AA543680  | AAS43670       | ADG77905 | AAQ82294 | AEF72123 | AEC22791 | ADG43900   | ADF77306 | ADE43868 | AAS45831 | AEB93316 | ADS73903 | AAT /24 /  | AEC3053      | AEC02602 | ADZ19613 | AD02666    | ADP29145     | AAZ6153 | AAQ42803 | AAQ1034     | AA008505 | AEC3443        | ADPB216 | ADP12009  | AD051535 | ADL3244       | ACC48831        | ABZ59163 | ABL9441 | ABL9429    | ABL4532  | AAK9523 | AAA71802 | AAZ48049   | ABZJII9    | AAD1269  | ACN0839 | ACNO646    | ADU84382 | ACA88981   | ACL4088 | ACL4 0111      | ACL40113 | ACL41021   | ADP85740 | ABQ84461 |
|   | 01 -     | , ,     |          | -        | 01 1     |          |           | , 0            | 0,       |          |          | 7        |            | , 0,     | ·w       |          | ٠, ١     |          |            | . #2         | 2        | ω (      |            | , 0          | ·w      | w        | 445         |          |                | ~ ~     | 1 01      | Ui       | , <del></del> | -,-             | - w      |         | 7 7        | - 0      |         | N        | ω.         | D K        | , ω      | N       | <b>5</b> F | - 20     |            | N U     | , <sub> </sub> | Ψ.       |            | - 0      | _        |
|   |          |         |          |          |          |          |           |                |          |          |          |          |            |          |          |          |          |          |            |              |          |          |            |              | •       |          |             |          |                |         |           |          |               |                 |          |         |            |          |         |          |            |            |          |         |            |          |            |         |                |          |            |          |          |
|   |          |         |          |          |          |          |           |                |          |          |          |          |            |          |          |          |          |          |            |              |          |          |            |              |         |          |             |          | •              |         |           |          |               |                 |          |         |            |          |         |          |            |            |          |         |            |          |            |         |                |          |            |          |          |
|   | Human    | 200     | Knoc     | Corn     | Corn     | Corn     | Corn      | Corn           | Cani     | Chro     | Huma     | Human    | Huma       | PCR      | Huma     | Mouse    | Human    | DMD o    | Human      | Human        | Human    | Human    | CODONE     | Human        | Prim    | Human    | Probe       | Segn     | Huma           | Huma    | Set       | Huma     | Clon          | Campylobacter ] | Nucl     | Mouse   | Human      | Anti     | Human   | FAA F    | Human      | Cand       |          |         | VNW        | Human    | Sele       | ABCC    | ABCC           | ABCC     | ABCC4 t    | Huma     | DPP1     |
| 4 | н        | TILUS   | k-dow    | eodesi   | eodesi   | eodesi   | eodesi    | Corneodesmosin | ne di    | mosom    | n FLAP   | n myo    | 727        | prime    | n eota   | PAR      | n siR    | gene :   | n CLL      | n locus-     | n IgE    | n siR    | 3 7        | . 5          | er 6U   | n IL-    | e to t      | ence o   | n FOE          |         | 2 rigi    | n ser    | e spe         | YLODA           | eotid    | e C/EBP | /mou       | ian chr  |         | E        |            | r a        | ın alpha | minus   | Amber      | ē        | 0          | = 5     | 4 target       | 4 SIRNA  | בים בי     | n Tal    | 0 PCR    |
|   | aE shor  | 918     | n tar    | mosin    | nosin    | nosin    | TERONIE L | mosin          | веаве    | e 11 (   | P gen    | cardi    | R4 an      | r #1     | axin     | P-2 a    | אא כי    | speci    | - J ge     | locus-specif | shor     | NACE     | וו רמנ     | secreted pro | for     | ğ        | the h       | of 5'    | R regulat      | -8860   | ht PCR pa | ine/t    | cific         | cter            | e sec    | BP bet  | ው የ        | 2 8      | A clc   | CIP1 in  | etal 5     | 7 0        | 2        | 里?      | rzyme      | AP-2     | n and      | NA ar   | get            | NA ar    | get ol     |          | prime    |
|   | מוני לי  | 3 0     | target   | PCR      | PCR      | PCR      | 3 2       | PCR            | mar      | (loc     | e al     | al i     | R4 ancise  | tor      | gene     | 2 antis  | ansc     | fic      | ine e      | ecif         | ťin      | rget     | בינו<br>כי | pro          | a hu    | be.      | uman        | ord      | nilat          | Clac    | CR pr     | threo    | PCR           | er jeju         | nenc     | ta p    | EBP        | igonic 2 | ne-s    | tera     | - UT       | ing G      | lpha     | nd H    | ne subs    | 2 hamm   | nd ampl    | tise    | ligo           | tise     | )ligo      | μ.       | er#      |
|   |          |         |          |          |          |          |           |                |          |          |          |          |            |          |          |          |          |          |            |              |          |          |            |              |         |          |             |          |                |         |           |          |               |                 |          |         |            |          |         |          |            |            |          |         |            |          |            |         |                |          |            |          |          |

ALIGNMENTS

RESULT 1
AAV33949/c
ID AAV33949 standard; DNA; 27 BP.

```
ACL41022
ID ACL4
XX ACL4
XX ACL4
XC ACL4
XX ACL4
XX C20c
XX C20c
XX C20c
XX Cytc
XX Cytc
XX Synt
XX Synt
   5
  밁
   Query Match
Best Local :
  Matches
   amplification of gibbon interleukin-3 cDNA (see AAV33946) minus the signal sequence. It includes a 5' BamHI site. The primer was used with a reverse primer (see AAV33950) to amplify the gibbon IL3 mature coding region. The PCR product was utilised in the construction of a prokaryotic expression plasmid encoding a fusion between human Fanconi anaemia complementation group C (FAC) protein (see AAW68546) and gibbon IL3 (see AAW68547). This conjugate, or a nucleic acid encoding it, can be used to deliver FAC to a haematopoetic progenitor cell, specifically to inhibit apoptosis, particularly in patients exposed to high doses of chemotherapy for treatment of non-myeloid cancers, also to treat Fanconi anaemia by complementation of the genetic defect
                              Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; short interfering RNA; gene silencing.
  New conjugate of Fanconi anaemia molecule and peptide selective for haematopoietic precursor cells - inhibits apoptosis of these cells, for treating Fanconi anaemia and patients undergoing high-dose chemotherapy
   Synthetic.
Hylobates lar.
   Fanconi anaemia complementation group C; FAC; apoptosis; haematopoiesis;
bone marrow; chemotherapy; gene therapy; interleukin-3; gibbon;
His-ILFAC; PCR; primer; ss.
 Synthetic
  Sequence 27
   Gibbon interleukin-3 forward primer.
  C20orf103 siRNA antisense sequence, SEQ ID 2094.
   Example 1; Page 27; 72pp; English.
  WPI; 1999-009774/01.
   Youssoufian
  15-MAY-1997;
   19-NOV-1998.
  WO9851792-A1
  15-FEB-1999
   AAV33949;
   ACL41022 standard; RNA; 21 BP
   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
  15-MAY-1998;
   Local Similarity
  is the nucleotide sequence of a forward primer for the PCR
   TGTCTGGGTCATGGGAGCGGATCCC
   rereregerearegegegeagarece 25
  ₽₽;
  Conservative
  (first entry)
   (first entry)
  98WO-US009975
   7 A;
  97US-0046546P
   92.0%;
  11 C;
  6 G; 3 T; 0 U;
   Score 21.8; DB pred. No. 6.9; 0; Mismatches
  DB 1; Length 27;
  0 Other;
  <u>ب</u>
  Indels
  0,
  Gaps
  0
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RESULT 3
ACL40867/c
ID ACL408
XX ACL408
XX ACL408
XX 24-MAR
XX CYCOST
XX CYCOST
XX HOMO 8
XX HOMO 8
XX HOMO 9
XX HOMAY
XX 19-MAY
XX 20-MAY
XX AMHP
  Query Match
Best Local Similarity
Whiches 8; Conserve
   밁
   δ
  ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNAS (siRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
  ве х,
  Cytostatic; Gene therapy; Vaccine;
  C20orf103 target oligonucleotide,
  24-MAR-2005
   ACL40867;
   ACL40867 standard; DNA; 21
  Sequence 21 BP; 2 A; 4 C; 3 G; 0 T; 12 U; 0 Other;
  The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level protein activity of a cancer-related transmembrane protein (CRTP) or
   Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
   20-MAY-2003; 2003US-0471729P
   19-MAY-2004; 2004WO-US015645.
                                  20-MAY-2003; 2003US-0471729P
  19-MAY-2004; 2004WO-US015645
   WO2005001092-A2
   Homo sapiens
   ftp.wipo.int/pub/published_pct_sequences
   Claim 3; SEQ ID NO 2094; 113pp; English
   treating
   WPI; 2005-075568/08
  WO2005001092-A2
   1 UUCUUGUUCUGCCAUGAUUUU 21
  Wei L,
  TTCTCCTTCTGCCATGATTTT 170
   Conservative
   (first entry)
  Slonim DK,
  7.5%;
   дB
   11; Mismatches
   Howes
  Score 17.8;
Pred. No. 21
  HS
  SEQ ID 1939
   RNA Interference; cancer; ss
   멂
   1; Length 21;
   اد
  Indels
  on level or (
   0,
   gene
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gene

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RESULT 4
ACL40869
      밁
   S
   Matches
   Query Match
Best Local
  protein activity of a cancer-related transmembrane protein (CRTP) or gene, an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polymucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACMAID, CDH6, CST, ENP93, FLJ11856, GRR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, stomach cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a target oligonucleotide from one such CRTP for which short interfering RNAs (siRNA) were produced. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
  Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
  Вe
  20-MAY-2003; 2003US-0471729P
   06-JAN-2005
   WO2005001092-A2
   short interfering
   Cytostatic; Gene therapy; Vaccine; RNA Interference;
   C20orf103 siRNA antisense sequence, SEQ ID 1941.
   24-MAR-2005
   ACL40869
  ACL40869 standard;
   Sequence
  ftp.wipo.int/pub/published_pct_sequences
   The present invention relates to a novel pharmaceutical composition
  Claim
  Вe
   19-MAY-2004; 2004WO-US015645
   ×
   2005-075568/08
  149
   ω
••
   21
   Wei L,
   Wei L,
  Similarity
  21
   CTTCTTGTTCTGCCATGATTT 1
  CTTCTCCTTCTGCCATGATTT 169
   SEQ ID NO 1939; 113pp; English
   BP; 11 A;
  (a) an
   Conservative
   (first
   Slonim
  Slonim
   RNA;
  agent capable of modulating an expression
   entry)
  90
   7.5%;
   3 C; 5
  봈
   Ŗ,
   gene silencing.
  21
  Howes
   Howes
  0;
   Score 17.8;
Pred. No. 21
   G; 2 T; 0 U;
   Mismatches
  SH
   HS
   0 Other;
  DB 1; Length 21;
  ν
•
   Indels
  cancer;
  0;
  level
  Gaps
  ç
  0;
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RESULT 5
AEC02687
Ś
  맑
  Matches
  Best Local
   Query Match
  CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orfl03, CACNALD, CDH6, CST, ENPP3, FIJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
  Watson JD,
Abernethy 1
  immediate type hypersensitivity; immunosuppressive; asthma; antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory; ear, nose, throat disease; inflammation; respiratory disease; immune disorder; IgE; short interfering nucleic acid; siNA;
   immunosuppressive; expression; RNA interference; allergy;
atopic dermatitis; urticaria; dermatological; dermatological disease;
  antiallergic; antiinflammatory; antiasthmatic; dermatolog immunosuppressive; expression; RNA interference; allergy;
   Human IgE short
   03-NOV-2005
   AEC02687 standard;
   Sequence
  , an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3,
  The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level
  WPI; 2005-591970/60.
  20-FEB-2004; 2004US-0546434P
  21-FEB-2005; 2005WO-NZ000021
  WO2005080410-A1
  Homo sapiens
  protein activity of
  Claim 3; SEQ ID NO 1941; 113pp; English
   treating cancer
  silencing; ss.
  149 CTTCTCCTTCTGCCATGATTT 169
  Н
   GENESIS RES & DEV CORP
   Similarity
9; Conserv
  CUUCUUGUUCUGCCAUGAUUU
   21 BP; 2
  z
   Murison GJ,
  Conservative
   (first entry)
  Webster
   interfering
   A; 5 C; 3 G; 0 T; 11 U;
   DNA;
  a cancer-related transmembrane protein (CRTP) or
  7.5%;
  G
   21
   Grigor MR,
   ₽P
  10;
   nucleic acid SEQ ID NO 290
  Score 17.8;
Pred. No. 2:
  21
   Mismatches
   Havukkala IJ,
   21;
   DB 1; Length 21;
   0 Other;
   2
   dermatological;
  Indels
   Munro
   ç
   0,
  Gaps
   유
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0,

New composition comprises small interfering nucleic acid molecule capable of reducing expression of a target gene that is active in mediated disorder, useful for treating, e.g. allergic rhinitis or

atopic b (SiNA)

dermatitis.

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Disclosure;
 SEQ
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290; 178pp; English.
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8x55555555555555555555555

CC The invention describes a composition comprising a small interfering CC nucleic acid molecule (siNA) capable of reducing expression of a target CC gene that is active in a IgE-mediated disorder, a genetic construct that CC expresses the siNA, and a binding agent that specifically binds to a CC target antigen expressed on the surface of the cell. Also described are: CC amethod for the treatment of an IgE-mediated disorder in a patient; cC prevention of IgE-mediated disorder in a patient; reduction of CC essinophilia in a patient; modulating an IgE-mediated immune response to a specific antigen in a patient; and preventing or reduction of the severity CC of an immune response to a specific antigen in a patient. The composition CC is useful in the preparation of a medicament useful for the treatment of CC urticaria, atopic dermatitis, food allergies, diseases that benefit from CC the reduction of essinophilia in the tissues of the respiratory system, CC or disorders having hypersensitivity immune reaction. This sequence CC represents a sinA for supression of human IgE expression. 21 BP; 7 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Sequence

Ś Query Match Best Local Matches 1 60 19; Similarity AGTGAGTTCACGTGAGAGCTG 80 Conservative 7.5**%**; 0 Pred. Score 17.8; Pred. No. 21; Mismatches DB 1; 2 Length 0;

0

ВÞ

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AATGAGTTCACATGAGAGCTG 21

lower PCR primer SEQ ID

RESULT 6
AAH37262;
ID AAH37262;
XX AAH37262;
XX AAH37262;
XX AAH37262;
XX SNP specific lower PCR prime;
XX SNP specific lower PCR prime;
XX SNPS; genotyping; agammaglobk
KW SNPE; genotyping; agammaglobk
KW SNPE; genotyping; agammaglobk
KW Lesch-Nyhan syndrome; muscula
polycystic kidney disease; of
KW acute intermittent porphyria;
KW polycystic kidney disease; of
KW acute intermittent porphyria;
XX Homo sapiens.
XX W acute intermittent porphyria;
XX Homo sapiens.
XX Homo sapiens.
XX W0200129262-A2.
XX W Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial pypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.

13-OCT-2000; 2000WO-US028436

99US-0160096P

ORCHID BIOSCIENCES INC

New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic

83pp; English

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPB. The present invention includes kits for determining the presence or absence of a SNP, using t

SNP flanking sequence, the SNPE primer is used as a genotyping primer. CC The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The colligonucleotides are useful for determining the presence, absence or colligonucleotides are useful for determining the presence, absence or clientity of a SNP and for genotyping nucleic acid samples, for e.g. to casses by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include disease e.g. caused by one or more SNPs. Phenotypic traits include disease, muscular cystrophy, familial hypercholesterolaemia, polycystic kidney disease, conteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial contended in the component is or may be genetic such as autoimmune continuation, cancer, nervous system diseases and infection by pathogenic inflammation, cancer, nervous system diseases investigations and microorganism. The method is also useful in forensic investigations paternity analysis. The present sequence represents a PCR primer spector a human SNP containing DNA sequence oligonucleotides of the invention. The PCR primers are used to amplify a specific

Sequence 19 BP; 6 A; 2 C; 9 G; 2 T; 0 U; 0 Other;

Ś Matches Query Match Local 147 18; Similarity cccrrcrcrrcreccare 165 Conservative 7.4%; 0 Pred. Score Mismatches 17.4; I No. 24; DB 1; Length 19; Indels 0 Gaps 0

밁 19 CCCTTCACCTTCTGCCATG 1

AEC36449 standard; RNA; 19 В₽

03-NOV-2005 (first entry)

VEGF/VEGFR2 multifunctional siNA VEGF target complement sequence #3.

RESULT 7
AEC36449
ID AEC36449
ID AEC36449
AC AEC3
XX AEC3
XX VEGF
XX VEGF
XX Shor
XX VIOR
XW ININ
XW VIOR
XW VIOR
XW CARD
XW C short interfering nucleic acid; siNA; short interfering RNA; siRNA; gene silencing; RNA interference; transplant rejection; pulmonary disease; respiratory-gen.; respiratory disease; injury; vulnerary; neurodegenerative disease; neuroprotective; neurological disease; cancer; neoplasm; cytostatic; infection; natimicrobial; ocular disease; ophthalmological; cardiovascular disease; ophthalmological; cardiovascular disease; reardiovascular-gen.; prion disease; cerebroprotective; degeneration; inflammation; antiinflammatory; renal disease; nephrotropic; endocrine disease; genitourinary disease; liver disease; hepatotropic; gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;

Unidentified

WO2005078097-A2

25-AUG-2005

09-FEB-2005; 2005WO-US004270.

10-FEB-2004; 2004US-0543480P. 24-MAY-2004; 2004WO-US016390.

(SIRN-) SIRNA THERAPEUTICS INC

Zinnen S

WPI; 2005-571603/58

New multifunctional short interfering nucleic acid (siNA), useful for modulating RNA function and/or gene expression in a cell or for treating or preventing pulmonary diseases, neurodegenerative conditions, cancers,

ocular

diseases

WPI; 2005-571603/58

```
RESULT 8
AEC36402/c
ID AEC36402 standard; RNA; 19 BE
XX
AC AEC36402;
XY
O3-NOV-2005 (first entry)
XY
VEGF/VEGFR2 multifunctional s
XX
Short interfering nucleic aci
XX
VIDEF/VEGFR2 multifunctional s
XX
Short interfering nucleic aci
XX
Short interfering nucleic aci
XX
Interary; neurodegenerative
Interary; neurodegeneration
Interary; neurodegenerative
Interary; neurodegenerative
Interary; 
  밁
  Ś
   acid (sina). This multifunctional sina molecule is of two formulae given of in the specification. The multifunctional sina of the invention is useful for modulating RNA function and/or gene expression in a cell. It can be used for down regulating or inhibiting the expression of one or more conditions that responds to modulation of gene expression or activity in conditions that responds to modulation of gene expression or activity in conditions that responds to modulation of gene expression or activity in carell, tissue, or organism, e.g. organ or tissue transplant, tissue tracting, or treatment of pulmonary disease (restenosis) or preventing conditions, or treating CNS lesions or injury, including treating conditions or injury, including treating consisting conditions (e.g. Alzheimer's disease, parkinson's conservative conditions (e.g. Alzheimer's disease, parkinson's conservative conditions (e.g. Alzheimer's disease, cardiovascular consesses, prion disease, inflammatory diseases, or methoduction condiseases, mitochondrial diseases, coular diseases, liver conservated diseases and conditions. AEC36400-AEC3640, or repredent target sequences from VEGF, for a multifunctional sina of the invention which conservate sequences to the tracet sequences.
   Query Match
Best Local S
Matches 12
   neurological disease; cancer; neoplasm; cytostatic; infection; antimicrobial; ocular disease; ophthalmological; cardiovascular disease; cardiovascular disease; cardiovascular disease; cardiovascular disease; cardiovascular disease; cardiovascular disease; prion disease; nephrotropic; inflammation; antiinflammatory; renal disease; nephrotropic; endocrine disease; genitourinary disease; liver disease; hepatotropic; gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;
   short interfering nucleic acid; siNA; short interfering RNA; siRNA; gene silencing; RNA interference; transplant rejection; pulmonary disease; respiratory-gen.; respiratory disease; injury; vulnerary; neurodegenerative disease; neuroprotective;
   09-FEB-2005; 2005WO-US004270
  VEGF/VEGFR2 multifunctional siNA VEGF target sequence
  Sequence 19
   Example
  (SIRN-) SIRNA THERAPEUTICS INC
   specification describes a multifunctional short interfering
  147 CCCTTCTCCTTCTGCCATG 165
  H
   n 7.4%;
Similarity 63.2%;
  7; SEQ ID NO 114; 168pp; English.
  cccuccuccuucugccaug 19
  BP; 1
   Conservative
  2004US-0543480P.
2004WO-US016390.
  the target sequences.
   A; 10 C; 2 G; 0 T; 6 U; 0 Other;
  ВP
  Score 17.4; DB 1; Length 19; pred. No. 24; 6; Mismatches 1; Indels
   #3
   ٥,
   Gaps
   0
```

```
The specification describes a multifunctional short interfering nucleic coacid (sinA). This multifunctional sinA molecule is of two formulae given in the specification. The multifunctional sinA of the invention is useful cor modulating RNA function and/or gene expression in a cell. It can be used for down regulating or inhibiting the expression of one or more conditions that responds to modulation of gene expression or or activity in a cell, tissue, or organism, e.g. organ or tissue transplant, tissue conditions that responds to modulation of gene expression or activity in a cell, tissue, or organism, e.g. organ or tissue transplant, tissue conditions (e.g. organ or tissue transplant, tissue conditions) or preventing constitual hyperplasia and atherosclerosis in grafts. It can further be used for treating CNS lesions or injury, including treating curodegenerative conditions (e.g. Alzheimer's disease, Parkinson's concers, infectious diseases, ocular diseases, cardiovascular diseases, prion disease, inflammatory diseases, renal diseases, liver consenses, prion disease, inflammatory diseases, renal diseases, liver consenses, from VEGF, for a multifunctional sinA of the invention which consenses the target segmences.
   New multifunctional short interfering nucleic acid (siNA), useful for modulating RNA function and/or gene expression in a cell or for treating or preventing pulmonary diseases, neurodegenerative conditions, cancers, or ocular diseases.
   Example 7; SEQ ID NO 56; 168pp; English
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밁
            ঠ
                            Matches
  Query Match
                                   госат
              147
19
                            18;
                                   Similarity
       CCCTTCTCCTTCTGCCATG 165
CCCTCCTCCTTCTGCCATG
                            Conservative
                                 7.48;
94.78;
                            0;
                                   Score 17.4;
Pred. No. 2
                            Mismatches
  DB 1;
                            1;
   Length 19;
                            Indels
                            0
                            Gaps
                            0
```

Sequence 19 BP; 6

A; 2 C; 10 G; 0 T; 1 U;

0 Other; to the target sequences.

```
ARBSULT 9
ARBO5616/6
ARD 5616/6
XX ARD 566
XX ARD 566
XX ARD 56
XX ARD 56
XX VASCUL
XX III-MAR
X
   AED05616 standard; RNA;
  (first entry)
   23
   ВP
```

Short interfering sense sequence targeting human VEGF 121, seqid 81.

vascular endothelial growth factor; RNA interference; gene silencing macular degeneration; ophthalmological; ocular disease; diabetic retinopathy; antidiatoratiovascular disease; cancer; cytostatic; neoplasm; asthma; antiasthmatic; immune disorder; inflammation; respiratory disease; angiogenesis disorder; antiangio; se, short interfering RNA; siRNA. antiangiogenic; silencing

```
WO2005089224-A2.
                         sapiens.
```

11-MAR-2005; 2005WO-US008182

12-MAR-2004; 2004US-0552620P 05-APR-2004; 2004US-0559824P 25-JAN-2005; 2005US-0647191P

(ALNY-) ALNYLAM PHARM INC

Fougerolles A, Frank-Kamenetsky M, Manoharan M, Rajeev ନ

Hadwiger

```
RESULT 10
AED05619/c
ID AED056
XX AED056
XX AED056
XX O1-DEC
XX Vascul
KW Vascul
KW Macula
KW diabet
KW Cytost
KW Inflam
KW 19; sh
XX Homo s
XX Homo s
XX Homo s
XX Homa s
XX Ho
   밁
   ફ
  synthesis of the iRNA agent, where the sense and antisense strands comprise at least one modification that stabilizes the iRNA agent against nucleolytic degradation; a pharmaceutical composition comprising the iRNA agent; inhibiting VEGF expression; and treating a human diagnosed with agent; inhibiting VEGF expression; and treating a human diagnosed with conductive amount of the iRNA agent. The isolated iRNA agent has the sense sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ CC ID NO: 2-401, not defined in the specification. The iRNA agent further comprises a non-nucleotide moiety. The iRNA agent further comprises a non-nucleotide moiety. The iRNA agent further comprises a phosphorothicate at the first internucleotide linkage at the 5' or 3' end of the antisense and sense sequences. The agent further comprises a phosphorothicate at the first internucleotide linkage at the 5' or 3' end of the antisense and sense sequences. The agent for treating adult macular degeneration, diabetic retinopathy, cancer, asthma cand angiogenic disorders. The present sequence is short interfering sense agent cand angiogenic disorders. The present sequence is short interfering sense companies.
   Matches
  Query Match
                                      12-MAR-2004; 2004US-0552620P.
05-APR-2004; 2004US-0559824P.
25-JAN-2005; 2005US-0647191P.
   vascular endothelial growth factor; RNA interference; gene si macular degeneration; ophthalmological; ocular disease; diabetic retinopathy; antidiabetic; cardiovascular disease; cytostatic; neoplasm; asthma; antiasthmatic; immune disorder;
   interfering ribonucleic acid (iRNA) agent comprising a sense sequence an antisense sequence, where the sense and the antisense sequences for an antisense sequence, where the sense and the antisense sequence for an RNA duplax. Also claimed are methods of reducing the amount of VEGF RNA in a cell, using the iRNA agent; making an iRNA agent by the
  The present endothelial
   New isolated 
sequence and
   WO2005089224-A2
   Homo sapiens
   ss; short interfering
   01-DEC-2005
  AED05619
   AED05619 standard;
   Sequence 23 BP; 7 A;
  Claim 1; SEQ ID NO 81; 200pp; English.
  11-MAR-2005;
   inflammation; respiratory disease; angiogenesis
  Local
   having or
  2005-658984/67.
   147 CCCTTCTCCTTCTGCCATG 165
  interfering
   23
   18;
  Similarity
   CCCTCCTCCTTCTGCCATG 5
  growth
   Conservative
   invention
   interfering ribonucleic acid (iRNA) agent comprising a sense an antisense sequence, useful for treating a human diagnosed
  an antisense sequence, useful for treating a h at risk for having adult macular degeneration.
   2005WO-US008182
   (first entry)
  sense sequence targeting human VEGF 121,
   ion relates to the use factor (VEGF). Specifi
   RNA;
  5 C; 10 G; 0 T; 1 U; 0 Other;
   94.7%;
   RNA; SIRNA
   7.48;
   23
  ΒP
   0;
  Score 17.4;
  Pred.
   Mismatches
   Specifically claimed is an
  No. 22;
  DB 1; Length
   1;
   Indels
  an
   antiangiogenic;
  silencing;
  seqid
  cancer;
   vascular
   0
  isolated
  Gaps
   84
  form
   and
   0
```

```
(ALNY-) ALNYLAM PHARM INC
   Fougerolles A,
   Frank-Kamenetsky M,
   Manoharan
   ž
   Rajeev
   ត
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New isolated interfering ribonucleic acid (iRNA) agent comprising a sense sequence and an antisense sequence, useful for treating a human diagnosed as having or at risk for having adult macular degeneration.

Claim SEQ ID NO 84; 200pp; English.

CC synthesis of the iRNA agent, where the sense and antisense atrands CC comprises at least one modification that stabilizes the iRNA agent against CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA cC agent; inhibiting VEGP expression; and treating a human diagnosed with CC adult macular degeneration (AMD), by administering a therapeutically CC effective amount of the iRNA agent. The isolated iRNA agent has the sense CC sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ CC ID NO: 2-401, not defined in the specification. The iRNA agent further CC comprises a non-nucleotide moiety. The iRNA agent further CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent CC further comprises a phosphorothioate at the first internucleotide linkage CC at the 5' or 3' end of the antisense and sense sequences. The agent CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma agent comprises a condition of the iRNA agent is useful for treating adult macular degeneration, diabetic retinopathy, cancer, asthma comprises a condition of the iRNA agent is useful for treating adult macular degeneration, diabetic retinopathy, cancer, asthma comprises a condition of the iRNA agent is useful for treating adult macular degeneration, diabetic retinopathy. The present invention relates to the use of siRNA targeting vascular endothelial growth factor (VEGF). Specifically claimed is an isolated interfering ribonucleic acid (iRNA) agent comprising a sense sequence an antisense sequence, where the sense and the antisense sequences for an RNA duplex. Also claimed are methods of reducing the amount of VEGF RNA in a cell, using the iRNA agent; making an iRNA agent by the sequence targeting human VEGF form and

Sequence 23 BP; 7 A; 4 C; 11 G; 0 T; 1 U; 0 Other;

```
S
                           Matches
                                 Query Match
Best Local
             147
20
                           18;
                                 Similarity
       CCCTTCTCCTTCTGCCATG 165
CCCTCCTCCTTCTGCCATG 2
                           Conservative
                                 7.48; 94.78;
                           0,
                                 Score
Pred.
                           Mismatches
                                   17.4;
No. 22;
  ВB
  ۲.
  Length
                           Indels
  23
                           0
                           Gaps
                           0
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RESULT 11
AED056
XX AED056
XX AED056
XX AED056
XX AED056
XX VASCU
DT 01-DEC
XX VASCU
LX Short
XX CYCOST
XX Sishor
XX Homo Six Short
XX WO2005
XX WO2005
XX 11-MAR
XX 11-MAR Short interfering sense sequence targeting human VEGF 121, seqid 01-DEC-2005 AED05618 standard; RNA; (first entry) 23 ВP

vascular endothelial growth factor; RNA interference; gene silencing; macular degeneration; ophthalmological; ocular disease; diabetic retinopathy; antidiabetic; cardiovascular disease; cancer; cytostatic; neoplasm; asthma; antiasthmatic; immune disorder; cytostatic; neoplasm; asthma; antiasthmatic; immune disorder; inflammation; respiratory disease; angiogenesis disorder; antiangiogenic; cabetic interference. interfering RNA; siRNA

sapiens

11-MAR-2005; 2005WO-US008182

12-MAR-2004; 2004US-0552620P

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RESULT 12
AED05620/c
  밁
  श
  CC synthesis of the iRNA agent, where the sense and antisense strands comprise at least one modification that stabilizes the iRNA agent against composition degradation; a pharmaceutical composition comprising the iRNA agent; inhibiting VEGF expression; and treating a human diagnosed with CC adult macular degeneration (AMD), by administering a therapeutically ceffective amount of the iRNA agent. The isolated iRNA agent has the sense composition of the iRNA agent. The isolated iRNA agent further comprises a non-nucleotide moiety. The iRNA agent further comprises a non-nucleotide moiety. The iRNA agent further comprises a phosphorothicate at the first internucleotide linkage cratther comprises a phosphorothicate at the first internucleotide linkage cat the 5' or 3' end of the antisense and sense sequences. The agent curther comprises a 2'-modified nucleotide. The iRNA agent is useful for treating adult macular degeneration, diabetic retinopathy, cancer, asthma cand angiogenic disorders. The present sequence is short interfering sense comprises a proper candified nucleotide.
  Matches
   Query Match
Best Local
   Short interfering
   diabetic
  vascular endothelial growth
  01-DEC-2005
   AED05620;
  AED05620 standard; RNA;
  endothelial growth factor (VEGP). Specifically claimed is an isolated interfering ribonucleic acid (INNA) agent comprising a sense sequence an antisense sequence, where the sense and the antisense sequences form an RNA duplex. Also claimed are methods of reducing the amount of VEGF RNA in a cell, using the IRNA agent, making an IRNA agent by the
  New isolated interfering ribonucleic acid (iRNA) agent comprising a sense sequence and an antisense sequence, useful for treating a human diagnosed as having or at risk for having adult macular degeneration.
   WO2005089224-A2
  macular degeneration;
diabetic retinopathy;
cytostatic; neoplasm;
  Sequence 23
  The present
   Claim 1;
  WPI; 2005-658984/67.
  Hadwiger
   De Fougerolles A,
   05-APR-2004;
25-JAN-2005;
  inflammation;
  sapiens
   147 CCCTTCTCCTTCTGCCATG 165
  21
  18;
   Similarity
  ALNYLAM PHARM INC
  CCCTCCTCCTTCTGCCATG 3
   SEQ ID NO 83;
   interfering
  BP; 7
   invention relates to the use of siRNA targeting vascular growth factor (VEGF). Specifically claimed is an isolate
  Conservative
   2004US-0559824P.
2005US-0647191P.
  (first entry)
  respiratory disease;
   sense sequence targeting human VEGF 121, seqid
  A; 5 C; 10 G; 0 T; 1 U; 0 Other;
   Frank-Kamenetsky M,
   7.4%;
  growth factor; RNA interference; gene silencing, ophthalmological; ocular disease; antidiabetic; cardiovascular disease; cancer; asthma; antiasthmatic; immune disorder;
   200pp; English.
  23
  дB
  0; Mismatches
   Score 17.4;
Pred. No. 2;
  angiogenesis
   Manoharan M,
   DB 1; Length 23;
  1;
  disorder;
  Indels
   Rajeev KG
  antiangiogenic;
  <u>,</u>
  Gaps
   and
  ٥,
```

```
RESULT 13
AED05617/c
ID AED056
밁
  Ś
  The present invention relates to the use of siRNA targeting vascular conditions of the interfering ribonucleic acid (iRNA) agent comprising a sense sequence and can antisense sequence, where the sense and the antisense sequences form conditions a cell, using the iRNA agent mixed and iRNA agent by the iRNA agent mixed and irea against comprise at least one modification that stabilizes the iRNA agent against comprise at least one modification that stabilizes the iRNA agent against comprise at least one modification that stabilizes the iRNA agent against concleolytic degradation; a pharmaceutical composition comprising the iRNA agent; inhibiting VEGF expression; and treating a human diagnosed with call that against defective amount of the iRNA agent. The isolated iRNA agent has the sense sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ CO ID NO: 2-401, not defined in the specification. The iRNA agent further comprises a non-nucleotide moiety. The iRNA agent further comprises one or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent further comprises a phosphorothioate at the first internucleotide linkage at the 5' or 3' end of the antisense and sense sequences. The agent for treating adult macular degeneration, diabetic retinopathy, cancer, asthma can and angiogenic disorders. The present sequence is short interfering sense can and eargeting human VEGF 121.
  Matches
  Query Match
Best Local
  vascular endothelial growth factor; RNA interference; gene silencing; macular degeneration; ophthalmological; ocular disease; diabetic retinopathy; antidiabetic; cardiovascular disease; cancer; cytostatic; neoplasm; asthma; antiasthmatic; immune disorder; inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;
   12-MAR-2004;
05-APR-2004;
25-JAN-2005;
   Short interfering
   01-DEC-2005
   AED05617;
   AED05617
  Sequence 23 BP; 8 A; 3 C; 11 G; 0 T; 1 U;
  Claim 1; SEQ ID NO 85; 200pp; English.
  New isolated
   De Fougerolles
  sequence and
  WPI; 2005-658984/67.
   (ALNY-) ALNYLAM PHARM INC.
   11-MAR-2005; 2005WO-US008182
   short interfering
  147
  19
  18;
  Similarity
  CCCTTCTCCTTCTGCCATG 165
   standard;
  CCCTCCTCCTTCTGCCATG 1
  o
r
  Conservative
  interfering ribonucleic acid (iRNA) agent comprising a sense an antisense sequence, useful for treating a human diagnosed at risk for having adult macular degeneration.
   2004US-0552620P.
2004US-0559824P.
   (first entry)
   2005US-0647191P
  ,
   sense sequence targeting human VEGF 121,
   RNA;
   Frank-Kamenetsky M,
  7.4%;
   RNA;
   23
   SIRNA.
   ВÞ
  0;
  Score 17.4;
  Pred. No.
  Mismatches
   Manoharan
  명
  0 Other;
  1; Length 23;
  1;
   Z,
  Indels
   Rajeev
   seqid 82.
  0;
  Gaps
```

WO2005089224-A2

Homo sapiens

```
RESULT 14
ABZ22095
ID ABZ22
XX ABZ22
XX ABZ22
XX I1-M2
AX Polya
XX Polya
XX Polya
XX Polya
XX Polya
XX WO200
XX WO200
XX WO200
XX WO200
   밁
   ঠ
   The present invention relates to the use of siRNA targeting vascular CC endothelial growth factor (VEGF). Specifically claimed is an isolated CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and CC an antisense sequence, where the sense and the antisense sequences form CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF CC RNA in a cell, using the iRNA agent; making an iRNA agent by the CC synthesis of the iRNA agent, where the sense and antisense strands CC comprise at least one modification that stabilizes the iRNA agent against CC cucleolytic degradation; a pharmaceutical composition comprising the iRNA agent; inhibiting VEGF expression; and treating a human diagnosed with CC adult macular degeneration (AMD), by administering a therapeutically CC effective amount of the iRNA agent. The isolated iRNA agent has the sense sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ CC ID NO: 2-401, not defined in the specification. The iRNA agent further CC comprises a non-nucleotide moiety. The iRNA agent further comprises one or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent further CC crasting adult macular degeneration, diabetic retinopathy, cancer, asthma CC and angiogenic disorders. The present sequence is short interfering sense cC sequence targeting human VEGF 121.
   Query Match
Best Local S
Matches 18
   New isolated interfering ribonucleic acid (iRNA) agent comprising a sense sequence and an antisense sequence, useful for treating a human diagnosed as having or at risk for having adult macular degeneration.
  12-MAR-2004; 2004US-0552620P.
05-APR-2004; 2004US-0559824P.
25-JAN-2005; 2005US-0647191P.
   03-OCT-2002
   Synthetic
   Polyanionic
  ABZ22095;
   ABZ22095 standard; DNA; 24 BP
  Claim 1; SEQ ID NO 82;
  WPI; 2005-658984/67.
   De Fougerolles A,
   29-SEP-2005
                                    WO200277036-A2
  Polyanionic polymer related oligonucleotide #49
   11-MAR-2003
   (ALNY-)
  147 CCCTTCTCCTTCTGCCATG 165
   22
  1 Similarity
18; Conserv
   ALNYLAM PHARM INC
   23
   CCCTCCTCCTTCTGCCATG 4
   B₽;
   polymer;
   Conservative
  2005WO-US008182
   (first
   7
   A,
   Frank-Kamenetsky M,
   entry)
   7.4%;
   bioactivity; water solubility; ss
   S
   C; 10
  200pp; English
   0
   Score 17.4;
Pred. No. 22
   ଜ;
୦
   Mismatches
   T; 1 U;
  22;
   Manoharan M,
  DB 1; Length 23;
   0 Other;
   1;
   Indels
   Rajeev
   0
   Gaps
   0
```

ADO51553
ADO51553
ADO51553
AC ADO51
AC ADO51
AC ADO51
XX
T12-AU
XX
DE Humar
XX
Serir
XW trans
XW trans
KW myris
KW myris
KW myris
XX
XX
XX
XX
XX
XX

12-AUG-2004 ADO51553;

(first

entry)

ADO51553 standard; DNA;

20

ВP

0

transforming growth factor-beta-stimulated factor 1; TSF1; myristylated and palmitylated serine/threonine kinase; MPSi hyperproliferative disorder; gene therapy; human; antisens phosphorothioate backbone; ss.

Serine/threonine kinase 16; PKL12;

serine/threonine kinase 16 antisense oligo,

ISIS 220645

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   CC monodispersed preparation of a polyanionic polymer (PP) larger than 10 CC kD. (M) involves inserting into an expression vector (EV) a ligating content of product formed by ligating together oligonucleotides that encode content for the protein (I) comprising EV in a host cell, and isolating CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is CC approximately of the same molecular weight. Also described: (1) a CC recombinant fusion protein (I) comprising a polyanionic polypeptide at either one end or at both ends of it; (2) a CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and CC comprises a nucleotide sequence encoding a polyanionic polymer and CC comprises a nucleotide sequence, where the polyanionic polymer and CC comprises a nucleotide sequence, where the polyanionic polymer and at comprises a nucleotide sequence, where the polyanionic polymer is CC polyglutamic acid or polyaspartic acid, (4) production of (I); (5) a cell CC (IV) comprising (III) or a vector that comprises a nucleotide sequence that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a recombinantly-produced polyanionic polymer (V) that is of any molecular CC weight or is larger than 10 kD, and is conjugated to another protein. (I) is useful for treating a disease or alment in an individual by caffective amount of a pharmaceutically acrive agent a therapeutic manner of a pharmaceutically acrive agent.
   Matches
   Query Match
Best Local
  Leung DW,
Waggoner |
  effective amount of a pharmaceutically active agent, a therapeutic protein or a drug to a patient in need of it, or for diagnostic and testing or research purposes. ABZ22045 to ABZ22131 and ABP56374 to ABP56400 represent sequences used in the exemplification of the property.
  Producing monodispersed preparation of polyanionic polymer for therapy, by expressing vector comprising ligation product of oligonucleotides encoding glutamate/aspartate residues in host cell and isolating the
  Sequence
   The present invention describes a method (M)
   Disclosure;
  21-MAR-2001; 2001US-0277705P
   21-MAR-2002; 2002WO-US008614
  (LEUN/) LEUNG D W.
   140 CTGCTCCCCCTTCTCTTCTGC 161
1 circiccrecirciciterec 22
   Similarity
   24
  Bergman PA,
   BP; 0
   Fig
   Conservative
   5; 74pp;
  A; 13 C; 0 G; 11 T; 0 U; 0 Other;
   86.4%;
  Lofquist A,
   English.
   <u>,</u>
   Score 17.2;
Pred. No. 23;
   Mismatches
  Pietz GE,
   BB
   1; Length
   for producing a
   ω
--
  Tompkins
   Indels
   24
   °,
   Gaps
  present
```

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RESULT 16
ACL40112/c
*******
   문
  ફ
  Query Match
Best Local
   Matches
   The invention relates to compounds, compositions and methods for modulating the expression of serine/threonine kinase 16 (also called PKLI2, transforming growth factor-beta-stimulated factor 1; TSP1 and myristylated and palmitylated serine/threonine kinase; MPSK). The composition comprise antisense oligonucleotides targeted to PKLI2 gene. The compound, composition and methods are useful for treating a disease or condition associated with serine/threonine kinase 16, such as a hyperproliferative disorder. They are also useful in research and diagnostics for modulating the expression of serine/threonine kinase 16. The invention is also useful in gene therapy. The present sequence is an antisense oligonucleotide targeted to human serine/threonine kinase 16 DNA. This sequence is used to illustrate the method of the invention.
           ABCC4 siRNA sense sequence, SEQ ID
   Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;
  New compounds, particularly oligonucleotides targeted to a nucleic acid encoding serine/threonine kinase 16, useful for treating diseases associated with serine/threonine kinase 16, e.g. hyperproliferative
   US2004097444-A1
   Homo sapiens.
Synthetic.
                                       24-MAR-2005
   ACL40112;
   ACL40112 standard; RNA; 21 BP
  Example 15;
  WPI; 2004-389186/36
  Dobie KW
   (ISIS-) ISIS
  16-NOV-2002; 2002US-00298953.
   16-NOV-2002; 2002US-00298953.
   20-MAY-2004.
   modified_base
  modified_base
   modified_base
   Local Similarity 90.0%;
es 18; Conservative
  106 CTCATTCTCCTGCTCCCACT 125
   CACATTCTCCTGCTCCCAAT 20
  SEQ ID NO 44; 36pp; English
                                       (first entry)
   PHARM INC
  Location/Qualifiers
1. .20
  /mod_base= OTHER
/mote= "2'-methoxyethyl (2'-MOE) bases"
16. . 20
   /mod_base= OTHER
/note= "Phosphorothioate backbone in which all cytidine
residues are 5-methylcytidines"
   note= "2'-methoxyethyl (2'-MOE) bases"
   *tag=
   *tag= a
   mod_base= OTHER
   7.1%;
   0
   Score 16.8;
Pred. No. 2
   Mismatches
   DB
  ۲,
   2
  Length 20;
  Indels
  0,
   Gaps
   0
```

```
RESULT 17
ACL41020/c
ID 40C4410
XX ACL410
XX ACL410
XX ACL410
XX ACL410
XX ACL410
XX C20oxf
XX Cytost
XX Cytost
XX Homo s
XX WO2005
XX HOMO s
XX HOMO s
XX HOMO s
YX H
   뭉
   8
   Query Match
Best Local Similarity
   Matches
  CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC3OA4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNAs (siRNA) ollgonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
   The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the
   C20orf103 target oligonucleotide, SEQ ID 2092.
  24-MAR-2005
   ACL41020 standard; DNA; 21 BP
   Sequence 21 BP; 4 A; 4 C; 6 G; 0 T; 7 U; 0 Other;
   Pharmaceutical composition comprising an agent capable of modulating expression level or protein activity of a gene, e.g. ABCC4, or a T constituted by the polypeptide or antibody, and a carrier, useful for
  06-JAN-2005
  WO2005001092-A2
  Homo sapiens
   Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer;
   Claim 3; SEQ ID NO 1184; 113pp; English.
   WPI; 2005-075568/08.
  20-MAY-2003; 2003US-0471729P
  19-MAY-2004; 2004WO-US015645
   06-JAN-2005
   WO2005001092-A2
   Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss; short interfering RNA; gene silencing.
  treating cancer.
  (AMHP ) WYETH.
  171
   20
  Wei L,
  AAGATTCCAGGGACTTCACA 190
   Conservative
  (first entry)
   Slonim
  90.0%;
   ,.
  Score 16.8;
Pred. No. 27
   Mismatches
   DB 1; Length 21;
   2;
   Indels
   0,
  88
  Gaps
   kidney
   gene
```

19-MAY-2004; 2004WO-US015645

```
ACL40781/c
ID ACL407
XX
AC ACL407
XX
AC ACL407
XX
ABCC4
XX
Cytost
KW Cytost
KW Short
XX
Synthe
XX
OS Synthe
AX
OS Synthe
A
  CC The present invention relates to a novel pharmaceutical composition CC comprising: (a) an agent capable of modulating an expression level or CC protein activity of a cancer-related transmembrane protein (CRTP) or gene CC; an antibody specific for a CRTP, or a T cell activated by a CRTP; and CC (b) a carrier. The pharmaceutical composition may also comprise a CC polynucleotide capable of inhibiting or decreasing the expression of the CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the CC invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENP3, CF, L11856, GPR54, HAVCR1, SLCSA3, SLC30A4, TRG, and TRPM4. The CC pharmaceutical composition is useful for trating cancer, e.g. colon CC cancer, stomach cancer, and esophageal cancer. The present sequence is a CC cancer, stomach cancer, and esophageal cancer. The present sequence is a CC target oligonucleotide from one such CRTP for which short interfering CC RNAs (sirNA) were produced. Note: The sequence data for this patent did cot form part of the printed specification, but was obtained in CC electronic format directly from WIPO at CC ftp.winc.inf/mh/mihliched or accer.
  र्
   RESULT 18
   밁
  Query Match
Best Local S
Matches 18
   Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
   Cytostatic; Gene t
short interfering
   06-JAN-2005
   Synthetic
  ABCC4 sirNA
   24-MAR-2005
  Sequence 21
  Claim 3; SEQ ID NO 2092; 113pp; English
  WPI; 2005-075568/08.
  ве х,
   20-MAY-2003; 2003US-0471729P
   19-MAY-2004; 2004WO-US015645.
  WO2005001092-A2
  ACL40781 standard; RNA;
  treating cancer.
   20-MAY-2003; 2003US-0471729P.
  (AMHP ) WYETH
   ftp.wipo.int/pub/published_pct_sequences
   Local Similarity
         2005-075568/08
  150
   21
   Wei L,
  Wei L, Slonim
  18;
   TTCTTGTTCTGCCATGATTT 2
  rrcrccrrcrcccarcarr 169
  BP;
   Gene therapy; Vaccine; RNA Interference; cancer; fering RNA; gene silencing.
   sense sequence,
   Conservative
  (first entry)
  Slonim DK,
   11 A;
   7.1%;
90.0%;
   DK,
  4 C; 4 G; 2 T; 0 U;
  21
  ВP
  Howes
  ; Score 16.8; D; Pred. No. 27; 0; Mismatches
  Howes
   SEQ ID 1853.
  HS
  ; HS
  DB 1;
   0 Other;
   2;
  Length 21;
   Indels
   0
   Gaps
   0,
```

```
Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
   Claim
  treating
   3; SEQ ID NO 1853; 113pp; English
   cancer.
```

The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or gene (C protein activity of a cancer-related transmembrane protein (CRTP) or gene (C in antibody specific for a CRTP, or a T cell activated by a CRTP; and (C polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the CC invention are selected from ABCC4, C200rf103, CACNAID, CDH6, CST, ENPP3, CF invention are selected from ABCC4, C200rf103, CACNAID, CDH6, CST, ENPP3, CC cancer, lung cancer, SICCA3, SICC30A4, TRG, and TRPM4. The CC pharmaceutical composition is useful for treating cancer, e.g. colon CC cancer, stomach cancer, and esophageal cancer. The present sequence is a CC cancer, stomach cancer, and esophageal cancer. The present sequence concer short interfering RNAs (siRNA) oligonucleotide. Note: The sequence cancer cancer in this patent did not form part of the printed specification, but the other cancer in the sequence of the solution of the solution of the solution of the context form with the cancer in the sequence of the solution of the soluti ftp.wipo.int/pub/published\_pct\_sequences

Sequence 21 BP; 4 A; 4 C; 6 G; 0 T; 7 U; 0 Other;

Query Match Best Local S Matches 18 l Similarity
18; Conserv Conservative 7.1%; <u>.</u> Score 16.8; Pred. No. 27; Mismatches BB 1; Length ν • Indels 21 0 Gaps 0

뮍 Ś 171 AAGATTCCAGGGACTTCACA 190 20 AAGATTCCAGGCGCTTCACA 1

21 ВÞ

entry)

C20orf103 target oligonucleotide, SEQ ID 1942

therapy; Vaccine; RNA Interference; cancer; ss

19-MAY-2004; 2004WO-US015645

20-MAY-2003; 2003US-0471729P

Slonim DK, Howes HS

RESULT 19
ACL40870/c
ID ACL40870 standard; DNA; 21
XX
ACL40870;
XX
ACL40870;
XX
ACL40870;
XX
Cytostatic; Gene therapy;
XX
Cytostatic; Gene therapy;
XX
OS Homo sapiens.
XX
W02005001092-A2.
XX
PN W02005001092-A2.
XX
PD 06-JAN-2004; 2004WO-US0156
XX
PD 08-WAY-2004; 2004WO-US0156
XX
ACLAMMAP ) WYETH.
XX
PR 20-MAY-2003; 2003US-047177
XX
PA (AMMP) WYETH.
XX
PHARMACEUTICAL composition PT expression level or protein expression Pharmaceutical composition comprising an agent capable of modulating expression level or protein activity of a gene, e.g. ABCC4, or a T constituted by the polypeptide or antibody, and a carrier, useful for ng an cell

3; SEQ ID NO 1942; 113pp; English.

(a) an agent capable a novel pharmaceutical composition of modulating an expression level õ

```
RESULT 20
ACL40872
        밁
  S
   protein activity of a cancer-related transmembrane protein (CRTP) or gene

in antibody specific for a CRTP, or a T cell activated by a CRTP; and

composition may also comprise a

polynucleotide capable of inhibiting or decreasing the expression of the

CRTP by RNA interference or an antisense mechanism. The CRTPs of the

invention are selected from ABCC4, C20orf103, CACNAID, CDHG, CST, ENPB3,

FLJ11856, GPRS4, HAVCR1, SLCGA3, SLC30A4, TRG, and TRPM4. The

concer, lung cancer, breast cancer, prostate cancer, e.g. colon

concer, stomach cancer, and esophageal cancer. The present sequence is a

carget oligonucleotide from one such CRTP for which short interfering

RNAs (siRNA) were produced. Note: The sequence data for this patent did

cont form part of the printed specification, but was obtained in

celectronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences
  Matches
   Query Match
The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCG4, C20orf103, CRCNAID, CDB6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon
   Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
  WPI;
   Be X,
   20-MAY-2003; 2003US-0471729P
  19-MAY-2004; 2004WO-US015645
  06-JAN-2005
   WO2005001092-A2
   short interfering RNA;
   Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; 88;
  C20orf103 siRNA antisense sequence, SEQ ID 1944.
  24-MAR-2005
   ACL40872;
   ACL40872 standard;
   Sequence 21
   (AMHP)
   госат
  2005-075568/08
  149
  20
   Wei L,
  18;
   Similarity
   SEQ
  CTTCTTGTTCTGCCATGATT 1
  CTTCTCCTTCTGCCATGATT 168
   BP; 10
  Conservative
   ID NO 1944; 113pp; English
  (first entry
   Slonim
   RNA;
   A; 3 C; 5 G; 3 T; 0 U; 0 Other;
  90.0%;
   DK,
   gene silencing.
   21
   Howes
  0
  Score 16.8;
Pred. No. 2
  Mismatches
   SH;
   DB 1;
  2
  Length 21;
  Indels
  0;
  1 for
  Gaps
  0
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RESULT 21
ABL58878
  នន្តន្តន្តន្តន្ត
Ś
  맑
  S
                           Query Match
Best Local S
Matches 18
  Query Match
Best Local S
Matches S
  The invention relates to marking DNA-containing samples by treatment with a marker oligonucleotide that is either an artificial microsatellite oligonucleotide or an artificial single nucleotide polymorphism (SNP) oligonucleotide for analysis. The oligonucleotides are useful as internal markers for identifying samples used for e.g. characterising or typing an animal for monitoring food production and in human or veterinary medicine. The present sequence is that of a artificial oligonucleotide used to exemplify the invention
  cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
  Sequence
   Disclosure; Page 6; 25pp; German.
  Marking DNA samples for identifying samples during subsequent analysis by adding microsatellite or single nucleotide polymorphism oligonucleotide.
   WPI; 2002-435855/46
   08-NOV-2000;
  07-NOV-2001; 2001WO-EP012880
  Synthetic
  Marker oligonucleotide; microsatellite; single nucleotide polymorphism; SNP; food production; veterinary; medicine; ss.
  Oligonucleotide
  22-JUL-2002
   ABL58878;
   ABL58878 standard;
  Sequence
  was obtained in electronic format direct
ftp.wipo.int/pub/published_pct_sequences
   16-MAY-2002
   WO200238804-A1
  140
   149
                             l Similarity
  N
   Similarity 9; Conserv
  AGROBIOGEN GMBH BIOTECHNOLOGIE
  24
 CIGCICCCCCTTCTCCTTCT 159
  CONCONGUNCOGCCAUGAUU
   CTTCTCCTTCTGCCATGATT 168
  21 BP; 3
  BP; 0
                             Conservative
  Conservative
  2000DE-01055368
  (first entry)
  A; 12 C;
   A; 5 C; 3
   DNA;
   45.0%;
   90.0%;
   7.1%;
  7.1%;
   24
  1 G; 11 T;
   ВP
                             0
  G; 0 T; 10 U;
                                      Score 16.8;
Pred. No. 2
   Score 16.8;
Pred. No. 2
  21
  Mismatches
  0 U; 0
   ВB
   DB
  0 Other;
  1,
  1;
  Other;
                             2
  2
   Length
  Length
                             Indels
   24;
   21;
                             0,
   0
                             Gaps
  Gaps
                             0
  0
```

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ທ

AEC36403/c

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The specification describes a multifunctional short interfering nucleic acid (siNA). This multifunctional siNA molecule is of two formulae given in the specification. The multifunctional siNA of the invention is useful for modulating RNA function and/or gene expression in a cell. It can be used for down regulating or inhibiting the expression of one or more target nucleic acid molecules. It is also useful for treating diseases or conditions that responds to modulation of gene expression or activity in a cell, tissue, or organism, e.g. organ or tissue transplant, tissue grafting, or treatment of pulmonary disease (restenosis) or preventing neointimal hyperplasia and atherosclerosis in grafts. It can further be used for treating CNS lesions or injury, including treating cued for treating the conditions (e.g. Alzheimer's disease, parkinson's cuedesses, epilepsy, dementia, Huntington's disease, or amyotrophic lateral sclerosis), cancers, infectious diseases, ocular diseases, crardiovascular diseases, prion disease, inflammatory diseases, renal diseases, liver diseases, mitochondrial diseases, sendorned diseases, or reproduction related diseases, and conditions. AEC14610-AEC36614 represent target
   New multifunctional short interfering nucleic acid (siNA), useful for modulating RNA function and/or gene expression in a cell or for treating or preventing pulmonary diseases, neurodegenerative conditions, cancers,
   related diseases and conditions. AEC36400-AEC36404 represent target sequences from VEGF, for a multifunctional siNA of the invention which targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary
  cardiovascular-gen.; prion disease; cerebroprotective; degeneration; inflammation; antiinflammatory; renal disease; nephrotropic; endocrine disease; genitourinary disease; liver disease; hepatotropic; gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;
   neurological disease; cancer; neoplasm; cytostatic; infection; antimicrobial; ocular disease; ophthalmological; cardiovascular disease;
   short interfering nucleic acid; siNA; short interfering RNA; siRN gene silencing; RNA interference; transplant rejection; pulmonary disease; respiratory-gen.; respiratory disease; injury; vulnerary; neurodegenerative disease; neuroprotective;
   Example 7; SEQ ID NO 57; 168pp; English
   WPI; 2005-571603/58.
   10-FEB-2004; 2004US-0543480P.
24-MAY-2004; 2004WO-US016390.
   AEC36403 standard; RNA; 19
  Jadhav V,
   09-FEB-2005; 2005WO-US004270
   25-AUG-2005.
  WO2005078097-A2
   VEGF/VEGFR2 multifunctional siNA VEGF target sequence
   (SIRN-) SIRNA THERAPEUTICS INC
  Unidentified
   ocular diseases.
  19
  Zinnen S
BP;
   the target sequences.
  (first entry)
σ
   nucleic acid; siNA; short interfering RNA; siRNA;
Α,
2 C;
10
ធ;
0
T; 1 U;
0 Other;
```

S

147 CCCTTCTCCTTCTGCCAT 164

Query Match Best Local S Matches 17

17; Conserv

Conservative

0

Score 16.4; DB 1; Length 19; Pred. No. 31; o; Mismatches 1; Indels

0

Gaps

0

Sequence 19 BP; 1 A; 10 C;

2 G;

0 T;

6 U;

0 Other

6.9%;

```
RESULT 23
AEC36450
  밁
acid (sinA). This multifunctional sinA molecule is of two formulae given in the specification. The multifunctional sinA of the invention is useful for modulating RNA function and/or gene expression in a cell. It can be used for down regulating or inhibiting the expression of one or more target nucleic acid molecules. It is also useful for treating diseases or conditions that responds to modulation of gene expression or activity in a cell, tissue, or organism, e.g. organ or tissue transplant, tissue grafting, or treatment of pulmonary disease (restences) or preventing neointimal hyperplasia and atherosclerosis in grafte. It can further be used for treating CNS lesions or injury, including treating neurodegenerative conditions (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, dementia, Huntington's disease, or amyotrophic lateral sclerosis), cancers, infectious diseases, or anyotrophic lateral since of the conditions of the cond
  pulmonary disease; respiratory-gen.; respiratory disease; injury; vulnerary; neurodegenerative disease; neuroprotective; underary; neurodegenerative disease; neuroprotective; neurological disease; cancer; neophasm; cytostatic; infection; antimicrobial; ocular disease; neuropological; cardiovascular disease; neuropological; cardiovascular disease; cardiovascular-gen.; prion disease; cerebroprotective; degeneration; inflammation; antiinflammatory; renal disease; nephrotropic; endocrine disease; genitourinary disease; hierardiction disease; hepatotropic;
   diseases, prion disease, inflammatory diseases, renal diseases, liver diseases, mitochondrial diseases, endocrine diseases, or reproduction related diseases and conditions. AEC36400-AEC36404 represent target sequences from VEGF, for a multifunctional sNNA of the invention which targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary
  New multifunctional short interfering nucleic acid (siNA), useful for modulating RNA function and/or gene expression in a cell or for treating or preventing pulmonary diseases, neurodegenerative conditions, cancers, or ocular diseases.
  The specification describes a multifunctional short interfering nucleic
   WPI; 2005-571603/58
   Jadhav V,
   10-FEB-2004; 2004US-0543480P
24-MAY-2004; 2004WO-US016390
   09-FEB-2005; 2005WO-US004270
  endocrine disease; genitourinary disease; liver disease; hepatotropic; gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;
   gene silencing; RNA interference; transplant rejection;
   short interfering nucleic acid; siNA; short interfering
  03-NOV-2005
  AEC36450
   AEC36450 standard; RNA;
   Example 7;
   WO2005078097-A2
   Unidentified
   VEGF/VEGFR2 multifunctional siNA VEGF target complement sequence #4.
   (SIRN-) SIRNA THERAPEUTICS
   18
  CCCTCCTCCTTCTGCCAT 1
   SEQ ID NO 115; 168pp; English
   the target
  (first
  entry)
   sequences.
   RNA; siRNA;
```

```
문
                       ঠ
  밁
  S
  Query Match
Best Local (
  Matches
  Matches
   Best Local
  against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, peridymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these
   PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORF encode polypeptides (see AAX36754-Y37949) which can be used as vaccines
   Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis, epidymitis; revvicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
  Sequence
   Disclosure; Page 1555; 1755pp; English.
  Genome sequence of Chlamydia trachomatis
   WPI; 1999-371125/31.
   04-NOV-1998;
   28-NOV-1997;
17-DEC-1997;
   27-NOV-1998;
  10-JUN-1999.
  WO9928475-A2
  Chlamydia trachomatis.
  Synthetic
  PCR primer used to amplify an ORF of Chlamydia trachomatis.
  07-OCT-1999
  AAZ02810;
  AAZ02810 standard; DNA;
  (GEST ) GENSET
   147
                 202 CTAACGCCATGCTTCTTG 219
w
  11;
  N
  Similarity
  Similarity
  CCCTTCTCCTTCTCCAT 164
  20 BP; 3
  cccuccuccuucueccau 19
   Conservative
   Conservative
   (first entry)
   97FR-00015041.
97FR-00016034.
98US-0107077P.
   98WO-IB001939.
  A; 6 C; 4 G; 7 T; 0
  6.9%;
  61.1%;
  20
  ₿P
20
   0,
   6
  Score 16.4;
Pred. No. 30
  Score 16.4; DB 1; Length 19; Pred. No. 31; indels
   U; 0 Other;
  30;
   DB 1; Length 20;
   <u>ب</u>
   Indels
   0,
   <u>,,</u>
   frames
These ORFs
   Gaps
  Gaps
   0
  0,
```

RESULT 25 ABL45056

RESULT 26
ABK96689
ID ABK96
XX
AC ABK96
XX
AC ABK96
XX
AC ABK96
XX
XX
XX
III
DI 24-SE
XX
XX
XX

ABK96689 standard; DNA; 21 BP

24-SEP-2002

(first entry)

Interleukin-3 (IL-3) reverse sequencing primer

밁

μ

CTCTCATCCTCCTGCTCC 18

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Ś
   The present invention describes a method of arraying genome clones. The comprises: (a) clones of the genomic libraries contained in cmultiwell plates numbered for discrimination are mixed in each of the cultiwell plates; (b) a primer designed based on the chromosome marker (c) a signal corresponding to the marker is detected from the resultant (c) a signal corresponding to the marker is detected from the resultant complified product to specify the discrimination Nos. of the multiwell complete containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to the marking in the specified discrimination Nos. to array the multiwell complete; (e) the clones in the multiwell plates of the specified complete; (e) the clones in the multiwell plates of the specified complete; (e) the clones in the multiwell plates of the specified complete; (e) the mixed clones are detected from the amplified by using the above primer; (g) signals can disteral directions; (f) the mixed clones are cultured and the complete are specified from the detected result; and (i) the clones in the multiwell complete are specified from the detected result; and (i) the clones are constituted as the positions on the chromosome and arrayed. The conformators is useful for gene analysis. ABL42937 to ABL45322 represent PCR primers for human chromosome 21922.1, which are specified for use in the present invention
                                   Query Match
Best Local Similarity
Matches 17; Conserv
   Sequence
  Claim 4; Page 46; 528pp; Japanese;
   20-NOV-2001.
  JP2001321190-A
   Human chromosome 1p36-35 PCR primer SEQ ID NO:2100
   ABL45056 standard; DNA; 20 BP
  (RIKA ) RIKAGAKU KENKYUSHO.
  10-MAR-2000; 2000JP-00066716.
   12-MAR-2001; 2001JP-00068285
  Homo sapiens.
  Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
   primer; ss.
104 CTCTCATTCTCCTGCTCC 121
   genome clones.
   20 BP;
  Conservative
  (first entry)
   N
   A;
   6.9%;
   10 C; 2 G; 6 T; 0 U; 0 Other;
  .
   Score 16.4;
Pred. No. 30
  Mismatches
   30;
  DB 1;
  ۲,
  Length
  Indels
  20
  0
  Gaps
```

```
RESULT 27
ABK96692/C
ID ABK966 XX
X ABK96
XX
AC ABK96
XX
AC ABK96
XX
Intel
XX
Intel
XX
Intel
XW
Intel

  밁
   र्
   The invention describes an isolated polynucleotide (I) comprising a cequence which is a polynorphic variant for a reference sequence for interleukin 3 (colony-stimulating factor) (II3) gene or its fragment (I) Is useful for studying the expression and biological function of II3, as well as in developing drugs targeting the II3 protein. A transgenic animal is useful for studying expression of II3 isogenes in vivo, for in vivo screening and testing of drugs targeted against II3 protein, and for the testing the efficacy of therapeutic agents and compounds for diseases of the central nervous system e.g. multiple sclerosis, Alzheimer's disease, Parkinson's disease and CNS injury, and immune or inflammatory disorders. The method described in the invention is useful in developing diagnostic tests and therapeutic treatments for diseases of the central nervous system and immune or inflammatory disorders. This sequence represents a sequencing primer used to sequence regions of the II-3 gene in order to central nervous in the order.
   Matches
  Query Match
Best Local (
  Chew
   Interleukin 3; colony-stimulating factor; IL3; transgenic animal;
IL3 isogene; central nervous system disorder; multiple sclerosis;
Alzheimer's disease; Parkinson's disease; CNS injury; immune disorder;
   Interleukin 3; colony-stimulating factor; IL3; transgenic animal; IL3 isogene; central nervous system disorder; multiple sclerosis; Alzheimer's disease; Parkinson's disease; CNS injury; immune diso
   Novel isolated polynucleotide comprising a sequence which is a polymorphic variant for a reference sequence for interleukin 3 gene useful for studying the expression and biological function of the
   ABK96692
   ABK96692 standard; DNA;
  Sequence 21
   06-JUN-2002.
   WO200244410-A1
  Homo sapiens.
   inflammatory disorder; sequencing; primer; ss
   Homo
  inflammatory disorder;
  Interleukin-3 (IL-3) forward sequencing primer
  24-SEP-2002
   Example 1; Page 25; 62pp; English
   (GENA-)
   28-NOV-2000; 2000WO-US032381
  28-NOV-2000; 2000WO-US032381.
  sapiens.
   polymorphisms
   GENAISSANCE PHARM INC
  Similarity
   TGTCTGGGTCATGGGGGC 18
   Denton RR,
  BP;
   Conservative
  (first entry)
  2 A;
   6.9%;
  'n
  4 C; 9 G; 6 T; 0 U;
  Nandabalan
   the
  sequencing; primer;
  21
  ΒP
  21
  0;
  Pred
   Score 16.4;
   ~
   Mismatches
  No.
   Stephens JC;
   29;
   0 Other;
  DB 1;
  1;
   #4.
   Length
   Indels
   sclerosis;
immune disorder;
  21;
  0
   Gaps
   0
```

```
The invention describes an isolated polynucleotide (I) comprising a sequence which is a polymorphic variant for a reference sequence for interleukin 3 (colony-stimulating factor) (II3) gene or its fragment (I) Is useful for studying the expression and biological function of II3, as well as in developing drugs targeting the II3 protein. A transgenic animal is useful for studying expression of II3 isogenes in vivo, for in vivo screening and testing of drugs targeted against II3 protein, and for testing the efficacy of therapeutic agents and compounds for diseases of the central nervous system e.g. multiple sclerosis, Alzheimer's disease, parkinson's disease and CNS injury, and immune or inflammatory disorders. The method described in the invention is useful in developing diagnostic tests and immune or inflammatory disorders. This sequence represents a system and immune or inflammatory disorders. This sequence represents a sequencing primer used to sequence regions of the IL-3 gene in order to
  Novel isolated polynucleotide comprising a sequence which is polymorphic variant for a reference sequence for interleukin useful for studying the expression and biological function of
   Example 1;
   28-NOV-2000; 2000WO-US032381.
  28-NOV-2000;
  06-JUN-2002
                                   polymorphisms in the gene
   GENAISSANCE
   Page
  2000WO-US032381.
   26;
  RR,
   62pp; English
   PHARM INC.
  Nandabalan
  ۲
  Stephens
  JC;
   is a
kin 3
  cin 3 gene
```

Sequence 21 BP; 6 A; 9 C; 4 G; 2 T; 0 U; 0 Other;

밁 Ś Query Match Best Local : Matches 18 μ l Similarity 17; Conserv TGTCTGGGTCATGGGGGC TGTCTGGGTCATGGGAGC 1 Conservative 6.9%; 18 0, Score Pred. Mismatches 16.4; No. 29; DB 1; Length Indels 21; 0 Gaps 0

```
RESULT 28
AEDO56
XX AEDO56
XX AEDO56
XX O1-DEC
XX Vascull
XW Wacull
XW Wacull
XW Inflam
XW inflam
XX SHOMO E
XX SHOMO E
XX SHOMO E
XX HOMO E
XX HO
  AED05621
  standard;
  RNA;
  23
  ВP
```

Short interfering sense sequence targeting human VEGF 121, seqid

01-DEC-2005

(first entry)

vascular endothelial growth factor; RNA interference; gene silencing, macular degeneration; ophthalmological; ocular disease; macular degeneration; ophthalmological; ocular disease; cancer; diabetic retinopathy, antidiabetic; cardiovascular disease; cancer; cytostatic; neoplasm; asthma; antiasthmatic; immune disorder; inflammation; short interfering sapiens respiratory disease; angiogenesis disorder; antiangiogenic; RNA; SIRNA

29-SEP-2005

11-MAR-2005; 2005WO-US008182

12-MAR-2004; 2004US-0552620P

WO200244410-A1

```
RESULT 29
ADD55615/C
ID ADD56
XX ADD56
XX ADD56
XX ADD56
XX VA6CUL
DE Short
XX VA6CUL
KW MACULA
KW MACULA
KW GYFOST
KW 1nflam
KW S9; Sh
OX Homo S
XX WO2005
XX XY
PD 29-SEP
PD 29-SEP
   밁
   Ś
  CC endothelial growth factor (VEGF). Specifically claimed is an isolated CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and CC an antisense sequence, where the sense and the antisense sequences form CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF CR NA in a cell, using the iRNA agent making an iRNA agent by the CC synthesis of the iRNA agent; where the sense and antisense strands CC comprise at least one modification that stabilizes the iRNA agent against CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA agent; inhibiting VEGF expression, and treating a human diagnosed with CC adult macular degeneration (AMD), by administering a therapeutically CC effective amount of the iRNA agent. The isolated iRNA agent further CC moprises a non-nucleotide moiety. The isolated iRNA agent further CC comprises a non-nucleotide moiety. The iRNA agent further CC comprises a non-nucleotide moiety. The iRNA agent further CC comprises a non-nucleotide moiety. The iRNA agent further CC comprises a phosphorothioate at the first internucleotide linkage CC at the 5' or 3' end of the antisense and sense sequences. The agent CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma CC and angiogenic disorders. The present sequence is short interfering sense CC semience targeting human VCGF 12'
   Query Match
Best Local !
  Matches
                     29-SEP-2005
  WO2005089224-A2
   vascular endothelial growth factor; RNA interference; gene silencing macular disease; macular disease; extinopathy; antidiabetic; cardiovascular disease; cancer; cytostatic; neoplasm; asthma; antiasthmatic; immune disorder;
   Short interfering sense sequence targeting human VEGF 121,
  01-DEC-2005
   AED05615 standard; RNA;
  Sequence
  Claim 1;
   New isolated interfering ribonucleic acid (iRNA) agent comprising a sense sequence and an antisense sequence, useful for treating a human diagnosed as having or at risk for having adult macular degeneration.
  WPI; 2005-658984/67.
   De Fougerolles A,
  05-APR-2004;
25-JAN-2005;
  (ALNY-)
   inflammation;
  sapiens
  147 CCCTTCTCCTTCTGCCAT 164
   18
   Similarity
  ALNYLAM PHARM INC
  ogenic disorders. The present sequence is targeting human VEGF 121.
   CCCTCCTCCTTCTGCCAT 1
  23
  SEQ ID NO 86; 200pp; English
   ion; respiratory disease; anglogenesis interfering RNA; siRNA.
  BP; 9 A;
   invention relates to the use of siRNA targeting vascular growth factor (VEGF). Specifically claimed is an isolate
  Conservative
  2004US-0559824P.
2005US-0647191P.
  (first entry)
   Frank-Kamenetsky M,
   6.9%;
  2 C; 11
   23
   ВP
  <u>,</u>
   Score 16.4;
Pred. No. 28
  G; 0 T; 1
  Mismatches
  U; 0 Other;
   Manoharan M,
   DB 1; Length 23;
  1;
   disorder;
  Indels
   Rajeev KG
  gene silencing
   antiangiogenic;
   seqid
  0
  Gaps
  0
```

```
ABX97349
ID ABX977
XX ABX97
XX ABX97
XX ABX97
XX UOVX,
XW NOVX,
XW NOVX,
XW hypot
KW hypot
KW human
XX
Homo
XX
WO200
XX
PD 19-SE
XX
  Ś
   밁
  The present invention relates to the use of siRNA targeting vascular CC endothelial growth factor (VEGF). Specifically claimed is an isolated CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and CC an antisense sequence, where the sense and the antisense sequences form RNA duplex. Also claimed are methods of reducing the amount of VEGF CRNA in a cell, using the iRNA agent; making an iRNA agent by the CC synthesis of the iRNA agent, where the sense and antisense strands CC comprise at least one modification that stabilizes the iRNA agent against CC comprise at least one modification that stabilizes the iRNA agent against CC comprise at least one modification that stabilizes the iRNA agent against CC comprise at least one modification that stabilizes the iRNA agent against CC comprise amount of the iRNA agent. The isolated iRNA agent that the sense sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ CC ID NO: 2-401, not defined in the specification. The iRNA agent further comprises a phosphorothioate at the first internucleotide linkage creating adult macular degeneration; diabetic retinopathy, cancer, asthma CC and angiogenic disorders. The present sequence is short interfering sense CC sequence targeting human VEGF 121.
  Best Local
Matches 1
  Query Match
   12-MAR-2004;
05-APR-2004;
25-JAN-2005;
   NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer; hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
   Human NOV-associated probe from primer-probe set Ag3550
  20-MAY-2003
  ABX97349;
  ABX97349 standard; DNA; 23
   Sequence 23 BP; 7 A; 5 C; 10 G; 0 T; 1 U; 0 Other;
   Claim 1; SEQ ID NO 80; 200pp; English.
  sequence and as having or
  New isolated
  De Fougerolles A, Hadwiger P;
  11-MAR-2005; 2005WO-US008182
   (ALNY-) ALNYLAM PHARM INC.
  148 CCTTCTCCTTCTGCCATG 165
   23
  17;
   probe;
  Similarity
  Conservative
  interfering ribonucleic acid (iRNA) agent comprising a sense an antisense sequence, useful for treating a human diagnosed at risk for having adult macular degeneration.
   2004US-0552620P.
2004US-0559824P.
2005US-0647191P.
  (first entry
  Frank-Kamenetsky M,
  6.98;
  먥
  0;
  Score 16.4;
Pred. No. 28;
  Mismatches
  Manoharan
  DB 1; Length 23;
  1;
  Σ,
  Rajeev
  <u>;</u>
  Gaps
```

WO200272757-A2

sapiens.

19-SEP-2002

```
08-MAR-2001
08-MAR-2001
08-MAR-2001
08-MAR-2001
08-MAR-2001
08-MAR-2001
11-MAR-2001
11-MAR-2001
11-MAR-2001
11-MAR-2001
11-MAR-2001
12-MAR-2001
20-MAR-2001
21-MAR-2001
22-MAR-2001
22-MAR-2001
21-MAR-2001
22-MAR-2001
21-MAR-2001
21-MAR
  Padigaru M, S
Zerhusen BD,
Patturajan M,
Fernandes ER,
Spaderna SK,
   08-MAR-2002;
   CURAGEN
  2001US-0274322P.
2001US-0274849P.
2001US-0275235P.
2001US-0275578P.
2001US-0275579P.
2001US-02756000P.
2001US-0276000P.
2001US-0276000P.
  2001US-027694P.
2001US-027723P.
2001US-027732P.
2001US-0277737P.
2001US-0277737P.
2001US-027793P.
2001US-0278999P.
2001US-0279934P.
2001US-0279934P.
2001US-0280802P.
2001US-0280802P.
2001US-028194P.
2001US-0288342P.
2001US-0288342P.
2001US-0288982P.
2001US-0288982P.
2001US-02889489P.
2001US-0294889P.
2001US-0294889P.
2001US-0294889P.
2001US-0294889P.
2001US-0294889P.
2001US-03931P.
2001US-03933146P.
2001US-03331846P.
2001US-03331846P.
2001US-03331846P.
2001US-03331849P.
2001US-03331849P.
2001US-03331849P.
2001US-0333184P.
                        Spytek KA,
Gusev V,
M, Gangolli I
   2002WO-US006908
      Catterton E,
   CORP.
                      ក្ន
                                       ,
E
Shenoy SG, Taupier RJ, Pena CEA,
Ji W, Gorman L, Miller CE, Kekuda
E, Vernet CAM, GOUO X, Tchernev V,
Malyankar UM, Gerlach V, Liu Y,
E, Burgess C, Leite M, Zhong H, /
      Anderson D;
  ۶. F.
                        Anderson
  ۲
    RESULT 31
ADN62252
ID ADN62252
XX ADN62
AC ADN62
AC ADN62
AC Humar
XX Humar
XX Humar
XX Humar
XX Haema
XX real
XX real
XX 10-M3
XX 10-M3
PR 08-M3
PR 08-M3
PR 08-M3
PR 08-M3
PR 08-M3
PR 113-M3
PR 1
   밁
   Š
  Best Loc
Matches
  Query Match
    08-MAR-2001;
08-MAR-2001;
08-MAR-2001;
08-MAR-2001;
09-MAR-2001;
13-MAR-2001;
13-MAR-2001;
13-MAR-2001;
13-MAR-2001;
14-MAR-2001;
16-MAR-2001;
19-MAR-2001;
20-MAR-2001;
   07-MAR-2002;
  04-MAR-2004
   01-JUL-2004
   Sequence
  Example
   US2004043382-A1
  Homo sapiens
   Lepley
   Local
  2002-723332/78.
   100
  l Similarity
18; Conserv
  N
   ¥,
  ü
  CCGCCTCTCCTTCTCCCGCTC
   23
  Page
   BP; 1
   Rieger
   (first
```

cancer, hypertension, atherosclerosis, DVX polypeptides and disorder associated 717; 1103pp; English polynucleotides, useful for preventing or treating with aberrant NOVX expression or activity e.g., atherosclerosis, cardiomyopathy or bronchial

This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABX13460-ABX13462 and ABX97186-ABX97593 represent PCR primers and probes used in the amplification and isolation of the NOVX polymucleotides represented in ABX97008-ABX97185 which encode the polypeptides represented in ABU65041-ABU65218. The probes described in the invention are modified at the 5'-end by TET and the 3'-end by TAMRA A; 13 C; 2 G; 7 ,, H 0 U; 0 Other;

CCCCCTCTCATTCTCCTGCTC 6.9%; ilarity 85.7%; Conservative 0; Score Pred. 120 Mismatches 16.2; No. 29; BB 1; Length

Indels

0,

Gaps

0

23;

22

Human NOV40a RTQ-PCR probe ADN62252 standard; DNA; entry) 23 ВР

cancer-associated cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; chronic disorder; real time quantitative pro probe; RTQ-PCR, anorexia;

2001US-0274194P.
2001US-0274281P.
2001US-0274829P.
2001US-0274849P.
2001US-0275579P.
2001US-0275579P.
2001US-0275601P.
2001US-0276706P.
2001US-0276776P.
2001US-027739P.
2001US-0277321P. 2002US-00092900 2001US-0274191P

```
16-AUG-2001

10-SEP-2001

12-SEP-2001

27-SEP-2001

27-SEP-2001

18-CCT-2001

31-CCT-2001

14-NOV-2001

14-NOV-2001
   20-MAR-2001
21-MAR-2001
21-MAR-2001
22-MAR-2001
23-MAR-2001
26-MAR-2001
27-MAR-2001
27-MAR-2001
28-MAR-2001
30-MAR-2001
02-APR-2001
03-MAY-2001
13-MAY-2001
15-MAY-2001
16-MAY-2001
16-MAY-2001
16-MAY-2001
11-MAY-2001
11-MAY-2001
11-MAY-2001
11-MAY-2001
11-MAY-2001
11-MAY-2001
 (GORM/)
(KEKU/)
(KEKU/)
(PATT/)
(GANG/)
(GURN/)
(GURN/)
(TCHE/)
(FERN/)
(FERN/)
(FALY/)
(GALY/)
(GALY/)
(GALY/)
(GALY/)
(GALY/)
(GALY/)
(GALY/)
(GALY/)
  (PENA/)
   (PADI/)
(SPYT/)
(SHEN/)
(TAUP/)
  21-NOV-200
  14-NOV-200:
   14-NOV-2001;
14-NOV-2001;
MILLER C E.

KEKUDA R.

PATTURAJAN M.

GANGOLLI E A.

VERNET C A M.

GUO X S.

TCHERNEV V T.

FERNANDES E R.

CASMAN S J.

MALYANKAR U M.

GERLACH V.

LIU Y.

ANDERSON D W.

SPADERNA S K.
   PADIGARU M.
SPYTEK K A.
SHENOY S G.
TAUPIER R J.
PENA C E A.
  ZERHUSEN B
   2001US-0288066P.
2001US-0288342P.
2001US-028852BP.
2001US-0291190P.
2001US-0291240P.
2001US-0291485P.
2001US-0294889P.
2001US-029489P.
2001US-029489P.
2001US-029489P.
2001US-029489P.
2001US-0299303P.
2001US-039310P.
2001US-0318462P.
   2001US-0278999P
2001US-0279934P
2001US-0279344P
2001US-0279995P
2001US-028080233P
2001US-0280802P
2001US-0280802P
2001US-0280802P
2001US-0281444P
2001US-0281444P
  2001US-0277327P.
2001US-0277338P.
2001US-0277791P.
2001US-0277833P.
   O
```

```
CC The invention relates to an isolated polypeptide (designated NOVX, or CC NOV1-NOV127) comprising a sequence selected from 178 fully defined amino acid sequences (and their mature forms, variants and fragments). Also CC included are an isolated nucleic acid molecule encoding NOVX, a vector CC comprising the nucleic acid, a cell comprising the vector, methods for determining the presence or amount of the polypeptide or the nucleic acid molecule in a sample, methods for determining the presence of or CC predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian CC subject, a method for identifying an agent that binds to the above polypeptide, a method for identifying a potential therapeutic agent for CC use in the treatment of a pathology that is related to aberrant CC expression or physiological interactions of the polypeptide, a method of screening for a modulator of activity or of latency or predisposition to CC a pathology associated with the polypeptide and a method for modulating CC are useful for diagnosing, preventing or treating diseases such as CC diabetes, obseity, infectious diseases, anorexia, cancer-associated CC diabetes, obseity, infectious diseases, anorexia, cancer-associated CC diabetes, and other chronic diseases. These may also be used in CC parkinson's disease, immune disorders, haematopoietic disorders. The composition and cc pharmacogenomics. The polypeptides are also useful as vaccines. The CC assay tissue specific axpression of a NOVX mRMA.
  Example C; SEQ ID NO 521; 786pp;
  New NOVX polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or
   pharmacogenomics.
   WPI; 2004-225693/21.
  Alsobrook JP,
  Anderson
   Patturajan
Fernandes E
  Zerhusen
   Padigaru
   (LEPL/)
(RIEG/)
  (LEIT/)
(ALSO/)
  BURG/)
                                    tissue
   ALSOBROOK J
LEPLEY D M.
RIEGER D K.
   CATTERTON
LEITE M W.
ZHONG H.
  BURGESS C E.
  DW,
  BD,
                                ence is an RTQ-PCR (r
specific expression
  Spytek KA, Shenoy SG, Taupier RJ, Pe
Gusev VY, Ji W, Gorman L, Miller CE
Gusev VY, Di W, Gorman LM, Miller CE
, Gangolli EA, Vernet CAM, Gerlach V,
, Casman SJ, Malyankar UM, Gerlach V,
Spaderna SK, Catterton E, Leite MW,
Lepley DM, Rieger DK, Burgess CE;
   Ξ
  ы
  ש
                                  of a
  English.
   Taupier RJ, Pena
man L, Miller CE,
CAM, Guo XS, Tch
r UM, Gerlach V,
                                    NOVX mRNA.
   Pena
  Pena CEA, Li
CE, Kekuda R;
Tchernev VT;
V, Liu Y;
V, Liu Y;
  īR;
   ۲
  acid
```

Sequence 23 BP; 1 A; 13 ü N Ģ 7 T; 0 U; 0 Other;

RESULT 32 ABN89272 밁 Ś Query Match Best Local S Matches 18 Local Similarity nes 18; Conserv 100 N CCCCCTCTCATTCTCCTGCTC 120 Conservative 6.9%; Score 16.2; D Pred. No. 29; 0; Mismatches 22 B 7: ω ' Length Indels 23; 0, Gaps

0

\*\*\*\*\*\*\*\*\* 29-AUG-2002 (first entry)

ABN89272 standard; DNA; 20

ВP

Human Talin antisense phosphorothioate oligonucleotide SEQ ID NO:85

Human; Talin; antimicrobial; antiinflammatory; cytostatic; inhibit antisense gene therapy; infection; inflammation; Talin inhibitor; inhibitor; tumour;

```
RESULT 33
ADG90535
ID ADG90
XX
AC ADG90
XX
AC ADG90
XX
AC ADG90
XX
AC ADG90
XX
   ঠ
  밁
   Matches
  Query Match
Best Local
  Talin in human cells or tissues comprising contacting the cells or tissues in vitro with (I) or (a). (I) has antimicrobial, antiminlammatory and cytostatic activities, and can be used in antisense gene therapy and as a Talin expression inhibitor. (I) can be used: to inhibit the expression of human Talin in human cells or tissues; to prevent or delay infection, inflammation or tumour formation; and in diagnostics, therapeutics, prophylaxis, and in research reagents and kits. The present sequence represents a human Talin antisense chimeric phosphorothicate oligonucleotide, having 2'-methoxyethyl (2'-MOE) wings of 5 nucleotides at the 5' and 3' ends and a 10 nucleotide deoxy gap in the middle, which
  The present invention describes an antisense compound (I), 16 to 30 bases in length targeted to specific base regions of a nucleic acid encoding human Talin. Also described: (a) an antisense compound up to 30 bases in length which inhibits the expression of human Talin; (b) a composition length which inhibits the expression of human Talin; (b) a composition (II) or (a); and (c) inhibiting the expression of human (II) comprising (I) or (a); and (c) inhibiting the expression of human (II) comprising (I) or (a); and (c) inhibiting the expression of human (II) comprising (I) or (a); and (c) inhibiting the expression of human (II) comprising (I) or (a); and (c) inhibiting the expression of human (II) comprising (I) or (a); and (c) inhibiting the expression of human (II) comprising (II) or (a); and (c) inhibiting the expression of human (II) comprising (II) or (a); and (c) inhibiting the expression of human (III) comprising (II) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression of human (III) or (a); and (c) inhibiting the expression (III) or
                              11-MAR-2004
  Sequence 20
  Claim 14; Col 42; 46pp; English.
  New antisense compound useful for inhibiting expression of Talin and preventing or delaying infection, inflammation or tumor formation.
   30-OCT-2000; 2000US-00702251.
  30-OCT-2000; 2000US-00702251.
   ADG90535;
   ADG90535 standard;
   16-APR-2002.
  US6372492-B1
  modified_base
   modified_base
  Homo sapiens
  antisense oligonucleotide; phosphorothioate; ss
  (ISIS-) ISIS
   modified_base
   used in an example from the present
   2002-470102/50
  105
   16;
   ω
  Similarity
  TCTCATTCTCCTGCTC 120
   TCTCATTCTCCTGCTC 18
  BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;
   Conservative
                              (first entry)
   Cowsert
  PHARM INC
  16. .20
  Location/Qualifiers
   /*tag= a
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
   note= "2'-methoxyethyl (2'-MOE) nucleotides'
  mod base= OTHER
  *tag=
  note=
   DNA; 20
  6.8%;
   _base= OTHER
  "phosphorothioate backbone"
   ი
   ВP
  Score 16; pred. No.
   0,
   Mismatches
   invention
  DB 1; Length 20; 33;
   0;
   Indels
  ç
   Gaps
  bases
   for
   0
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Sequences ADG90460-ADG90539 represent phosphorothioate targeted to the CC human talin gene, which inhibit its expression. The antisense were considered to target different regions of human talin RNA, and were considered to their effect on talin expression by quantitative real-time CC PCR. Talin is a cytoplasmic protein which links cytoskeletal proteins considered to their effect on talin expression by quantitative real-time CC regulation of cellular advisor and cell morphology. Talin is highly considered to the contractill morphology. Talin is highly considered to the contractill morphology. Talin is highly considered to the contractill morphology. Talin is highly considered to the cardiomy a role in platelet adhesion as its conduction as it has been found to confide the contractill force to the extracellular conductions. The expression at myotendinous junctions. The expression of talin is contribute to the development of prostate tissues, a phenomenon known to contribute to the development of prostate tissues, a phenomenon known to contribute to the development of prostate tissues, a phenomenon known to contribute to the development of prostate tissues, a phenomenon to talin is such as those related to cellular adhesion. The coligonucleotide concertation for a particular cell line.
  Query Match
Best Local Similarity
Matches 16; Conserv
  Sequence
   New antisense oligonucleotides targeted to nucleic acid molecules encoding human Talin, useful for inhibiting the expression of human Talin and for treating a human having a disease or condition associated with
   Bennett
   prostate cancer; talin-related disorder;
cellular adhesion-related disorder; expression inhibition;
antisense therapy; phosphorothicate; antisense oligonuclectide; ss.
  oligonucleotide
  Example 15;
  (ISIS-)
   22-FEB-2001; 2001US-00791942.
  30-OCT-2001; 2001WO-US048435
   06-SEP-2002
  WO200268446-A1.
   Homo sapiens
  cardiomyocyte; platelet; prostate; androgen
   Human talin phosphorothioate antisense oligonucleotide,
  modified_base
105 TCTCATTCTCCTGCTC 120
  talin; cellular adhesion; muscle strength; cardiac function;
   CF,
   ISIS PHARM INC.
BOEHRINGER INGELHEIM PHARM INC.
   20
  6.8%;
ilarity 100.0%;
Conservative
  BP; 1 A;
   SEQ ID NO 85; 114pp; English
   Rothlein R,
  concentration for a particular cell line.
   /*tag= a
/mod base
/mod_base
/note= "This oligonucleotide has a phosphorothioate
/mote= "This oligonucleotide has a phosphorothioate
backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
and 3' ends, which are 5 nucleotides in length. Also all
cytosine nucleotides are 5-methylcytosines"
   Location/Qualifiers
  7 C; 2 G; 10 T; 0 U; 0 Other;
   Kishimoto TK,
  0;
   Score 16;
Pred. No.
   Mismatches
  33;
   Cowsert
  1.
   downregulation;
   0
  Length 20,
   ;
K
   Indels
   SEQ ID NO:85
  0
  Gaps
  0
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  RESULT 34
ABQ84461/c
  The present invention describes a new isolated nucleic acid sequence (I) comprising a DPP10 mRNA sequence. DPP10 is a dispeptidyl peptidase (also CK known as prolyloligopeptidase). (I) has antiinflammatory, antiasthmatic, currently of the manufacture of a medicament for regulating before the manufacture of a medicament for regulating DPP10 expression or for preventing or treating inflammatory disease e.g., inflammatory cor for preventing or treating inflammatory disease e.g., inflammatory cor bewel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can be used in an assay for detecting or measuring DPP10 in a sample. A host cell comprising (I) can be used for producing recombinant DPP10 gene products, or in drug screening systems to identify agents for diagnosis or treatment of individuals having or susceptible to inflammatory cor treatment DPP10 is located on chromosome 2, more specifically chromosome 2q14. ABQ84254 to ABQ84612 and ABP55569 to ABP55629 represent of sequences used in the exemplification of the present invention
   Query Match
Best Local S
Matches 16
  Sequence
  New nucleic acid sequence comprising DPP10 mRNA, useful for the manufacture of a medicament for regulating DPP10 protein expression or for preventing or treating inflammatory disease e.g., inflammatory bowel
   DPP10; dipeptidyl peptidase; prolyloligopeptidase; enzyme; asthma; antiinflammatory; antiasthmatic; antipsoriatic; antiarthritic; antirheumatic; vaccine; gene therapy; inflammatory disease; inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
  Claim 43; Page 314; 321pp; English
   Cookson
  24-APR-2001; 2001GB-00010044.
24-APR-2001; 2001GB-00010046.
12-OCT-2001; 2001GB-00024575.
12-OCT-2001; 2001GB-00024594.
   24-APR-2002;
   31-OCT-2002.
  WO200286113-A2
  Synthetic
   Homo sapiens.
   chromosome 2q14; PCR primer; ss.
   20-FEB-2003
   ABQ84461;
   ABQ84461 standard; DNA;
   (ISIS-)
   2003-093132/08
                            191
  PCR
18
   16;
  ISIS
  Similarity
   ₩OCM,
  20
                           AGAAGCAAATGCTAAC 206
  BP; 4
   6.8%; Solarity 100.0%; Conservative 0;
  INNOVATIONS
   2002WO-GB001887.
   (first entry)
   Moffat MF,
  A; 5 C; 3
   20
  LTD.
   k; Score 16; DB
k; Pred. No. 33;
0; Mismatches
   Allen
   ₽P
  G; 8
  Z,
  T; 0 U; 0
   Lench
   DB 1; Length 20; 33;
  z
  Other;
   <u>.</u>
   Indels
   0
   Gaps
  gene
   0
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RESULT 35

RESULT 36 ACL41021/c

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ADP85740
XX
ADP85740;
AC ADP85740;
AC ADP85740;
AC ADP85740;
AC ADP85740;
AC ADP85740;
AC ADP85740;
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AC ADP857
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  Matches
  Query Match
Best Local
  The invention relates to novel antisense compounds targeted to a nucleic acid molecule encoding human Talin to and inhibit its expression. The invention is useful for treating a disease or condition associated with Talin such as a disease or condition e.g. muscular, haematologic, cardiac or hyperproliferative disorder such as cancer. The present sequence is ar antisense oilgonucleotide targeted to human Talin DNA.
  New compounds, particularly antisense oligonucleotides targeted to nucleic acid encoding talin, useful for treating muscular, cardiac, hematologic, or hyperproliferative disorders.
   30-OCT-2000;
30-OCT-2001;
   Homo sapiens.
Synthetic.
   Claim 3; SEQ ID NO 85; 48pp; English.
   WPI; 2004-440384/41.
   modified_base
  Antisense; Talin; cardiac disorder;
  Bennett CF, Cowsert
   11-SEP-2003; 2003US-00415463
   US2004110705-A1
   modified_base
  modified_base
  phosphorothioate;
  Human Talin antisense oligonucleotide,
  26-AUG-2004
  105 rerearrerecte 120
  16;
w
   BENNETT C
  Similarity
   20 BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;
  standard;
   6.8%; Score 16; llarity 100.0%; Pred. No. Conservative 0; Mismatc
  2000US-00702251.
2001WO-US047585.
  (first entry)
   /note= "
16. .20
   /mod
   /*tag= a
/mod_base= OTHER
/note= "2'-methoxyethyl
   residues are 5-methylcytidines"
  Location/Qualifiers
   /*tag=
  /mod_base= OTHER
/note= "Phosphorothicate backbone where all cytidine
   note=
  3 স
   muscular disorder; haematologic disorder;
hyperproliferative disorder; cancer; human;
  DNA;
   Z
  base= OTHER
  "2'-methoxyethyl (2'-MOE) nucleotides"
  a
  ۵
   20
  Mismatches
  No.
   DB 1;
   ISIS #109184
   (2'-MOE)
  0,
  Length 20;
   nucleotides"
  Indels
  ologic, cardiac
sequence is an
  0
  Gaps
  Ö
  0,
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RESULT 37
ACL40780/c
ID ACL407
XX
AC ACL407
XC
AC ACL407
XC
DT 24-MAR
XX
DE ABCC4
XX
CYtost
   밁
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  Matches
  Query Match
Best Local :
   ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, FLJ11856, GPR54, HAVCRI, SIC6A3, SIC50A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
  The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level of protein activity of a cancer-related transmembrane protein (CRTP) or
  Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
 Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer;
   Sequence 21 BP; 10 A; 3 C; 4 G; 0 T; 4 U; 0 Other;
   Be X,
   06-JAN-2005
  Synthetic
   Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer;
   C20orf103 siRNA sense sequence, SEQ ID 2093.
  24-MAR-2005
                               ABCC4 target oligonucleotide,
  24-MAR-2005
  ACL40780;
   ACL40780 standard; DNA;
   Claim 3;
  WPI;
  20-MAY-2003; 2003US-0471729P
  19-MAY-2004; 2004WO-US015645
   WO2005001092-A2
  short interfering RNA; gene silencing.
  (AMHP ) WYETH
  ACL41021 standard; RNA; 21 BP
  150 TTCTCCTTCTGCCATGATT 168
  19
   1 Similarity
17; Conserv
   Wei L, Slonim DK,
   SEQ ID NO 2093; 113pp; English.
   Conservative
  (first entry)
  (first entry)
   6.7%;
   21
  Howes SH;
   ВP
   0; Mismatches
  Score 15.8;
Pred. No. 3
                                 SEQ ID 1852.
   DB 1;
   2
   Length 21;
   Indels
   ٥,
   88;
   Gaps
  õ
   0
```

19-MAY-2004; 2004WO-US015645

06-JAN-2005 WO2005001092-A2 Cytostatic; Gene therapy; Vaccine; RNA Interference;

cancer;

interfering

RNA;

gene silencing.

ABCC4 siRNA antisense sequence, SEQ ID 1185

24-MAR-2005

(first entry)

ACL40113 standard; RNA;

```
ACL40113
ID ACL40
XX ACL40
AC ACL40
XX ACL40
AC ACL40
XX ACC4
AC CYTOS
KW CYTOS
KW Short
XX Synth
XX Synth
XX WO200
XX IS O6-JA
XX IS MO-JA
XX IS ACC4
  맑
  S
   CC The present invention relates to a novel pharmaceutical composition CC comprising: (a) an agent capable of modulating an expression level or CC protein activity of a cancer-related transmembrane protein (CRTP) or gene CC; an antibody specific for a CRTP, or a T cell activated by a CRTP; and CC (b) a carrier. The pharmaceutical composition may also comprise a CC polynucleotide capable of inhibiting or decreasing the expression of the CC (CRTP by RNA interference or an antisense mechanism. The CRTPs of the CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENP3, CF LJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The CC pharmaceutical composition is useful for treating cancer, e.g. colon CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CC target oligonucleotide from one such CRTP for which short interfering CC RNAs (sirNA) were produced. Note: The sequence data for this patent did cnot form part of the printed specification, but was obtained in CC electronic format directly from WIPO at
  Matches
  Query Match
Best Local
  Sequence 21 BP; 5 A;
   Claim 3; SEQ ID NO 1852; 113pp; English
  Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
  WPI; 2005-075568/08
   ве х,
   19-MAY-2004; 2004WO-US015645.
  06-JAN-2005
   WO2005001092-A2
   Homo sapiens
   ftp.wipo.int/pub/published_pct_sequences
  creating
  20-MAY-2003; 2003US-0471729P
   (AMHP ) WYETH
  l Similarity
17; Conserv
   Wei L,
  AGATTCCAGGGACTTCACA 190
   cancer.
  AGATTCCAGGCGCTTCACA 3
  Conservative
   Slonim DK,
  6.7%;
89.5%;
  4 C; 7 G; 5 T; 0 U; 0 Other;
   Howes
  0;
  Score 15.8;
Pred. No. 3
  Mismatches
   SH;
   DB 1; Length 21;
  2;
  Indels
  ٥,
  Gaps
  0
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  RESULT 39
ACL40111/c
   문
   Query Match
Best Local :
   Matches
   comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisence mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, FLJ11856, GRF54, HAVCRI, SLC6A3, SLC3OA4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNAs (sIRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
Pharmaceutical composition comprising an agent capable of modulating
  ве х,
   20-MAY-2003; 2003US-0471729P
   19-MAY-2004; 2004WO-US015645
   WO2005001092-A2
   Homo sapiens
  Cytostatic; Gene
   ABCC4 target oligonucleotide, SEQ ID 1183.
   24-MAR-2005
   ACL40111;
  ACL40111 standard;
  Sequence
  Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
  WPI;
  ве х,
  20-MAY-2003; 2003US-0471729P
   The present invention relates to a novel pharmaceutical composition
  Claim 3;
  ftp.wipo.int/pub/published_pct_sequences
  (AMHP ) WYETH
  (AMHP ) WYETH
                             2005-075568/08
  172
  2005-075568/08
   13;
  _
   Wei L,
   Wei L,
   Similarity
   AGATTCCAGGGACTTCACA 190
  21
  AGAUUCCAGGCGCUUCACA 19
  SEQ ID NO 1185; 113pp; English.
  BP; 5 A; 6 C; 4 G; 0 T; 6 U; 0 Other;
   Conservative
  (first entry)
  Slonim
  Slonim DK,
   therapy; Vaccine; RNA Interference; cancer;
  DNA;
   6.7%;
  묫
  21
  ВÞ
  Howes
  Howes
  4;
   Score 15.8;
Pred. No. 34;
   Mismatches
  HS
  SH;
  DB 1; Length 21;
  <u>ب</u>
   Indels
  0;
  88
  Gaps
 an
  0
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cc protein activity of a cancer-related transmembrane protein (CRTP) or gene ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and C(b) a carrier. The pharmaceutical composition may also comprise a collected capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the creation are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPD3, C111856, GPR54, HAVCR1, SLC6A3, SLC3OA4, TRG, and TRPM4. The Cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a carget oligonucleotide from one such CRTP for which short interfering CRNAS (siRNA) were produced. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in the componing format directly from WIPO at the proper cancer is a concer in the print of the print of the proper was obtained in the componing format directly from WIPO at the proper cancer is a concer in the print of the print of the proper was obtained in the concert of the print of the proper was obtained in the concert of the print of the pri
Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
  The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level of protein activity of a cancer-related transmembrane protein (CRTP) of protein activity.
   expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
  ftp.wipo.int/pub/published_pct_sequences
  SEQ ID NO 1183; 113pp; English
   cancer.
```

Query Match 6.7
Best Local Similarity 89.5
Matches 17; Conservative 172 21 AGATTCCAGGGACTTCACA 190 AGATTCCAGGCGCTTCACA 3 6.7%; <u>.</u>. Score 15.8; Pred. No. 3 Mismatches DB 1; 2 Length Indels 21; 0 Gaps

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RESULT 40
ACL40868/c
ID ACL408
XX ACL408
XX ACL408
XX CYCOORF
XX C Synthetic short interfering RNA; C20orf103 siRNA sense sequence, 24-MAR-2005 ACL40868 WO2005001092-A2 Cytostatic; standard; Gene therapy; Vaccine; RNA Interference; (first entry) RNA; 21 BP gene silencing. SEQ ID 1940. cancer; 88;

06-JAN-2005

19-MAY-2004; 2004WO-US015645

20-MAY-2003; 2003US-0471729P

(AMHP ) WYETH

Wei L, Slonim 봈 Howes

2005-075568/08

Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for treating cancer.

Claim 3; SEQ ID NO 1940; 113pp; English

The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level ( o R

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Matches
   Query Match
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  protein activity of a cancer-related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polymucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, FLJ11856, GRR54, HAVCR1, SLC6A3, SLC3AA4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNAS (sixNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
               The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDM6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon
  Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
  Be
  Claim 3;
  WPI; 2005-075568/08
  (AMHP ) WYETH
   20-MAY-2003; 2003US-0471729P
  19-MAY-2004; 2004WO-US015645
   06-JAN-2005
  WO2005001092-A2
   Synthetic
  short interfering
   Cytostatic;
  ABCC4 siRNA antisense sequence, SEQ ID 1854.
   24-MAR-2005
   ACL40782;
  ACL40782 standard; RNA;
   Sequence 21 BP; 9 A; 3 C; 5 G; 0 T; 4 U; 0 Other;
   ftp.wipo.int/pub/published_pct_sequences
  149
   19
   Wei L,
  17;
   Similarity
Bunt
   CTTCTCCTTCTGCCATGAT 167
   cancer
   SEQ ID NO 1854; 113pp; English
   CTTCTTGTTCTGCCATGAT 1
  Gene therapy; Vaccine; RNA Interference; cancer;
  Conservative
cancer,
  (first entry
  Slonim
   RNA;
   6.7%;
breast
  봈
   gene silencing.
   22
   ВP
  Howes
cancer, prostate cancer, liver cancer, kidney
   0; Mismatches
   Score 15.8;
Pred. No. 3
  ;HS
   멂
   ۲.
   2;
   Length
  Indels
  21;
   0;
  Gaps
   0
```

Query Match

Sequence

22

BP;

2 A;

8 C; 2

G; 10 T; 0 U;

0 Other;

15 6,

BB

Length

```
RESULT 42
ACA88981
ID
ACA88981
XX
ACA88981
ACA89881
ACA89
   នន្តន្តន្តន្ត្
  밁
   Ş
   Query Match
Best Local
   The invention describes a method of selecting genetic markers as targets for nucleic acid sequence amplification comprising selecting each of the genetic markers according to a heterozygosity index of 0.5 or greater. Selecting and amplification of genetic markers are useful as targets for nucleic acid sequence amplification, for genetic testing or facilitating multiplex PCR amplification from limiting amounts of target nucleic acid. The methods are also useful for improving genetic diagnostic and screening methods, such as prenatal diagnostic testing, foetal sex determination or genetic identification, e.g. DNA profiling or DNA fingerprinting. The nucleic acid sequence amplification is also useful in forensic analysis of degraded, old, ancient and difficult samples that are difficult to amplify and identify. This sequence represents a PCR
   cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
   Selecting genetic markers as targets for nucleic acid sequence amplification, useful for improving genetic testing, e.g. fetal sex determination, comprises selecting each of the genetic markers according
   Genetic marker selection; multiplex PCR amplification; prenatal diagnostic testing; foetal sex determination; genetic identification; DNA profiling; DNA fingerprinting; forensic analysis; PCR; primer; ss.
   ACA88981 standard; DNA; 22
  Sequence 21
  17-APR-2003
  Homo sapiens
   Selection and
  08-JUL-2003
  ACA88981
  Claim 36; Page 40; 64pp; English
  WPI; 2003-381725/36.
   12-OCT-2001; 2001AU-00008234
12-OCT-2001; 2001AU-00008235
   14-OCT-2002; 2002WO-AU001388
   (UYQU ) UNIV QUEENSLAND
   WO2003031646-A1
  heterozygosity index.
  172
  13;
   used
   Similarity
   AGATTCCAGGGACTTCACA 190
  AGAUUCCAGGCGCUUCACA 19
   B₽;
   in the
  Matthews
  Conservative
  (first entry)
   amplification of genetic markers
   5 A;
   selection
  PL,
   68.4%;
   6 C; 4
  Mulcahy
   股
  4.
   G; 0 T; 6 U;
   Score 15.8;
Pred. No. 3
   and amplification of genetic markers
   Mismatches
  BK;
   34;
  0
   띪
   Other;
  1;
  2
  PCR related
   Length
   Indels
   21;
   primer
  0
  Gaps
  ij
   0
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RESULT 43
ADU84382
    밁
   ठ
  Matches
   Best Local Similarity
   08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
29-DEC-1999;
30-DEC-1999;
   31-AUG-1999;
27-SEP-1999;
27-SEP-1999;
27-SEP-1999;
  Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-LB; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitits B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; CANZYme; cancer; breast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression genes encoding protein-tyrosine-phosphatase-lb (PTB-LB), methionine aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presentiin-1 (ps-1)
   WPI,
   The present invention relates to the use of molecules (e.g. ribozymes) to modulate gene also methods for their use to down regulate
   Example
  Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes
   Stinchcomb
  Mcswiggen
Karpeisky
  04-FEB-2000;
20-MAR-2000;
  30-AUG-2000;
  08-MAR-2001
  WO200116312-A2
  Homo
   Human MetAP-2
  ADU84382
  (RIBO-)
   10-FEB-2005
   2001-244406/25.
   sapiens
  144
  18;
   μ
  and
  RIBOZYME PHARM
  , A,
   standard;
   ricrectreactricieccare 22
  TCCCCCTTCTCCTTCTGCCATG
   Page 249; 717pp;
   99US-00474432
99US-0173612P
99US-00476387
2000US-00498824
2000US-00531025
2000US-0197769
2000US-00578223
2000US-00636385
  heart disease.
  Conservative
  2000WO-US023998
   (first
  Usman N, Blatt L,
Matulic-Adamic J, S
Beaudry A, Zinnen
  hammerhead ribozyme substrate sequence #391.
  99US-00406643.
99US-0156236P.
99US-0156467P.
   99US-00436430.
99US-0169100P.
   DNA;
   81.8%;
   INC.
   Blatt
  17
  ВÞ
  English
   0
  t L, Beigelman L, Burgin
J, Sweedler D, Draper K,
innen S, Lugwig J, Sproat
   Pred.
  165
  Mismatches
   ŏ.
  enzymatic nucleic acid
   4
  Sproat BS
   Indels
   Α,
  Chowrira
  0
  Gaps
 n factor (ps-1),
   of
f
  0
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RESULT 44
ACNO8391
ID ACNO8391
ACNO8391
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ACNO8391
   밁
  5
   Query Match
Best Local S
Matches 16
  for treating cancer, in particular breast cancer, Alzheimer's disease, disbetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences
   New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
  WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
   Sequence
  presentiin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatinucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNazyme motifs. The methods of the invention are useful for the protein of the invention of the invention.
   (RIBO-)
   20-OCT-2000; 2000US-0242411P
   19-OCT-2001;
   WO200268637-A2
   West Nile Virus
  WNV minus
   22-APR-2004
   ACN08391;
  ACN08391
   associated
   Local Similarity
   2002-706994/76
   ŗ
   75
  16;
   μ
   RIBOZYME PHARM INC
BLATT L.
   MCSWIGGEN J
   standard; RNA; 17
   GAGCTGGTTGTTTGAAA
   17 BP; 4 A; 1 C;
   GAGCTGGTTTTTGAAA
  Mcswiggen JA;
  strand Hammerhead
  with them.
  Zinzyme; ss
  Conservative
   2001WO-US048350.
  (first entry)
   Þ
   6.5%;
   ഗ
   17
   91
   ВÞ
  G; 7
  Ribozyme substrate
  0,
  Score 15.4; Di
Pred. No. 41;
O; Mismatches
   ..
..
   0 U;
   0
  B
   Other;
   1;
  ۲,
  SEQ
  Length
  Indels
  IJ
  ö
  0,
   enzymatic
  Gaps
```

0;

The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (MNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

hepatocellular carcinoma or cirrhosis. The nucleic acid lected from the group of ribozymes consisting of payme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

molecule

r failure, hepatoc cule is selected ( erhead, Inozyme, (

Claim

23;

SEQ

ID NO 8394;

495pp;

English

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밁 8

0

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RESULT 45
ACN06460/c
   Matches
  Query Match
Best Local
   least ten 2'-O-methyl m
least three of the 5' t
3'-3' inverted abasic m
are claimed; however, S
in the specification. T
molecule of the inventi
                  molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed, however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid
  The invention relates to nucleic acid molecules that modulate replication the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
   MNV; West Nile Virus; antinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
  Sequence 17
  New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
  06-SEP-2002.
are claimed; however, in the specification. molecule of the invent
   WPI; 2002-706994/76
   20-OCT-2000; 2000US-0242411P
   19-OCT-2001; 2001WO-US048350
   WO200268637-A2
  WNV Amberzyme substrate SEQ
  22-APR-2004
  ACN06460
  nucleic acid
  (RIBO-)
   BLAT/)
   Nile
   143
  RIBOZYME
BLATT L.
   MCSWIGGEN J A.
   Similarity 9; Conser
   crececrrerection 159
  standard; RNA;
  cucucccuucuccuucu 17
   SEQ ID NO 6463; 495pp; English.
   Mcswiggen
  Virus
   BP; 0
   the invention
   Conservative
  molecules further comprise at least five ribose residues, at -Q-methyl modifications, phosphorothioate linkages on at of the 5' terminal nucleotides and a 3' end modification of a ed abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 however, SEQ ID NO 2194-2206 and 17502-17514 are not given fication. The present sequence is that of a nucleic acid
  (first entry)
   ::
  PHARM
   Α;
  88
  6.5%;
  9 C; 0.G; 0
  H
   7;
   Score
Pred.
  ğ
   Mismatches
  T; 8
  6463
   15.4;
No. 4;
  ď;
  0 Other;
   멂
  1;
   ۳.
  Length
   Indels
   17;
   0
  replication
   Gaps
   0
```

Query Match Best Local S Matches 9

Similarity

6.5%;

Score 15.4; Pred. No. 41

DB 1;

Length 17;

Mismatches

۲,

Indels

0

Gaps

0

Conservative

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SX X
  吊
  Ś
  Query Match
Best Local S
Matches 16
                      or the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least three of the 5' terminal nucleotides and a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nuclei-
  WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
  Sequence 17
   Claim 23; SEQ ID NO 8395; 495pp; English.
  (RIBO-)
  West Nile Virus
   ACN08392
   pancreatitis, meningitis,
  06-SEP-2002
  WNV minus strand Hammerhead Ribozyme substrate
  22-APR-2004
  New nucleic acid molecule that modulates replication of West Nile (WNV), useful for treating a condition related to WNV infection e.
   WPI; 2002-706994/76
   20-OCT-2000; 2000US-0242411P
  19-OCT-2001; 2001WO-US048350
   Amberzyme; Zinzyme;
   (MCSW/)
   144 TCCCCCTTCTCCTTCTG 160
  al Similarity
16; Conserv
  17
  RIBOZYME
BLATT L.
   MCSWIGGEN J A.
  17
   standard; RNA; 17
  rerecerrerectricie 1
   Mcswiggen JA;
   B₽;
 BP;
  Conservative
  (first entry)
   œ
 0
   PHARM
   Þ
 ð
   6.5%;
  1 C;
  8
 ç
  щ
   8
   hepatocellular
 <u>ဂ</u>
  <u>,</u>
   <u>.</u>
   Score 15.4;
Pred. No. 4
  0
   0
   Mismatches
   нј
  Ţ,
   0
  œ
  ۲;
   Ç
  0
  carcinoma
   0
   DB
  Other;
   Other;
  ۲.
  SEQ
  Length
   Indels
  g
  ij
   infection e.g. cirrhosis.
  g
   17;
  8395
  ٥,
  Gaps
```

```
RESULT 47
AAD12693/c
ID AAD126
XX AAD126
XX AAD126
XX Human
XX Human;
XW Gene r
XX Gene r
CC Gend nemb
CC Gend nemb
CC Gend nemb
CC Gend nemb
CC Gend ne
CC Gend nemb
CC Gend Geriva
CC Gend nemb
CC Gend nemb
CC Gend nemb
CC Gend Nebrid
CC Sequen
  δ
  S
  BXXXB
   밁
  밁
  ABZ31192/c
  RESULT 48
  Query Match
Best Local S
Matches 16
  30-JAN-2003
                                       ABZ31192;
   ABZ31192 standard;
   Sequence
   derivative, corresponding to a alpha-catenin binding protein. The invention also relates to a novel human zinc finger protein binding with a member of the a-catulin/vinculin family, preferably with a human isoform of alpha N-catenin (neural form). The invention also relates to the field of drug discovery, diagnosis, prognosis and treatment of cancer and neurological disorders. The present sequence is a PCR primer which is used for sequencing and cloning human alphaE/alphaN-chimeras in pGBT9 two
   The invention relates to human catenin-binding proteins and their corresponding cDNA molecules which functions in signal transduction gene regulatory pathways. The invention also provides an isolated an recombinant nucleic acid or its functional fragment, homologue or
   Disclosure; Page 69; 160pp; English.
   Novel recombinant nucleic acids useful for diagnosing, prognosing and/or treating cancer and neurological disorders, corresponds to a protein binding to alpha-catenin protein and with signal transduction function.
  WPI; 2001-418220/44.
   23-DEC-1999;
   18-MAY-2000; 2000WO-EP004535
  WO200147954-A2
  Homo sapiens.
   Human; ANC_2H01 protein; catenin-binding protein; signal transduction; gene regulation; zinc finger protein; alphaN-catenin; drug screening; therapy; cancer; neurological disorder; cytostatic; neuroprotective; alphaE/alphaN-chimera; primer; ss.
   Human alphaE/alphaN-chimeric cDNA sequencing primer,
   AAD12693;
  AAD12693 standard;
   25-SEP-2001
   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
   Local Similarity
  182
   17
  16;
   20
   GACTTCACAAGAGGCAA 1
  GACTTCACAAGAAGCAA 198
  TCCCCCTTCTCCTTCTG 160
  ucucccuucuccuucus 17
  Conservative
   BP; 2 A; 4 C; 5 G; 9 T; 0 U; 0 Other;
  Vanlandschoot A,
   (first entry)
(first entry)
   99EP-00204512
   DNA;
  DNA;
   6.5%;
   20
  20
   ВÞ
  BP.
  0
   Score 15.4;
Pred. No. 38;
  Janssens
  Mismatches
  B
   DB 1; Length 20;
  1;
  Indels
   FVR1479F
  <u>.</u>
  Gaps
  and/or
   and
  0
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RESULT 49 AEF40118/c

AEF40118;

AEF40118 standard; DNA;

22

ВP

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                                   S
   CC cells in which both alleles of a gene are modified, comprising modifying CC one allele by insertion or replacement by a cassette having an CC expressible selectable marker and modifying other allele by CC recombination, of a promoter replacement fragment with a heterologous CC promoter, so that expression of the second allele is regulated by the CC promoter. (MI) is useful for constructing a strain of diploid fungal CC cells in which both alleles of a gene are modified. The diploid fungal CC cells in which both alleles modified are useful for identifying a gene that CC is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene CC that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus dasase. (MI) is useful for identifying a compound which modulates the CC activity of a gene product, preferably enzymatic activity, carbon CC compound catabolism, biosynthetic, transporter, transcriptional, CC translational, signal transduction, DNA replication and cell division CC ability to inhibit growth or proliferation of C. albicans cells and for CC treating infection by C. albicans. The present sequence is that of a PCR CC primer used in the method of the invention. Note: The sequence data for CC this patent is not represented in the printed specification but is based CC on sequence information supplied to Derwent by the European Patent Office
  Matches
  Query Match
Best Local
   Sequence
  Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
  Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal; PCR; primer;
   The invention relates to constructing (M1) a strain of diploid
  Claim 36; SEQ ID NO 5411; 167pp + Sequence Listing; English.
   WPI; 2002-566694/60
  Roemer T,
   29-DEC-2000; 2000US-0259128P
20-FEB-2001; 2001US-00792024
22-AUG-2001; 2001US-0314050P
  26-DEC-2001; 2001WO-US049486
   Candida albicans.
   Candida albicans GRACE strain PCR
  (ELIT-)
                                     38
 19
  l Similarity
16; Conserv
  ELITRA PHARM INC.
                       TAGTGCCATCCCCTTGG 54
   20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
TAGTGCCATCCCATTGG
  Jiang B,
  Conservative
  94.1%;
  Boone C,
  6.5%;
 w
  0
  Score 15.4;
Pred. No. 3
  Bussey H, Ohlsen
  Mismatches
   primer SEQ ID
  38;
  DB 1;
  ۲.
   ö
  Length
  <u>7</u>
  Indels
   5411
  0
  Gaps
  88.
  of
  0
```

```
ARZAGULT 50
ARZAGOA9/4
ID ARZAGOA9/4
XX ARZAGOA9/4
AC ARZA
  문
  ई
  Matches
   Query Match
Best Local
  The invention relates to a method for the recombinant production and purification of a human vascular endothelial growth factor (VEGF) protein encoded by a polynucleotide originally obtained from human hepatocarcinoma tissue. The method involves the inducible expression of the VEGF protein in Escherichia coli, followed by protein extraction and affinity chromatography to yield high purity VEGF protein. The invention also relates to the isolation and cloning of the hepatocarcinoma-associated VEGF polynucleotide, and to the use of the recombinantly expressed VEGF protein or variants and derivatives thereof in the diagnosis or treatment of hepatocarcinoma. Sequences AEF40119-AEF40119 represent human VEGF PCR primers which are specifically claimed for
  Homo
  tumour; inhibition; antisense oligonucleotide; phosphorothioate;
metastasis; antitumour; antiproliferative; angiogenesis; apoptosis;
tumour cell migration; proliferative disease; atherosclerosis; psoriasis;
  Chinese Han nationality vascular endothelial growth factor recombinant gene, useful in hepatic carcinoma clinical diagnosis and treatment.
   Protein production; protein purification; tumor marker; cytostatic; diagnosis; vascular endothelial cell growth
   Human hepatocarcinoma-associated VEGF
  23-MAR-2006
   Synthetic
  Human foetal
   AAZ48049 standard; DNA; 20
   Sequence
   Claim 2; Page 3; 10pp; Chinese
  WPI; 2005-726682/75
   Hu J,
  02-DEC-2003; 2003CN-01116861.
  02-DEC-2003; 2003CN-01116861.
   22-JUN-2005.
  Ното варіелв
  PCR; primer; 88.
  sapiens.
   149
  Yang J;
  Similarity
  22
  CTTCTCCTTCTGCCATG 165
   the hepatocarcinoma-associated VEGF polynucleotide.
   6.5%;
ilarity 94.1%;
Conservative
  BP; 7
   5'-UTR IGF-II antisense oligonucleotide GTI4009
  (first
   (first
  insulin-like
   Location/Qualifiers
   A;
  entry)
   entry)
   5 C; 9
  თ
   9: Score 15.4; D
9: Pred. No. 36;
0; Mismatches
   growth factor II; cell growth modulation;
   G; 1 T; 0 U; 0 Other;
   PCR
  primer
  DB 1;
  1;
  Length 22;
   Indels
   hepatocarcinoma; factor; VEGF;
  0
  Gaps
   protein
  0
```

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밁
   S
  RESULT
   Matches
   Query Match
Best Local
  (i) the autocrine and paracrine functions of IGF-II which promote tumour induced angiogenesis and tumour cell migration; and (ii) autocrine growth of tumour cells, possibly including induction of apoptosis. (I) may also function as ribozymes. (I) are used for inhibiting growth and metastasis of mammalian tumours, also: (i) for treatment of other proliferative diseases, e.g. atherosclerosis and psoriasis; (ii) when labeled, as probes for detecting IGF-II mRNA; and (iii) as molecular weight markers. (I) that bind to the 5'-untranslated region of the foetal transcript (the form present in tumour cells) should not affect the adult transcript. They are effective against drug-resistant tumours
   FAA: FANCIP1; Fanconi anemia protein of complementation group A; interactor; antitumor; anticytopenia; defective DNA repair; gene therapy; cell-cycle aberration; tumorigenesis; tumor progression; PCR primer; ss.
   08-JAN-2001
  AAA71802 standard;
   Sequence 20 BP; 5 A; 4 C; 11 G; 0 T; 0 U; 0 Other;
  oligonucleotides (I) complementary to the mRNA of human insulin-like growth factor II (IGF-II). The present invention also describes a method for inhibiting growth or metastasis of mammalian tumours by administering (I). (I) have antitumour and antiproliferative activity, and inhibits:
  Antisense oligonucleotides against mRNA of insulin-like growth factor II, for treating tumors and other proliferative diseases.
  04-NOV-1999
  modified_base
   FAA FANCIPI
  AAA71802;
  Claim 4;
   Wright JA,
   23-APR-1998;
   23-APR-1999;
   WO9955854-A2
   Unidentified
  AAZ48041 to AAZ48070
   WO200046244-A1
  (GENE-) GENESENSE TECHNOLOGIES
  al Similarity
17; Conserv
  20
  86
  GGCCCCCTCTCATTCTCCTG 117
   Page 18; 72pp; English
  GGCCCCCCCTCTTTCTCCCG
  interactor PCR primer FANCIP1-SP1.
   Young AH,
   Conservative
   (first entry)
   98US-0082791P
  99WO-CA000323
   /*tag= a
/mod_base
/note= "phosphorothicate linkages"
  DNA;
  6.4%;
  represent specifically claimed
  Lee YS;
  20
   <u>,,</u>
   Score 15.2;
Pred. No. 4
   Mismatches
   40;
   DB 1; Length 20;
   °.
   Gaps
   0
```

24-JAN-2000; 2000WO-EP000506.

10-AUG-2000.

05-FEB-1999;

99DE-01004650

```
밁
  S
   #X#X#X#X##X#XDDDDDDDDDDDDDDDDDD
   This invention describes a novel nucleic acid (I) encoding an interactor control the Fanconi anemia protein of complementation group A (FAA), described as FANCIP1. The products of the invention have antitumor and anticytopenia activity. The protein encoded by (I) interacts with FAA, and becomes part of the complex or signal transduction cascade that, when defective, results in Fanconi anemia. (I) is used to express the corresponding polypeptide (II) and this is used to express the corresponding polypeptide (II) and this is used to raise specific antibodies (Ab), or to identify compounds (A) that react with and/or alter regions of (II). Compositions containing (I), vectors or cells that contain (I), (II), Ab or (A) are used for diagnosis of disease associated with defective DNA repair, cell-cycle aberrations, cytopenia, tumorigenesis and/or tumor progression, or predisposition to the disorders, and to treat or prevent the diagnosed diseases, e.g. by gene therapy, Modified forms of (I) are useful as antisense sequences and ribozymes. This sequence represents a PCR primer used in the isolation of the invariance in the reactor protein FANCIP1 which is described in the method of
  Best Local Similarity Matches 17; Conserv
  Query Match
              WPI; 2001-524255/58
  Wakamateu
   08-JUL-1999;
11-JAN-2000;
   07-JUL-2000;
  05-SEP-2001.
  EP1130094-A2
   Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer;
  Human cDNA clone-specific primer, SEQ ID NO: 4477.
   06-NOV-2001
   AAK95232;
   AAK95232 standard; DNA;
  Sequence 20 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 0 Other;
   Disclosure; Fig 4; 33pp; German
  WPI; 2000-524414/47.
  (MULT-) MULTIGENE BIOTECH GMBH
   'n
   nucleic acid encoding Fanconi anemia protein interactor, useful diagnosis, treatment and prevention of tumors and cytopenia.
  sapiens
  103
  20
  Nishikawa T,
   HELIX RES INST.
  ccrcrcarrerecrecrece 122
  Ą,
   Conservative
   99JP-00194486.
2000JP-00118774.
2000JP-00183765.
   2000EP-00114089.
  (first entry)
  Sugiyama
   6.4%;
85.0%;
  Isogai T,
a T, Nagai
  Hoehn H,
  20
  0;
  Score 15.2;
Pred. No. 4
   Mismatches
  Hayashi K,
K, Kojima
  Herterich
   40;
  DB
  Ś
  1;
  Ishii S,
  ω
--
  Otsuki
  Length 20;
  Indels
  Kawai Y;
T, Koga
  0
  Ħ;
   Gaps
  e.g.
  0
```

```
RESULT 53
ABL45325/c
         밁
   á
  The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified and lateral directions; (f) the mixed clones are cultured and the resultant cultures are amplified by using the above primer; (g) signals
   Query Match
Best Local :
   Matches
  clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA ilbraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a primer used to amplify a human cDNA clone provided in the invention
   (RIKA )
(GENO-)
  Claim 6; Page 52; 528pp; Japanese
   WPI; 2002-144136/19.
   20-NOV-2001.
  JP2001321190-A
   11-APR-2002
  ABL45325;
  ABL45325
  Sequence
  10-MAR-2000;
   12-MAR-2001; 2001JP-00068285
   Homo sapiens.
  Human; chromosome
   Human chromosome 21q22.1 PCR primer SEQ ID NO:2369
   Example 18; Page 134; 1380pp + Sequence Listing; English
   830 Primers useful for synthesizing full length cDNA clones and their use
   in genetic
   primer;
  141
  20
   l Similarity
17; Conserv
   RIKAGAKU KENKYUSHO.
GENOTEX YG.
  TGCTCCCCCTTCTCCTTCTG 160
  genome clones.
  standard; DNA;
  20 BP; 9 A; 4 C; 7
  TGCTCCTGCTTCTGCTTCTG 1
   manipulation.
   Conservative
  2000JP-00066716
   (first entry)
  relates to
  1p36-35; chromosome 21q22.1; genetic analysis; genome;
  6.4%;
  20
  primers
   0
  G; 0 T; 0
   Score 15.2;
Pred. No. 40
   Mismatches
  for synthesising
  U; 0 Other;
   40;
  DB 1;
   ω
••
  Length
  full length
  20;
   0,
  CDNA
   Gaps
  ö
```

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밁 5

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RESULT
ABV7223
   Query Ma
Best Loc
Matches
                               Matches
  Query Match
Best Local
   ABV7223-37 represent antisense oligonucleotides which are targeted to human insulin-like growth factor II (IGF-II) foetal mRNA. The oligonucleotides are complementary to the 5 untranslated region consisting of exons 4, 5 or 6 of human fetal IGF-II mRNA. The antisense oligonucleotides of the invention are useful for inhibiting the growth human tumour, where a chemotherapeutic agent is also administered. They are also useful for treating proliferative disorders including various forms of cancers, psoriasis, and atherosclerosis, as hybridisation prob to detect the presence of IGF-II mRNA in mammalian cells, and as molecular weight markers
   are detected from the amplified products; (h) the clones in the multiwell plates are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1936-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21922-1, which are specifically claimed for use in the present invention
   2231/c
ABV72231
  1 54
1231/
  tumour growth; proli
atherosclerosis; ss.
  Sequence 20 BP; 4 A;
  Sequence
  Novel antisense compounds targeted to insulin-like growth factor mRNA, useful for inhibiting tumor growth and metastasis in mammals.
  WPI; 2002-634739/68
   (GENE-) GENESENSE TECHNOLOGIES
   23-APR-1998;
  22-APR-1999;
   09-JUL-2002.
   US6417169-B1
  Homo
   Antisense oligonucleotide;
  Antisense oligonucleotide targeting human IGF-II foetal mRNA.
  05-DEC-2002
   ABV72231;
  Match
   ocal
  sapiens
98
  20
   16
   1 Similarity
                                 Similarity
17; Conserv
   GGCAGATCCCTCATGAATGG
GGCCCCCTCTCATTCTCCTG
  GGCAGAGTCCTCATGAATCG 1
  20
  standard; DNA;
  BP; 5
  Young
   Conservative
                                 Conservative
   10;
  (first
  98US-0082791P
  proliferative disorder; cancer;
  9905-00295593
   40pp;
  Þ
  AH,
  entry)
  6.4%;
85.0%;
  6 C; 5
  6.4%;
  4 C; 11 G; 0
   English.
  Lee
  20
  ВP
   SY
   insulin-like growth
   0
                                 0;
  G; 5 T; 0 U; 0 Other;
  Score
Pred.
  Score 15.2;
  Pred. No.
   35
   INC
   Mismatches
                               Mismatches
  T; 0 U;
   No. 40;
  40
  B
  0 Other;
  ₽B
  1;
  1;
   ω
--
                                 ω
--
  psoriasis;
   factor II; IGF-II;
  Length 20;
  Length
                                 Indels
   Indels
   0
                                 0
   antisense
   Gaps
                                 Gaps
   probes
  They
   of.
   0
                                 0
```

5

primarily

regulates

hormone responsiveness

and oxidative

stress

responses

```
ABL94297
ID ABL94
AC 
  밁
                       Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha) gene, which inhibit its expression. The antisense oligonucleotides were designed to target different regions of the human and/or mouse C/EBP alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels by quantitative real-time PCR. The C/EBP family of proteins are a family of transcription factors which regulate the expression of a wide range of genes that control normal tissue development, cellular function, cellular proliferation and functional differentiation. C/EBP beta (also known as C/EBPZ, LAP, TCPS, CRP2, NFIL6, IL69BP, NF-M, AGP/EBP and Apc/EBP)
   Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EPB2 human; LAP; TCF5; CRP2; NFIL6; IL6DB; NF-M; AGP/EBP; Apc/EBB; transcription factor; tissue development; cellular function; proliferation; differentiation; hormone responsiveness; oxidative stress response; IL-6 signalling mediator; interleukin-6; carbohydrate metabolism; immunity; Th1 response; female fertility; gluconeogenesis; ovarian; cancer; tumour formation; type II; diabetes; infection; inflammation; expression inhibition; phosphorothioate;
  modified_base
  modified_base
  ABL94297
   14-JUN-2000; 2000US-00593711
   US6271030-B1
   modified_base
  Human/mouse
  ABL94297;
  Claim 1;
   WPI; 2002-214451/27.
  14-JUN-2000; 2000US-00593711
  07-AUG-2001.
   Homo sapiens
   29-JUL-2002
  (ISIS-) ISIS PHARM INC
  musculus
  antisense compound targeted to nucleic acids encoding human og CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro iting expression of human or mouse C/EBP beta in cells/tissues
  ВP
   20
   standard; DNA; 20
   Col 43-44;
  GGCCCCCGCTCTTTCTCCCG
   oligonucleotide;
  Butler MM,
  C/EBP beta antisense oligonucleotide,
   (first entry)
  /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE)
cytosines are 5-methylcytosine"
   cytosines
   /note= "2'-methoxyethyl (2'-MOE)
  /*tag=
   Location/Qualifiers
   note= "Phosphorothicate linkages"
   /*tag=
  mod_base= OTHER
  69pp;
  .20
  _base= OTHER
  English
   股
   nucleotides.
   nucleotides.
   SEQ
  cells/tissues.
   ID:63
   A11
   A11
  9
  ń
  ν
  for
```

MOE

```
RESULT 56
  Matches
  Query Match
   modified_base
  and is a mediator of II-6 (interleukin-6) signalling. C/EBP beta is thought to be involved in carbohydrate metabolism, immunity, the Th1 response, female fertility and gluconeogenic pathways. C/EBP beta is expressed in the liver, lung, spleen, kidney, brain, and testis, with the highest expression found in the lung. It is also expressed at a higher level in malignant ovarian tissue compared with normal ovarian tissue, and its expression in pancreas is upregulated in response to chronically elevated levels of glucose, indicating that it is involved in the impairment of insulin secretion in type II diabetes. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with C/EBP beta expression, such as cancer (particularly ovarian cancer), tumour formation, diabetes (particularly type II diabetes), infection, or inflammation
  modified_base
  modified_base
   carbohydrate metabolism; immunity; Th1 response; female fertility gluconeogenesis; ovarian; cancer; tumour formation; type II; diab infection; inflammation; expression inhibition; phosphorothioate; antisense oligonucleotide; ss.
  transcription factor; tissue development; cellular function; proliferation; differentiation; hormone responsiveness;
(ISIS-) ISIS
  14-JUN-2000; 2000US-00593711.
  14-JUN-2000;
   07-AUG-2001
   US6271030-B1
   Mus musculus
   prollieration; watterness, signalling mediator; interleukin-6 oxidative stress response; IL-6 signalling mediator; interleukin-6 oxidative stress response; female fertility;
   Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EPB2; LAP; TCF5; CRP2; NFIL6; IL6DBP; NF-M; AGP/EBP; Apc/EBP;
  Mouse C/EBP beta phosphorothioate antisense oligonucleotide,
  29-JUL-2002
  ABL94414;
  ABL94414 standard; DNA; 20
   Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;
   Local
  133 GAGACACCTGCTCCCCCTTC 152
   _
  17;
  Similarity
  GCGACAGCTGCTCCACCTTC 20
  Conservative
PHARM INC
  2000US-00593711
  (first entry)
  /note= "2'-methoxyethyl (2'-MOE) nucleotides.
cytosines are 5-methylcytosine"
  cytosines are 5-methylcytosine"
  /*tag= b
/mod_base= OTHER
/mote= "2'-methoxyethyl (2'-MOE) nucleotides.
  Location/Qualifiers
  /note=
  *tag=
  mod_base= OTHER
  *tag= a
   85.0%;
   base= OTHER
  "Phosphorothicate linkages"
  റ
  ВP
   0
   Pred.
   Score 15.2;
Pred. No. 4
  Mismatches
  40;
  formation; type II; diabetes;
   DB 1; Length 20;
  u
T
   Indels
  interleukin-6;
  0
   SEQ ID:180.
  A11
   A11
  Gaps
  ń
   ń
  MOE
  MOE
   0
```

Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 U; 0 Other;

0;

8 5

```
CC to the human or mouse CCAAP(enhancer-binding protein alpha (C/EBP alpha)

CC gene, which inhibit its expression. The antisense oligonucleotides were

CC designed to target different regions of the human and/or mouse C/EBP

CC alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels

CC of transcription factors which regulate the expression of a wide range of

CC genes that control normal tissue development, cellular function, cellular

CC proliferation and functional differentiation. C/EBP beta (also known as

CC C/EPB2, LAP, TCP5, CRP2, NFIL6, IL6DBP, NF-M, ACP/EBP and Apc/EBP)

CC primarily regulates hormone responsiveness and oxidative stress responses

CC and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is

CC expressed in the liver, lung, spleen, kidney, brain, and testis, with the

CC expressed in the liver, lung, spleen, kidney, brain, and testis, with the

CC injhest expression found in the lung. It is also expressed at a higher

CC level in malignant ovarian tissue compared with normal ovarian tissue,

CC elevated levels of glucose, indicating that it is involved in the

CC officients associated with C/EBP beta is

CC conditions associated with C/EBP beta is

CC conditions associated with C/EBP beta is

CC conditions associated with compared with normal ovarian tissue,

CC officients of succession in type II diabetes. The oligonucleotides

CC conditions associated with C/EBP beta expression, such as cancer

CC conditions associated with C/EBP beta expression, such as cancer

CC conditions associated with C/EBP beta expression, such as cancer

CC conditions associated with C/EBP beta expression, such as cancer

CC conditions associated with C/EBP beta expression, such as cancer

CC conditions associated with C/EBP beta expression, such as cancer
   Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)
   Example 17; Col 51-52; 69pp; English
   Novel antisense compound targeted to nucleic acids encoding human or mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro finhibiting expression of human or mouse C/EBP beta in cells/tissues.
  WPI; 2002-214451/27
   Monia BP,
   Butler MM,
   Wyatt J;
  human or
n vitro for
```

```
RESULT 57
ABZ59163/c
ID ABZ591
XX ABZ591
XX ABZ591
XX Nucleo
XX Nucleo
XX Nucleo
XX AChE;
KW AChE;
KW AChE;
KW AChE;
KW AChE;
KW WO2003
XX WO2003
PN WO2003
XX PD 09-JAN
XX Y
PF 23-MAY
XX PF 23-MAY
XX PF 24-MAY
XX PR 24-MAY
  밁
  Ś
   Matches
  Query Match
   24-MAY-2001; 2001IL-00143379
   23-MAY-2002; 2002WO-IL000411.
   09-JAN-2003
   WO2003002739-A1
   Rattus
  Synthetic
  AChE; acetylcholinesterase; neuroprotective; relaxant; vasotropic; anticonvulsant; neuroleptic; gene therapy; antisense; rat; ss.
   Nucleotide sequence of antisense oligo r-invEN102
   28-APR-2003
   ABZ59163;
   ABZ59163 standard; DNA; 20
   (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM
  Local
  136 ACACCTGCTCCCCCTTCTCC 155
   đs
  Н
  l Similarity
17; Conser
   (first entry)
   Conservative
   6.4%;
   ВP
  ٥,
  Score 15.2;
Pred. No. 4
  20
   Mismatches
  40;
  DB 1;
  <u>ب</u>
  Length 20;
   Indels
  0;
  Gaps
```

Soreq H;

```
ACC48831/
ID ACC4
XX
AC ACC4
AC ACC4
AC Camp
DE Camp
XX
INfe
KW Drim
XX
WO20
CAMP
DN WO20
XX
OS Camp
DN WO20
XX
OS Camp
OS Cam
  RESULT 58
  片
   ঠ
   Query Match
Best Local
   abnormalities, e.g. myasthenia gravis, Eaton-Lambert disease, muscular dystrophy, amyotrophic lateral sclerosis, post-traumatic stress disorder (PTSD), multiple sclerosis, dystonia, post-stroke sclerosis, post-injury muscle damage, excessive re-innervation, post-surgery paralysis of unknown origin, or post-exposure to AchE inhibitors. The composition is also useful for improving stamina in physical exercise or in decreasing muscle fatigue. This is also useful for treating conditions affecting the central nervous system, where the BBB would normally impede their
  prevention of a progressive neuromuscular disorder, for improving stamina, and/or for use in chronic muscle fatigue. This composition facilitates the passage of compounds through the blood-brain barrier (BBB). It is useful for treating and/or preventing a progressive neuromuscular disorder, particularly a disorder associated with an excess of AChE mRNA or protein, an excess of acetylcholinesterase 'readthrough' variant or isoform (AchE-R) mRNA, or impairment of cholinergic transmission. The composition is also useful for treating muscle preventing a progressive neuromuscular disorder involving muscle distortion, muscle re-innervation or neuromuscular junction (NNJ)
  New composition comprising an the antisense oligodeoxynucleotide hEN101, useful for treating or preventing a progressive neuromuscular disorder, e.g. myasthenia gravis, Eaton-Lambert disease, muscular dystrophy or
  04-SEP-2001;
  03-SEP-2002; 2002WO-EP009857
  Campylobacter jejuni
  Infection; primer; 88
   Campylobacter jejuni wlaK gene PCR primer LS16.
   delivery, e.g. ischaemia, brain tumours, hypoxia, epilepsy, and schizophrenia. The present sequence represents a rat AchE mRNA
   The invention relates to a pharm antisense oligonucleotide hEN101
  Example; Page 37; 84pp; English.
                                  Carlton RM,
   13-MAR-2003
   WO2003020958-A2
  11-AUG-2003
   ACC48831;
   ACC48831 standard; DNA;
  Sequence
  WPI; 2003-210276/20
  (acetylcholinesterase) mRNA. The composition is for the treatment and/or prevention of a progressive neuromuscular disorder, for improving
  (EXPO-) EXPONENTIAL BIOTHERAPIES
   102
  20
  Similarity
   20
   CCCTCTCATTCTCCTGCTCC 121
  oligo
  classification; glycosylation; wlak gene; antibacterial; PCR;
  BP;
  Conservative
  2001EP-00307499
  (first entry
  7
  ð
  0
   85.0%;
  C; 13
   20
   BP
   pharmaceutical composition, which PEN101 that inhibits the human AChE
  Score 15.2; D
Pred. No. 40;
0; Mismatches
  0,
  Ģ
  0
  T;
  0
  U;
   DB 1;
  0
   Other;
  ω
••
  Length 20;
   Indels
  anxiety or
  <u>,,</u>
   comprises
  Gaps
  0
```

```
SXCCCCCCCCCCCCCXSXATTTTXX
   Producing progeny of bacteriophages having genes encoding proteinaceous molecules allowing binding of the phage to Campylobacter spp, by contacting phage with Campylobacter mutant devoid of component present in the contacting phage with Campylobacter mutant devoid of component present
```

in

WPI; 2003-300898/29.

Example 1; Page 26; 66pp; English.

The present sequence is PCR primer LS16 for the Campylobacter jejuni wlak gene. LS16 was used in the construction of an insertional knockout mutant of the wlak gene of C. jejuni NCTC 1168. Mutagenesis of the gene was shown to disrupt binding by SBA lectin, and a role in protein glycosylation was indicated. The invention relates to methods for the detection, diagnosis and treatment or prevention of Campylobacter infections, especially in poultry. A method is provided for producing or selecting for progeny of phage comprising a nucleic acid encoding a protein allowing targeting or binding of the phage to Campylobacter spp. This involves contacting a phage library with a Campylobacter spp. mutant devoid of a surface component present in the wild-type, e.g. a glycosylated component. The phage can be used in the classification of a C. jejuni variant, and in a pharmaceutical composition for treating a Campylobacter infection

Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Matches Query Match Local l Similarity 17; Conserv Conservative 6.4**%**; 85.0**%**; <u>,,</u> Score 15.2; Pred. No. 40; DB 1; Length 20 Indels <u>,,</u> 0

밁 S 117 GCTCCCACTCTTGCATGAGA 136 20 GCTCCCACACTCACATGAGA 1

RESULT 59
ADG47261/c
ID ADG472
XX ADG472
XX ADG472
XX INSULI
KW Gene t
XX INSULI
KW Gene t
XX HOMO S
PN US2002
XX HOMO S
XX US2002
YN INSULI
YN IN 11-MAR-2004 ADG47261 standard; DNA; 20 (first entry) Β₽

Human IGF-II antisense oligonucleotide #GT14009.

Insulin like growth factor II; IGF-II; tumour; metastasis; cytostatic; gene therapy; antisense; human; ss.

Homo sapiens

US2002187954-A1.

17-APR-2002; 2002US-00125181

23-APR-1998; 22-APR-1999; 98US-0082791P. 99US-00295593.

GENESENSE TECHNOLOGIES

Wright JA, Young AH, Lee YS;

WPI; 2004-040950/04.

Inhibiting the growth of a human tumor by administering antisense oligonucleotide of twenty to one hundred nucle ering a cytostatic nucleotides.

Claim 7; SEQ ID NO 9; 41pp; English.

The present invention relates to oligonucleotides complementary to insulin like growth factor II (IGF-II) genes which modulate tumour growth in mammals. The invention is useful for inhibiting the growth the growth or

```
RESULT 60
ADL32444/c
ID ADL32
XX ADL32
AC ADL32
XX DT 20-MJ
DT 20-MJ
DT 20-MJ
DT 01igc
XX Oligc
XX Oli
밁
                                   ई
  밁
  δ
  ន្តន្តន្ត
   Query Match
Best Local (
  Matches
  Matches
   Query Match
  L32444/c
  Ota T, Ni
Wakamatsu
  This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that rare potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This oligonucleotide sequence is a human clone specific PCR primer used in an exemplification of the
  the metastasis of tumour. I growth factor II (IGF-II )
   Sequence 20
  Example 18;
  New oligonucleotide primers (830 cDNAs) useful
  WPI; 2004-204755/20
   11-JAN-2000;
02-MAY-2000;
  08-JUL-1999;
   07-JUL-2000;
  EP1396543-A2
  Homo sapiens
  human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; PCR; primer.
  Clone specific
   20-MAY-2004
  ADL32444;
   ADL32444 standard; DNA; 20
  Sequence
   (REAS-)
   10-MAR-2004.
   Local
   141
  20
   98 GGCCCCCTCTCATTCTCCTG 117
  20
   human
  Nishikawa T,
   Similarity
   RES ASSOC BIOTECHNOLOGY
   Similarity
   TGCTCCCCCTTCTCCTTCTG 160
  GGCCCCGGCTCTTTCTCCCG 1
  20
  ۶
  99JP-00194486.
2000JP-00118774.
2000JP-00183865.
2000EP-00114089.
   BP; 9
  SEQ ID NO 4477;
  Conservative
  BP; 5
   Conservative
   CDNAs.
   2003EP-00025638.
  (first entry)
  Sugiyama
   PCR primer to amplify human full length cDNA SeqID 4477.
  A,
   A; 4 C; 7 G; 0 T; 0 U; 0 Other;
   85.0%;
   6.4%;
85.0%;
   4 C; 11
  Isogai T,
na T, Nagai
  The present sequence is human insulin like antisense oligonucleotide.
   BP
  1340pp; English
   0,
   <u>.</u>
   Score 15.2;
Pred. No. 4
   Score 15.2;
Pred. No. 4
  G; 0 T; 0 U; 0 Other;
   Mismatches
  Mismatches
  Hayashi K,
K, Kojima
   40
  DВ
  DB 1;
  ູດ
  Ishii S,
S, Otsuki

    Length 20;

   ω.
   س
  for
  Length
   Indels
   Indels
  synthesizing
  Kawai Y;
T, Koga
  20
  Koga
   0
   <u>..</u>
   Gaps
  H;
   Gaps
   0
   0
```

Query Match Best Local Similarity

6.4**%**; 85.0**%**;

Score 15.2; Pred. No. 40;

Length

20;

Sequence

20

B₽;

N

A;

7 C; 3 G; 8 T; 0 U;

0 Other; B 1;

```
RESULT 61
ADO51535
ID ADO51
  The invention relates to compounds, compositions and methods for modulating the expression of serine/threonine kinase 16 (also called PKL12, transforming growth factor reta-stimulated factor 1; TSP1 and myristylated and palmitylated serine/threonine kinase; MPSK). The composition comprise antisense oligonucleotides targeted to PKL12 gene. The compound, composition and methods are useful for treating a disease or condition associated with serine/threonine kinase 16, such as a hyperproliferative disorder. They are also useful in research and a superproliferative disorder. They are also useful in research and a superproliferative disorder.
diagnostics for modulating the expression of serine/threonine kinase 16 The invention is also useful in gene therapy. The present sequence is a antisense oligonucleotide targeted to human serine/threonine kinase 16 DNA. This sequence is used to illustrate the method of the invention.
  New compounds, particularly oligonucleotides targeted to a nucleic acid encoding serine/threonine kinase 16, useful for treating diseases associated with serine/threonine kinase 16, e.g. hyperproliferative
   transforming growth factor-beta-stimulated factor 1; TSF1; myristylated and palmitylated serine/threonine kinase; MPSK; hyperproliferative disorder; gene therapy; human; antisense;
   Example 15;
   WPI; 2004-389186/36
   modified_base
   modified_base
   Serine/threonine kinase 16; PKL12;
   ADOS1535 standard; DNA; 20 BP
  16-NOV-2002;
  16-NOV-2002;
  20-MAY-2004
  US2004097444-A1
  modified_base
   Synthetic
   Homo sapiens.
  Human serine/threonine kinase 16 antisense oligo, ISIS 220609.
  12-AUG-2004
   (ISIS-) ISIS
  SEQ ID NO
   growth factor beta-stimulated factor 1; TS and palmitylated serine/threonine kinase;
  2002US-00298953
  PHARM
  2002US-00298953
  (first entry)
   /mod_base=
/note= "2'-
16. .20
   residues are
   Location/Qualifiers
   note= "Phosphorothioate backbone in which all cytidine esidues are 5-methylcytidines"
   *tag= a
   _base= OTHER
e= "2'-methoxyethyl (2'-MOE)
   _base= OTHER
   26; 36pp;
   ი
  88.
  -methoxyethyl
  OTHER
  English.
  (2'-MOE)
  bases"
   bases"
   an
```

```
RESULT 62
ADP12005/c
ID ADP120
XX ADP120
XX ADP120
XX Eransp
XW transp
XW transp
XW inflam
XX Homo s
PN W02004
XX 21-MAY
XX 21-MAY
XX 21-MAY
XX 24-APR
PR 24-APR
PR 24-APR
PR 20-DEC
XX Wohlge
PI Rosenb
XX WPI; 2
XX The pr
CC reject
PT the gent
XX The pr
CC reject
PR Claim
XX The pr
CC reject
PR CC indivi
CC indivi
CC an ind
CC of all
XX Sequen
SQ Sequen
   CC The present invention relates to diagnosing or monitoring transplant CC rejection, e.g. cardiac or kidney transplant rejection, in an individual CC comprises detecting the expression level of one or more genes. The CC methods, system and kits are useful in diagnosing or monitoring CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic CC islet, lung, bone marrow or stem cell transplant rejection, in an CC individual. The method is also useful in assessing the immune status of CC an individual. The methods are also useful in diagnosing and monitoring CC diseases that involve the immune system, e.g. rheumatoid arthritis, CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or CC viral, bacterial or fungal infection. The present sequence represents a CC primer for a 50 mer oligonucleotide marker for diagnosis and monitoring CC of allograft rejection and other disorders.
   8
  밁
   Ś
밁
  Query Match
Best Local S
  Matches
   Matches
  Claim 58; SEQ ID NO 2014; 1762pp; English.
  pancreas, pancre
  Diagnosing
   WPI; 2004-400724/37.
   24-APR-2002;
20-DEC-2002;
   24-APR-2003; 2003WO-US012946.
  transplant rejection; immune system; inflammatory bowel disease; multiple
  Set 2 right PCR primer for marker probe #111.
   Sequence 20
  Rosenberg S;
   Wohlgemuth J,
  WO2004042346-A2
   ADP12005;
   ADP12005 standard;
   (EXPR-)
   Homo sapiens
   12-AUG-2004
   134
   110
20
  17;
  μ
  17;
  Similarity
   EXPRESSION DIAGNOSTICS
   AGACACCTGCTCCCCCTTCT 153
  TTCTCCTGCTCCCACTCTTG 129
AGACCCCTCCTTCCCCTTCT 1
   ng or monitoring transplant rejection, e.g. heart, kidney, liver pancreatic islet, lung, bone marrow or stem cell transplant n, in an individual, comprises detecting the expression level of
  Conservative
   Conservative
  BP; 6 A; 1 C; 11 G; 2 T;
   2002US-00131831.
2002US-00325899.
  (first entry)
  Fry K,
   DNA;
  6.4%;
  Woodward R,
   20
   В₽
   0;
   0; Mismatches
   Score 15.2;
Pred. No. 40;
   INC
  Mismatches
  Ly N,
  0 U;
   rheumatoid arthritis;
sclerosis; HIV; AIDS;
  DB 1;
   0 Other;
   Prentice J,
   ω
--
  ω
••
  Length
   Indels
  Indels
  Morris
   lupus;
ss; primer
  0,
  0
  3
  Gaps
   Gaps
   liver,
   0
```

RESULT 63 ADP82177/c

```
0
   RESULT 64
ADP82163
 용
   Ś
  Best Loc
Matches
  Query Match
   The present sequence is directed to antisense oligonucleotides targeted to DR1-associated protein 1 [also known as DRAP1 and negative cofactor 2 alpha (NC2-alpha)] and which modulates to the expression of DR1-associated protein 1. The invention is useful for treating a disease or condition associated with DR1-associated protein 1 such as a developmental disorder. The present sequence is human DR1-associated protein 1 target oligonucleotide. This sequence is used in the
   New compounds, particularly oligonucleotides targeted to a nucleic acid encoding DR1-associated protein 1, useful for treating diseases associated with DR1-associated protein 1, e.g. developmental disorders.
   developmental disorder; therapy;
phosphorothicate backbone; ss.
   Human DR1-associated protein 1 antisense oligonucleotide ISIS #171311.
  26-AUG-2004
  ADP82163;
  Sequence 20
  DR1-associated protein 1; DRAP1; negative cofactor 2 alpha; NC2-alpha; developmental disorder; therapy; human; ss.
          modified_base
   Homo sapiens
Synthetic.
   DR1-associated protein 1; DRAP1;
  ADP82163
  exemplification of the invention.
  Example 15;
  WPI; 2004-440383/41
  Chiang
   10-DEC-2002; 2002US-00317279
   10-DEC-2002; 2002US-00317279.
  10-JUN-2004
   Homo sapiens
  Human DR1-associated protein 1 target oligonucleotide
  26-AUG-2004
   ADP82177 standard; DNA; 20 BP
   US2004110703-A1
  (ISIS-) ISIS PHARM INC.
   Local
   20
  z,
   l Similarity
17; Conserv
   CATTCTCCTGCTCCCACTCT 127
   standard;
  CATCCTCCTGCTCCGAGTCT
  Dobie
  SEQ ID NO 56; 33pp; English.
  BP; 6 A; 3 C; 9 G; 2 T;
  Conservative
  (first entry)
   (first entry)
/*tag=
                      Location/Qualifiers
  Š
            . 20
   DNA;
   6.4%;
85.0%;
   20
   0,
   Score 15.2; D
Pred. No. 40;
0; Mismatches
   μ
  human;
   negative cofactor 2
   0
  ;
   antisense;
   0 Other;
  DB
   ۲.
  ω
--
   Length
  Indels
  20;
  0
  Gaps
  acid
```

```
AEC34439/C
ID AEC344
XX AEC344
XX AEC344
XX AEC344
XX GYOST
CYCOST
XX GYCOST
XY GYCOST
   밁
  S
  Query Match
Best Local :
  Matches
   The present sequence is directed to antisense oligonucleotides targeted to DR1-associated protein 1 (also known as BRAP1 and negative cofactor; alpha (NC2-alpha)) and which modulates to the expression of DR1-associated protein 1. The invention is useful for treating a disease or condition associated with DR1-associated protein 1 such as a developmental disorder. The present sequence is human DR1-associated protein 1 antisense oligonucleotide. This sequence is used in the exemplification of the invention.
  ss; primer;
cytostatic;
  New compounds, particularly oligonucleotides targeted to a nucleic acid encoding DRI-associated protein 1, useful for treating diseases associated with DRI-associated protein 1, e.g. developmental disorders.
  Human EGFR regulatory region SNP detection primer SEQ ID NO:10.
   17-NOV-2005
  AEC34439 standard; DNA;
                              01-MAR-2005; 2005WO-US006559.
  15-SEP-2005.
   WO2005085473-A2
  AEC34439;
  Sequence 20 BP; 2 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
   Example 15; SEQ·ID NO 42; 33pp; English.
  Chiang M,
   10-DEC-2002;
  10-DEC-2002; 2002US-00317279.
  10-JUN-2004.
  US2004110703-A1.
   modified_base
  modified_base
  (ISIS-) ISIS PHARM INC
   Local
   Bapiens
   2004-440383/41
  108 CATTCTCCTGCTCCCACTCT 127
  1 CATCCTCCTGCTCCGAGTCT 20
   Similarity
   Dobie KW
  PCR; Epidermal growth factor receptor; EGFR; neoplasm; polymorphism; diagnostic.
  Conservative
   2002US-00317279
   (first entry)
   /*tag= a
/mod_base= OTHER
/note= "2' -metho:
16. .20
  /note= "Phosphorothioate backbone where all cytidines
5-methyl cytidines"
   note= "2'
   *tag= c
  mod_base= OTHER
  6.4%;
85.0%;
  base= OTHER
   20
  ВP
   ; Score 15.2; DI
; Pred. No. 40;
0; Mismatches
   -methoxyethyl nucleotides"
  -methoxyethyl nucleotides"
  DB 1; Length 20;
   u
.
  Indels
  cancer,
   0
   Gaps
  are
  N
   0
```

```
The invention relates to a method of evaluating (MI) the potential CC efficacy of an epidermal growth factor receptor (EGFR)-targeting CC therapeutic agent for treating cancer or a disease associated with the CC regulation of EGFR in a patient, comprising determining the sequence of a CC polymorphism in one or both EGFR genes in the patient. Also included are: CC predicting (M2) the clinical prognosis for a cancer patient, comprising CC determining the sequence of a polymorphism in one or both EGFR genes in the patient, comprising CC the patient; evaluating (M3) a patient's risk of toxicity to an EGFR-CC targeting therapeutic agent, comprising determining the sequence of a CC polymorphism in one or both EGFR genes in the patient; predicting the CC expression level of EGFR in a cell, comprising determining the sequence CC at position 216 in one or both alleles of the EGFR gene in the cell, CC where thymine at position 216 in one or both alleles of the EGFR gene in the cell, CC where thymine at position 216 in one or both alleles of the EGFR gene in the cell, CC polymorphism in an EGFR gene locus. (M1) is useful for evaluating the color potential efficacy of EFGR-targeting therapeutic agent, where the EGFR-CC targeting therapeutic agent is an EGFR-tyrosine kinase inhibitor or CC detect single nuclectide polymorphisms (SNPs) in the human EGFR used to
  Example 1; SEQ ID NO 10; 66pp; English
  Evaluating potential efficacy of epidermal growth factor receptor (EGFR)-targeting therapeutic agent for treating cancer or disease associated with dysregulation of EGFR, by determining sequence of polymorphism in
   01-MAR-2004; 2004US-0549069P
   regulatory
  WPI; 2005-630736/64.
  (UYCH-) UNIV CHICAGO
  genes
  3
   region.
  in patient.
   ξ
  Innocenti F;
```

밁 Ś Best Loc Matches Query Match 101 20 17; Similarity CCCCTCTCATTCTCCTGCTC 120 CTCCTCGCATTCTCCTCCTC Conservative 6.4%; ٥, Score 15.2; Pred. No. 4 Mismatches 40; DB 1; <u>ن</u> Length 20; Indels 0 Gaps

0

Sequence

20 BP; 7

A; 1 C; 11

G; 1

Η. ou;

0 Other;

RESULT 66
AAQ08505/c
ID AAQ085 25-MAR-2003 29-MAR-1992 AAQ08505; AAQ08505 standard; DNA; (revised)
(first entry) 21 B₽.

Sequence of 5' probe, complementary to a sequence encoding human interleukin-3 (huIb-3) leader. part оf.

Lymphokine; bone marrow proliferation; cytopenia therapy; ss

Homo sapiens.

WO9001039-A.

14-JUN-1989; 89WO-US002599

08-FEB-1990

20-JUL-1988; 88US-00221699

(IMMV ) IMMUNEX CORP

```
RESULT 67
AAQ10344/c
ID AAQ103
XX AAQ103
XX AAQ103
XX Probe
XX Probe
XX HuIL-3
XX Homo 8
XX Homo 8
XX WO9100
XX WO9100
XX U701
XX U701
XX U701
XX U701
XX I U701
XX U701
XX I MMV
XX I U701
XX I U70
  밁
   ঠ
  Query Match
Best Local S
Matches 17
  amt. of a recombinant human interleukin-3 protein analogue, rhuIL-3, (Asp15,Asp70). The rhuIL-3 analogue has AA SQ in AAR09326. The compsn. may also comprise the N-terminal octapeptide in AAR09327, and a diluent and 1 or more than 1 biological response modifier. The compsn. has a biological specific activity of equal to or more than 4.0 x 10 to the 7 mcg/mg in a human bone marrow proliferation assay, and a binding affinity for human monocyte IL-3 receptors of equal to or more than 4.0 x 10 to the 10 (M to the minus 1). (Updated on 25-MAR-2003 to correct PA field.)
                     Probes were used in the isolation of human II-3, which was then expressed in a modified form, with a mutation in the N-glycosylation sites. The modified II-3 does not result in ulticaria or infiltration of mast cells and lymphocytes into the dermis. It stimualtes granulopoiesis,
  Compans. contg. recombinant non-glycosylated human interleukin-3 - has increased biological activity and binding affinity, for treating
     and lymphocytes into the dermis. It stimualtes granulopoiesis, erythropoiesis and thrombopoiesis in vivo and may used to treat
  Non-glycosylated human interleukin-3 analog proteins - transformed yeast of Saccharomyces cerevisiae which do
  30-JUN-1989;
  30-JUN-1989;
  Example; Page 10; 23pp; English
   Example
   detectable urticaria.
   WPI; 1991-036745/05
  10-JAN-1991
  WO9100350-A.
   Homo sapiens
   neutropaenia;
   huIL-3; urticaria;
  Probe to the
  25-MAR-2003
10-APR-1991
   AAQ10344;
  Sequence
   The inventors claim a pharmaceutical
   Anderson
  (IMMV ) IMMUNEX CORP
   AAQ10344 standard;
   107
  1990-067162/09
   DL,
   20
  l Similarity
17; Conserv
   21 BP;
   ¥,
   TCATTCTCCTGCTCCCACTC 126
   TCCTGCTCCTGCTCCAACTC 1
   Page 7; 18pp;
   Sassenfeld
   Conservative
  (revised)
(first en
   human interleukin-3 gene
   anaemia; thrombocytopaenia;
   Cosman
  89US-00374667
  89US-00374667
  6 A;
  DNA;
   granulopoiesis; erythropoiesis;
  entry)
   3 C;
  6.4%;
85.0%;
   걸
   Ξ
   21
  English.
   10 G;
   Price
   ВP
   0
   Score 15.2;
Pred. No. 39
   2 T; 0 U;
   ş
   Mismatches
   compsn. which contains an effective
  39,
  88.
   DB 1;
   0 Other;
   ω
--
  Length 21;
   Indels
   thrombopoiesis;
   expressed not give
   0;
   Gaps
  γď
   0
```

RESULT 69
AAZ61533/c
ID AAZ615
XX
AC AAZ615

standard;

DNA;

21

ВÞ

AAZ61533; AAZ61533

```
RESULT 68
AAQ42803/c
ID AAQ428
XX Seques

O Seques
   Ş
   ន្តន្តន្ត
밁
   밁
                  S
  Best Loc
Matches
   Matches
  Query Match
Best Local :
   Query Match
   Two oligonucleotides were synthesised, with sequences complementary to selected 5' and 3' sequences of the huIL-3 gene. The 5' probe, complementary to a sequence encoding part of the huIL-3 leader, has the sequence given in AAQ42803. The 3' probe, corresp to a region encoding amino acids 123-130 of the mature protein, has the sequence given in AAQ42804. (Updated on 25-MAR-2003 to correct PN field.)
  Sequence 21
  MGF-interleukin-3 fusion proteins having enhanced activity - regulating immune and inflammatory responses.
  WPI; 1993-182546/22.
  Synthetic
   Mast cell growth factor; interleukin; haematopoietic progenitor cell; bone marrow cell; proliferation; differentiation; functional activation; peripheral blood leukocyte; circulating granulocyte; ss.
  25-MAR-2003
15-SEP-1993
   AAQ42803;
  AAQ42803
  neutropaenia, anaemia and thrombocytopaenia. correct PA field.)
  Example 1;
  Williams
  22-NOV-1991;
  19-NOV-1992;
   27-MAY-1993.
   WO9310229-A1
   Human IL-3 probe
   (IMMV) IMMUNEX
  Local
                     107
  107
   20
20
   17;
   17; Conserv
  Similarity
  21
            TCATTCTCCTGCTCCCACTC 126
   standard;
   TCATTCTCCTGCTCCCACTC 126
TCCTGCTCCTGCTCCAACTC
  TCCTGCTCCTGCTCCAACTC 1
  Page 17; 41pp; English
  BP; 6
  BP; 6 A; 3 C; 10 G; 2 T; 0 U; 0 Other;
  Conservative
   Conservative
  (revised)
(first en
  CORP
  91US-00797553.
  92WO-US009848.
   Đ,
   6.4%;
85.0%;
  CDNA;
  entry)
  6.4%;
  w
   Ç
   21
  10 G;
   ВP
  <u>,</u>
  ۰,
   Score
Pred.
  Score 15.2;
Pred. No. 39;
   Mismatches
   2 T;
  Mismatches
  No. 39;
   0
U;
  DB
   BB
   0 Other;
  1; Length
  1;
   (Updated
   ω
-
   Length
   Indels
   Indels
  9
   21;
  21,
  25-MAR-2003 to
  0
   0
   used
  encoding
  has the
  Gaps
   Gaps
   for
   0
  0;
```

```
RESULT 70
ADP29145
ID ADP29
XX
AC ADP29
XX
AC ADP29
XX
DT 12-AU
XX
Humar
XX
KW Cytos
KW Cance
XX
OS Homo
XX
  밁
  ঠ
  Best Local
Matches 1
  Query Match
Best Local (
   PCR primers and probes AAZ61533-34 are used to amplify and identify human 5'OT-EST (oxytoxin expressed sequence tag) cDNA sequences. The 5'-OT EST gene is involved in the control of obesity and fertility in males. 5'-OT EST nucleic acids are useful for producing transgenic animals. The transgenic animals created serve as a model for human late onset obesity and other related disorders and are also used for identifying the genetic cause of obesity. Compounds which modulate 5'-OT EST expression or activity are useful in the treatment or modulation of late onset visceral obesity or male infertility particularly in the disorders related to these conditions such as wasting, or anorexia, or cachexia associated with prolonged illness, or malabsorptive states or catabolic states associated with other diseases such as inflammatory conditions, Crohn's disease or AIDS wasting, or burns, or cancer, or bone disease
  Oxytoxin expressed sequence tag; 5'-OT EST; obesity; fertility; male; transgenic animal; human late onset obesity, late onset visceral obesit; male infertility; wasting; anorexia; cachexia; malabsorptive state; catabolic state; inflammatory condition; Crohn's disease; AIDS wasting; burn; cancer; bone disease; PCR primer; probe; ss.
                   Homo sapiens
   Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; ds; human secreted protein.
  Human secreted protein encoding sequence SEQ ID #1143.
  12-AUG-2004
  ADP29145;
  ADP29145 standard; DNA; 21 BP
   Sequence
   Disclosure; Page 26; 162pp; English.
   New anti-obesity polypeptide useful for treating obesity or infertility in mammals.
   WPI; 2000-224331/19
   Robinson ICAF,
   12-AUG-1998;
06-MAY-1999;
   24-FEB-2000.
   WO200009686-A1
  Primer 6U
  19-JUN-2000
   12-AUG-1999;
   (MEDI-) MEDICAL RES COUNCIL.
  139
  20
   ch 6.4%;
l Similarity 85.0%;
17; Conservative (
   CCTGCTCCCCCTTCTCCTTC 158
  21
  cerecrececrecree 1
  for a human 5'-OT EST
   BP; 6 A; 3 C; 12
  (first entry)
  (first entry)
   98GB-00017566.
99GB-00010522.
   Stoye JP, Flavell D, Wells SE,
  99WO-GB002658.
  0,
  Score 15.2; |
Pred. No. 39;
   G; 0 T; 0 U; 0 Other;
  Mismatches
  (oxytoxin expressed sequence tag).
  human secreted protein
   DB 1; Length 21;
  ω
••
  Indels
   Le Tissier P;
  0
   Gaps
  obesity;
  0,
   17-SEP-2002
17-SEP-2002
17-SEP-2002
17-SEP-2002
17-SEP-2003
18-APR-2003
18-APR-2003
18-APR-2003
18-APR-2003
02-MAY-2003
02-MAY-2003
02-MAY-2003
02-MAY-2003
19-MAY-2003
19-MAY
   17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
   17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
  29-AUG-2002;
29-AUG-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
   17-SEP-2002;
17-SEP-2002;
   17-SEP-2002
17-SEP-2002
   17-SEP-2002;
17-SEP-2002;
   17-SEP-2002;
17-SEP-2002;
   17-SEP-2002;
   17-SEP-2002;
   17-SEP-2002;
   17-SEP-2002;
  WO2004035732-A2
2002US-040658BP
2002US-0406612P
2002US-0406612P
2002US-0406612P
2002US-0406640P
2002US-0406659P
2002US-0410946P
2002US-0410949P
2002US-0410949P
2002US-0410959P
2002US-0410959P
2002US-04110959P
2002US-04110959P
2002US-04110059P
2002US-04110059P
2002US-04110059P
2002US-04110059P
2002US-0411005P
2003US-0463710P
2003US-048532P
2003US-048532P
2003US-048532P
2003US-0486890P
2003US-0486890P
2003US-0486890P
2003US-0486890P
2003US-0486890P
2003US-0486890P
2003US-0486890P
2003US-0486890P
2003US-048690P
2003US-048690P
2003US-048693370P
  2003WO-US026780
```

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CCXXX PTXX PTI
  밁
   ঠ
  Query Match
Best Local
  The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein encoding sequence. The present sequence is available on WIPOWEB and is not in the specification.
   Arts GJF,
Griffioen
  New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
  Williams LT, Halenbeck RF,
   New knockdown sequences, useful in lowering the amount of RNA and/or protein production in cells used in drug development process.
   04-NOV-2004.
   ds; RNA production;
  ADU26666 standard; DNA;
   Claim 1; SEQ ID NO 1143; 428pp; English.
  WPI; 2004-348438/32.
                       Claim 11; SEQ ID NO
   WPI; 2004-775940/76
   24-APR-2003; 2003WO-EP004362
  24-APR-2003; 2003WO-EP004362
  WO2004094636-A1
   Unidentified
   Knock-down target sequence #64
   27-JAN-2005
  ADU26666;
  Sequence 21
  Pierce K,
   08-AUG-2003;
  (GALA-) GALAPAGOS GENOMICS (VSCH/) VAN DER SCHUEREN J.
   knock-down target.
  (FIVE-) FIVE
   Similarity
  corcordorecreción 20
   CCTGCTCCCCCTTCTCCTTC 158
  Wang Y,
   Lambrecht MJY,
S, Bergs CJL;
   BP; 1 A;
  Conservative
   PRIME THERAPEUTICS INC
  (first entry)
  2003US-0493577P
   Chu K, Lee E, 1
Huang MM, Koth
  Chu K,
   Bergs
                      67; 402pp; English
   protein production; drug development;
  6.4%;
   13 C; 0 G; 7 T; 0 U; 0 Other;
  21
  E, Hestir K, Beaurang PA, Behren
Kothakota S, Haishan L, Linnemann
GP, Wu G, Zhang H;
   Ş
  ВP
  Djokic
  0; Mismatches
  Score 15.2;
Pred. No. 3:
  ۲
  Clasen
   DB 1;
  짇
  ω
••
   Length
   Indels
  Megic
  0
  Gaps
  0
```

The invention relates to a polynucleotide comprising an RNA sequence.

The

Query Match Best Local

Sequence 21

BP; 9 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Matches

l Similarity 17; Conserv

Conservative

6.4%;

; Score 15.2; D; Pred. No. 39; 0; Mismatches

DB

Length

21;

Indels

0

0

```
RESULT 72
ACL41023/c
ID ACL410
XX ACL410
XX ACL410
XX Cytost
XX Cy
   밁
   ន្តន្តន្ត្
   Ś
  The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or grotein activity of a cancer-related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polymucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C2000rf103, CACNAID, CDH6, CST, ENPP3, FLJ11855, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRMM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, stomach cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a target oligonucleotide from one such CRTP for which short interfering RNAs (siRNA) were produced. Note: The sequence data for this patent did electronic format directly from WIPO at flow was obtained in celectronic format directly from WIPO at
  Query Match
Best Local
  Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
   polynucleotides, vector, libraries, and method are useful in lowering the amount of RNA and/or protein production in cells used in drug development process. The present sequence represents a knock-down target sequence.
  Cytostatic; Gene
   C20orf103 target oligonucleotide,
  24-MAR-2005
  ACL41023;
   ACL41023
   Sequence
  Claim 3; SEQ ID NO 2095; 113pp; English
  treating
  WPI; 2005-075568/08
  20-MAY-2003; 2003US-0471729P
  19-MAY-2004; 2004WO-US015645.
  WO2005001092-A2
  Homo sapiens
   24
   l Similarity
17; Conserv
   N
  Wei L,
  CCTCATGAATGGTTTAGTGC 43
   21
   standard; DNA;
  CATCATGGAGGGTTTAGTGC 21
  BP; 5 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
  Conservative
  (first
  Slonim DK,
  therapy; Vaccine;
   entry)
  6.4%;
   21
  0,
   Score 15.2;
Pred. No. 39;
   Mismatches
  HS
   SEQ ID 2095.
  RNA Interference; cancer;
  DB 1;
  Length
   Indels
  0
```

ş

146

CCCCTTCTCCTTCTGCCATG

165

0

```
RESULT 73
ADZ19613
밁
  This invention relates to a novel screening method for identifying a gene convenies to the effect of an agent on a cell of a cell type. Specifically, it refers to identifying lethal/ synthetic lethal contexactions between a gene (or its product) and an agent such as a drug, sinkly interference. The present invention describes screening of an sirnA library for genes that interact with inhibitors of the KSP gene convenient interact with inhibitors of the KSP gene convenient interact with inhibitors of the KSP gene convenient in particular it illustrates STK6 and TPS2 as two genes that each independently exhibit synthetic lethal convenient conv
                                       is an siRNA olig
cell killing by
exemplification
  Example 3; SEQ ID NO 497; 284pp; English
  Identifying a gene product modulating the effect of an transfecting the cells with small interfering RNAs.
  Linsley
   22-SEP-2003;
27-FEB-2004;
  22-SEP-2004; 2004WO-US031629.
  07-APR-2005.
  WO2005031002-A2
  misc_feature
   Homo sapiens
  screening; synthetic lethal interaction; RNA interference; gene silencing; siRNA; short interfering RNA; tumor suppressor; cancer; cytostatic; ss.
  Human siRNA targeted against the human PIK3CB gene Seg 497
   16-JUN-2005
   ADZ19613 standard;
  20
  ,Sd
   MERCK & CO INC.
   CCACTTCTTGTTCTGCCATG
  2003US-0505229P.
2004US-0548568P.
2004US-0554284P.
   Mao M,
  (first entry)
   of the invention
  Location/Qualifiers 20. .21
  note=
   *tag=
   RNA;
   Kim AS,
   a
"dTdT dinucleotide to enhance siRNA binding"
   21
   Friend SH,
   Bartz
   SR,
   Cleary MA
   agent comprises
```

Query Match Best Local Similarity

65.0%;

Score Pred.

No. 39; В

۲.

Length

Query Match Matches

Local

l Similarity 17; Conserv

Conservative

0,

Mismatches

u T

0

Gaps

0,

6.4%; 85.0%;

Score 15.2; Pred. No. 39

39;

DB 1;

Length 21; Indels

Sequence

21

BP; 4

A.

3 C; 7 G; 2 T; 5 U; 0 Other;

```
밁
   Ş
   Matches
   gene that is active in a IgE-mediated disorder, a genetic construct that expresses the siNA, and a binding agent that specifically binds to a target antigen expressed on the surface of the cell. Also described are: a method for the treatment of an IgE-mediated disorder in a patient; prevention of IgE-mediated disorder in a patient; prevention of IgE-mediated disorder in a patient; prevention of a specific antigen in a patient; and preventing or reduction of a specific antigen in a patient; and preventing or reducing the severity of an immune response to a specific antigen in a patient. The composition is useful in the preparation of a medicament useful for the treatment of an IgE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis, urticaria, atopic dermatits, food allergies, diseases that benefit from the reduction of eosinophilia in the tissues of the respiratory system, or disorders having hypersensitivity immune reaction. This sequence
   New composition comprises small interfering nucleic acid molecule (siNA) capable of reducing expression of a target gene that is active in a IgE-mediated disorder, useful for treating, e.g. allergic rhinitis or atopic
   immunosuppressive; expression; RNA interference; allergy; atopic dermatitis; urticaria; dermatological, dermatological disease; immediate type hypersensitivity; immunosuppressive; astima; antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory; ear, nose, throat disease; inflammation; respiratory disease; immune disorder; IgE; short interfering nucleic acid; siNA;
Sequence
   The invention describes a composition comprising a small interfering nucleic acid molecule (siNA) capable of reducing expression of a target
   Disclosure; SEQ ID NO 205; 178pp; English
  Watson JD, 1
Abernethy N,
  20-FEB-2004; 2004US-0546434P
   21-FEB-2005;
  01-SEP-2005
  Human IgE short interfering nucleic acid SEQ
  AEC02602 standard; DNA;
   dermatitis
   WO2005080410-A1
  Homo sapiens.
   antiallergic;
  03-NOV-2005
  (GENE-) GENESIS RES & DEV CORP LTD
   silencing; ss.
  64 AGTTCACGTGAGAGCTGGTT
   13;
   N
 21
   AGUUCAUGUCAGGGCUGGTT
                                  a
                             having ny
 BP; 3
   Murison GJ,
   Conservative
   2005WO-NZ000021
  (first entry)
   Webster
   antiinflammatory;
 P
 7 C;
   Ö.
                                supression of human
  21
  Grigor MR,
 ຫ
   4.
 G; 6 T; 0 U;
   21
  83
   antiasthmatic;
   Mismatches
  Havukkala IJ,
 0 Other;
                                IgE expression.
   ij
   ω
••
   dermatological;
   ö
   Indels
  Munro
  ດ
   <u>,</u>
   Gaps
```

```
RESULT 75
RECOUNT 175
RECOUNTS 110
RECOUNTS 117-NC
RECOUNTS 11
  밁
The invention relates to a method of identifying the nucleotide for each of a set of single nucleotide polymorphisms (SNPs) in the major CC histocompatibility complex (MHC) region in a population of individuals, CC comprising providing the HLA type for the individuals and identifying an CC SNP haplotype in the population that correlates with the HLA type, where CC the SNP haplotype comprises the SNPs in the MHC region. The invention CC also relates to a method of predicting the HLA type of an individual, a CC method of determining the presence or absence of an allelic variant of an CC MHC gene in an individual, a method of identifying an SNP haplotype that CC correlates with susceptibility to a disease or condition, and a method of condition. The disease or condition and a method of condition selected from inflammatory bowel disease, ulcerative colitis, CC condition selected from inflammatory bowel disease, ulcerative colitis, CC myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease, gastritis, autoimmune hepatitis, dermatomy. Systemic CC purpus erythematosus, systemic sclerosis, polymyositis, dermatomyositis, pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia cCC purpura, Sjoegren's syndrome, multiple sclerosis, Reiter's syndrome and
  gastrointestinal-gen.; antiulcer; immunomodulator; immunosuppressive; antiarthritic; antirheumatic; antidabetic; muscular-gen.; neuroprotective; dermatological, antithyroid; hepatotropic; antianemic; hemostatic; ophthalmological; uropathic; antipsoriatic; ss;
  Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP; major histocompatibility complex; MHC; HLA; human leukocyte antigen; immune disorder; inflammation; hiflammatory bowel disease; ulcerative colitis; Crohns disease; rheumatoid arthritis; diabetes; diabetes mellitus; myasthenia gravis; vitiligo; Graves disease; Hashimotos disease; gastritis; autoimmune hepatitis; rheumatism; systemic lupus erythematosus; scleroderma; polymyositis; rheumatism; systemic lupus erythematosus; scleroderma; polymyositis; dermatomyositis; pernicious anemia; primary biliary cirrhosis; diopathic thrombocytopenia purpura; Sjoegrens syndrome; lipie sclerosis; Reiter's syndrome; psoriasis; antiinflammatory; multiple sclerosis; Reiter's syndrome; psoriasis; antiinflammatory;
  Identifying single nucleotide polymorphism (SNP) haplotype that correlates with the HLA type, useful for diagnosing an immunological inflammatory condition, comprises providing SNPs in the major histocompatability complex region.
  Oliphant A,
  09-SEP-2005
  Human locus-specific oligonucleotide #1822
  17-NOV-2005
  AEC30534;
  AEC30534 standard; DNA; 21
  (ILLU-) ILLUMINA INC
  26-FEB-2004; 2004US-0547823P
  28-FEB-2005; 2005WO-US006628
  WO2005082110-A2
  31
  N
   AATGGTTTAGTGCCATCCCC 50
  AATGGCTTGGTGCCTTCCCC
  SEQ ID NO 6554; 175pp; English.
  Murray S;
  (first entry
  21
```

```
RESULT 76
AAT72472/c
ID AAT724/c
XX AAT724
XX 29-SEP
XX 29-SEP
XX Mammal
KW Mitoch
KW polyme
XX W09716
XX W09716
XX W09716
XX W1; 1
XX W1; 1
XX ATT24
XX ATT24
XX ATT24
XX ATT24
CC Comple
CC Comple
CC XJMS 1
CC CII-3
CC SATOCH
XX Sequen
   SSSS
   망
  Ş
S
  Best
  Query Match
   Query Match
  Primers HuQPS1.Forw1 (AAT72472) and pJOS2.T7 (AAT72473) are respectively complementary to exon A (see also AAT72462) and fragment Y (see also AAT72462) and fragment Y (see also AAT72462) of the human CII-3 gene that encodes a subunit (AAW21674) of complex II of the human mitochondrial electron transport chain. They were used to amplify genomic DNA from HeLa cells, hamster B9 cells, hamster XMW5.1.1(+) cells containing a complete human chromosome 1, XMW5.1.1(-) cells, and hamster XEWB.2.3 cells contg. mammalian artificial chromosome MACB.2.3. A PCR product of expected size (1.05 bp) was obtd. from HeLa, XMW5.1.1(+) and XEWB.2.3 cell DNA, indicating that cloned human genomic CII-3 sequences are present on chromosome 1, including the portion of chromosome 1 comprising MACB.2.3
   psoriasis. This sequence represents a human locus-specific oligonucleotide used in the scope of the invention.
   Sequence
  New mammalian artificial chromosomes - comprising a mammalian centromere and a unique cloning site, used for stable expression of large fragments
  WPI; 1997-272103/24.
   Scheffler IE
   31-OCT-1995;
  29-OCT-1996;
   09-MAY-1997
  mitochondrial electron transport chain complex II; transgenic polymerase chain reaction; PCR; primer; ss.
   Mammalian artificial chromosome; MAC; selectable marker; CII-3;
   Human CII-3 gene exon A primer HuQPS1.Forw1.
  29-SEP-1997
   AAT72472 standard; DNA; 20
   Example 2; Page 45; 71pp; English.
  (REGC ) UNIV CALIFORNIA
  Local
   Local
  174
   \vdash
   l Similarity
17; Conserv
   l Similarity
15; Conserv
   20
  ATTCCAGGGACTTCACAAGA 193
   21
        CAGGGACTTCACAAG 192
   ATTCCAGAAGCTTCACAAGA 20
  BP; 8
   6.4%; So liarity 100.0%; I Conservative 0;
   BP; 3
   Conservative
   (first entry)
   95US-00550717
  96WO-US017476
   P,
   A; 6 C; 3 G; 4 T; 0 U;
   6.4%;
85.0%;
   5 C; 5
   ВP
   G; 7
   0,
                                       Score 15; DB 1; Length 20.
Pred. No. 42;
0; Mismatches 0; Indels
   Score 15.2;
Pred. No. 39;
   Mismatches
   T; 0 U; 0 Other;
   0 Other;
  B
  1; Length 21;
   ω
••
   Indels
   0;
   0,
   animal;
   Gaps
   Gaps
   0
   0
```

밁

16

CAGGGACTTCACAAG

```
밁
   ঠ
  RESULT 77
ADK96774/c
   Matches
  Query Match
  1903/c
ADS73903 standard; RNA; 19 BP.
   The present invention relates to a polymucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
  DMD; Duchenne muscular dystrophy; collagen VI alpha 1; COL6A1; myotubular myopathy 1; MTM1; dysferlin; DYSF; laminin-alpha 2; LAMA2; emery-dreyfuss muscular dystrophy; EMD; calpain 3; CAPN3; antisense; ss.
           21-MAR-2003; 2003WO-NL000214
                                 22-MAR-2004; 2004WO-NL000196.
   WO2004083446-A2
  Synthetic
   DMD gene specific antisense oligonucleotide h59AON2
  16-DEC-2004
  Sequence 20
  Claim 2; SEQ ID NO 5803; 2627pp; Japanese.
  nucleotide polymorphism in human gene.
   Novel polynucleotide useful for PCR amplification along with two DNA fragment from another set of sequences, or for detecting single
  WPI; 2004-093977/10
  08-MAR-2002; 2002JP-00064373.
  08-MAR-2002;
  JP2003259875-A
   human; single nucleotide polymorphism; SNP; ss; primer
   Primer of the invention #2494.
   06-MAY-2004
   ADK96774;
  ADK96774 standard; DNA; 20
  (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
  Local
   cal Similarity
15; Conserva
   103 CCTCTCATTCTCCTG 117
   19
   CCTCTCATTCTCCTG 5
   Conservative
  BP; 7 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
  (first entry)
   2002JP-00064373.
   (first entry)
  100.0%;
  BP.
   <u>,</u>
   Score 15;
Pred. No.
   Mismatches
  DB 1;
42;
   0
   Length 20
   Indels
  ٥,
   Gaps
   0
```

```
(ZIEK-) ACAD ZIEKENHUIS LEIDEN
  Ommeren GB,
  Deutekom JCT,
  Den Dunnen JT,
  Aartsma-Rus
  P
```

determining from a structure of RNA istructure hybridized to another part Generating an oligonucleotide for treating diseases, comprises in the structure RNA from an exon, a region that assumes a part of the RNA and a region that is not

Example 1; Page 89; 117pp; English.

CC oligonuclectide is complementary to a consecutive part of 14-50 confidence of the RNA. It also comprises RNA, where the RNA contains a CC modification, preferably a 2'-0-methyl modified ribose (RNA) or CC deoxyribose (DNA) modification. The pre-mRNA comprising the exon exhibits cundesired splicing in a subject. The absence of the exon from mRNA CC produced from the pre-mRNA generates a coding region for a protein. The gene from which the RNA comprising the exon is transcribed encodes an CC gene from which the RNA comprising the exon is transcribed encodes an CC gene (COLGA1), a myocubular myopathy 1 gene (DMD), a collagen VI alpha 1 (C gene (COLGA1), a myocubular myopathy 1 gene (MPMI), a dysferlin gene (DYSF), a laminin-alpha 2 gene (LAMA2), an emery-dreyfuss muscular CC dystrophy gene (EMD), and/or a calpain 3 gene (CAPN3). Preferably, the gene is the DMD gene. The oligonucleotide, its equivalent, or the compound is useful for at least in part altering recognition of the exon CC exons in a pre-mRNA; for the preparation of a medicament for the cc treatment of an inherited disease; for inducing exon skipping in a pre-mRNA; for altering exon-recognition in a pre-mRNA; for altering the efficiency with which a splice donor or splice acceptor sequence is used by a splicing machinery; for inducing exon-skipping of two, three, or correct exons in a pre-mRNA, or for inducing skipping of the at least two exons and a sequence located between the att exon exons (intervening sequence) on the pre-mRNA, where intervening sequence further comprises coligonucleotides (ADNs) used to study targeted skipping of 15 different common exons. Sequences ADS73865-ADS73903 represent antisense The invention relates to generating an oligonucleotide and involves determining from a secondary structure of RNA from an exon, a region assumes a structure that is hybridised to another part of the RNA (cl structure) and a region that is not hybridize in the structure (open structure), and subsequently generating an oligonucleotide, where at least a part of the oligonucleotide is complementary to the closed structure and at least another part of the oligonucleotide is complementary to the open structure. In generating an oligonucleotide the open and closed structures are adjacent to each other. The oligonucleotide is complementary to a consecutive part of 14-50 In generating an oligonucleotide, h, a region that the RNA (closed

Sequence 9 BP; 3 A; 3 C; 5 G; 0 T; 8 U; 0 Other;

Matches Query Match Best Local 16; Similarity Conservative 6.3%; 0 Score 14.8; Pred. No. 49 Mismatches 45; DB 1; *ب* Length 19; Indels 0, Gaps 0

```
멼
                    171 AAGATTCCAGGGACTTCA 188
19
AAGACTCCAGGAACTTCA 2
```

AEB93316/c
ID AEB933
XX
AEB933
AC AEB933
AC 03-NOV
XX
DE Human
XX
KW Short
KW Short
KW pharma
XX
OS Homo E
XX 03-NOV-2005 AEB93316; AEB93316 standard; DNA; 19 (first entry)

Human siRNA transcribed in the inventive optimized system, SEQ ID 79

Short interfering RNA; ds; pharmaceutical; siRNA. gene silencing; RNA

Homo sapiens

```
ID AAS4
XX XX AAS
AC AAS
XX 18-
XX 18-
XX MOU
XX MOU
KW CYC
KW CYC
   RESULT 80
  밁
   δ
  CC of the nucleotides 0 to +5 of the natural promoter of a DNA-dependent RNA CC molecule encoding the siRNA, an expression vector, a transfected/infected with the vector, a transgene comprising the DNA, a CC host cell transfected/infected with the vector, a transgene comprising the DNA, a CC the DNA and/or vector, a transgenic non-human animal (one or more of its CC cells comprising the transgenic non-human animal (one or more of its CC cells comprising the transgenic animal resulting in the animal expressed in one CC ribonucleic acid interference (RNAi) of the transgene is expressed in one CC ribonucleic acid interference (RNAi) of the target gene by the expressed of RNA), a cell derived from the transgenic animal and producing an siRNA CC by in vitro-method (involving providing the expression vector, admixing the vector with a recombinant DNA-dependent RNA-polymerase, and purifying CC ribonucleotides, suitable buffers and RNAse inhibitor, incubating the CC mixture at a suitable temperature for 30 minutes-24 hours for CC transgenic animal. The siRNA is useful for generating a non-human for transgenic animal models. The siRNA enables high-throughput projects in genomic CC research, in target gene validation, in pharmaceutical industry.
  Query Match
Best Local :
  Matches
   Small interfering RNA molecule useful for generating transgenic non-human animal, comprises 5 prime-protruding end that corresponds to consensus sequence of nucleotides of natural promoter of DNA-dependent RNA-
   11-FEB-2004;
03-AUG-2004;
  The invention relates to a small interfering (siRNA) molecule (I), comprising a 5'-protruding end that corresponds to the consensus sequence of the nucleotides 0 to +5 of the natural promoter of a DNA-dependent RNA
  03-FEB-2005;
Mouse; ss; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide; cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic; immunosuppressant; hyperproliferative disorder; cancer; cellular injury;
   Sequence 19
  biological interference with vector-based siRNA systems. The siRNA is biocompatible, cost effective, easy to use and suitable for automatization. The present sequence is a human siRNA produced by the method of the invention. NOTE: The present sequence is described as a
   Truss
   WO2005078089-A1
  Mouse PARP-2 antisense inhibitor ISIS #110297.
   18-DEC-2001
  AAS45831;
  AAS45831 standard; DNA;
  siRNA but is clearly a DNA molecule.
  Example 1; SEQ
  WPI; 2005-582878/59
  (UYBE-)
   109
  19
  16;
  UNIV BERLIN CHARITE
  Similarity
  ATTCTCCTGCTCCTTCTC 2
   ATTCTCCTCCTCCCACTC 126
   Hagemeier
   B₽;
  Conservative
   2004EP-00003079.
2004EP-00018376.
  2005WO-EP001079.
   (first
  ID NO 79; 56pp; English
   8
   ?
   entry)
  6.3%;
   1 C; 9
  20
  ВÞ
  <u>,</u>
  Score 14.8;
Pred. No. 4
   G; 1 T; 0
  Mismatches
   ς,
  45,
   0 Other;
  DB 1;
  ა
•
  Length 19;
  Indels
  <u>,</u>
  Gaps
  0
```

RESULT 81
ADE43868/c
ID ADE438
XX
AC ADE438

standard;

DNA; 20 BP

ADE43868; ADE43868 밁 Ś

```
Query Match
Best Local !
   Matches
  The invention relates to antisense oligonucleotides targeted to human PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly (ADP-ribose) polymerase plays an important role in chromatin decondensation, DNA replication, DNA repair, gene expression, malignant transformation, cellular differentiation and apoptosis. The antisense oligonucleotide inhibitors are useful for inhibiting the expression of PARP in human cells or tissues. They are also useful for treating a human with a disease associated with PARP especially hyperproliferative
  oxidative stress; neurological disorder; parkinsonism; apoptosis; meningitis-associated intracranial complication; ischaemia; probe inflammatory disorder; autoimmune disorder; arthritis; diabetes.
   Sequence
   disorders (e.g. cancer), cellular injury resulting from oxidative stress, neurological (e.g parkinsonism, meningitis-associated intracranial complications and ischaemia), inflammatory and autoimmune disorders (e.g arthritis) and diabetes. The present sequence is an antisense
   Antisense compound useful for treating hyperproliferative, neurological, inflammatory and autoimmune disorders and diabetes inhibits human PARP.
  WPI; 2001-602570/68
   02-MAR-2000; 2000US-00517467
   01-MAR-2001; 2001WO-US006572
   07-SEP-2001
   WO200164955-A1
  modified_base
  modified_base
   Mus musculus
  oligonucleotide of the invention
   Example 17; Page 89; 168pp; English.
   Popoff I,
  modified_base
   modified_base
   (ISIS-) ISIS PHARM INC
   4
   l Similarity
16; Conserv
                           TGCCATCCCCTTGGTGAT
   20 BP; 2 A; 8 C; 3 G; 7 T; 0 U; 0 Other;
TCCCATCCCCTTGGTGCT 18
   Cowsert LM
   Conservative
   /*tag=
/mod_ba
   /note=
16. .20
   /*tag=
   /*tag=
  Location/Qualifiers
   /note=
   /note= "2'
  note=
   mod.
   _
mod
   mod_base=
   6.3%;
  base=
   base=
  base= OTHER
  "2'-methoxyethyl
  "All
   "Phosphorothioate backbone"
   മ
  methoxyethyl nucleotides"
   OTHER
   OTHER
   OTHER
   58
   0; Mismatches
  cytidine
  Pred.
  Score 14.8;
Pred. No. 4
  residues are 5-methyl cytidine"
  44;
  nucleotides"
   멂
   2;
   Length
   Indels
   20;
   0,
   Gaps
   0
```

```
RESULT 82
ADP77306/c
ID ADP77306 E
XX ADP77306;
AC ADP77306;
XX ADP77306;
XX PCR primes
DE PCR primes
XX Bingle-str
KW amplification
KW antiasthma
KW eosinophil
  밁
   8
  Query Match
Best Local S
Matches 16
   The invention relates to diagnosing or predicting asthma or an inflammatory condition of respiratory tissues that is associated with tissue accumulation of eosinophils, comprising identifying a nucleic acid sequence that exhibits a polymorphism in an eotaxin gene, where the polymorphism comprises a substitution of adenine for guanine 67 base pairs following the ATG initiation code of the gene, and where counting is initiated at the A in that codon. The method uses a single-strand conformation polymorphism (SSCP) technique or by amplification refractory mutation system (ARMS) technique. The method is useful in diagnosing, predicting and treating asthma, rhinitis and other inflammatory conditions associated with eosinophil accumulation in respiratory tract and other tissues. The present sequence is an SSCP primer used in the
single-strand conformation polymorphism; SSCP;
amplification refractory mutation system; ARMS; inflammatory condition;
eosinophil accumulation; respiratory tissue; rhinitis; atopy;
antiasthmatic; antiallergic; antiinflammatory; dermatological; human;
   Asthma; polymorphism detection; eotaxin;
  26-FEB-2004
  Sequence
   Claim 12;
  Diagnosing, predicting or treating asthma or other inflammatory conditions of respiratory tract and other tissues, comprises identifying a nucleic acid sequence that exhibits a polymorphism in an eotaxin gene.
   16-MAY-1997;
  US6548245-B1
  Homo
  Human; ss; primer; eotaxin; SNP; single nucleotide polymorphism; antiasthmatic; antinflammatory; antiallergic; gene therapy; asth rhinitis; inflammatory condition; eosinophil accumulation; respiratory tract; single-strand conformation polymorphism; SSCP; amplification refractory mutation system; ARMS; PCR.
  29-JAN-2004
   PCR primer #1 for human eotaxin gene.
  method of the invention to detect the polymorphism.
  12-MAY-1998;
   (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
  sapiens.
   3
  eotaxin
  20
  70
  16;
  Similarity
   CGTGAGAGCTGGTTGTTT 87
  20
   standard;
  CGTGAGAGGTGGTGGTTT 3
  SEQ ID NO 2; 12pp; English.
   Luster AD,
  Conservative
  BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;
  (first entry)
   (first
  gene
   97US-0046720P
  98US-00076259
   DNA;
  SSCP PCR primer
   entry)
  6.3%;
   20
  <u>.</u>
  Score 14.8;
Pred. No. 44;
  Mismatches
  DB 1; Length 20;
  <u>ب</u>
  Indels
  therapy; asthma;
  <u>.</u>
  Gaps
  0
```

RESULT 83
ADG43900/c
ID ADG439
XX ADG439
XX ADG439
XX ADG439
XX BS; du
XX BS; du
XX DYRK4;
XX Inflam
XX Synthe
XX Synthe
XX US2003
XX US2003
XX US2003
XX YS 13-NOV
PP 10-MAY
XX

inflammation;

tumour; antisense.

ss; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase DYRK4; Down syndrome; mental retardation; cancer; infection;

Human DYRK4 antisense oligonucleotide ISIS 206819.

26-FEB-2004 ADG43900;

(first entry)

ADG43900 standard; DNA;

20 BP

13-NOV-2003.

US2003211606-A1

10-MAY-2002; 2002US-00144140

밁

20

CGTGAGAGGTGGTGTTT

w

0

```
S
   Matches
   Query Match
Best Local 9
   The present invention relates to a method for diagnosing and/or predicting asthma. The method comprises identifying a nucleic acid sequence exhibiting a polymorphism in an eotaxin gene, where the polymorphism comprises a substitution of adenine for guanine 67 bp following the ATG initiation codon of the gene, where counting is initiated at the A in that codon. The method involves amplifying the nucleic acid by PCR, and testing the nucleic acid by a single-strand conformation polymorphism (SSCP) or by an amplification refractory mutation system (ARMS) technique. The method of the invention is useful for diagnosing, predicting and/or treating asthma or an inflammatory condition associated with eosinophil accumulation in respiratory and other tissues, including rhinitis and atopy. The present sequence represents a PCR primer used in the method of the present invention.
   Sequence
   conditions associated with eosinophil accumulation in respiratory other tissues, such as rhinitis and atopy, using an eotaxin coding
   Claim 8; SEQ ID NO 2; 12pp; English.
  sequence
  WPI; 2003-898062/82.
  Lilly CM,
   14-APR-2003; 2003US-00413255
  04-SEP-2003
   16-MAY-1997;
12-MAY-1998;
  PCR; primer; ss.
  (BGHM ) BRIGHAM & WOMENS HOSPITAL
   sapiens
         70
  1 Similarity 16; Conserv
CGTGAGAGCTGGTTGTTT
   20 BP; 7
   polymorphism.
   Luster AD,
  predicting and/or treating asthma or other inflammatory associated with eosinophil accumulation in respiratory as
  Conservative
   97US-0046720P.
98US-00076259.
   A; 9 C; 2
  6.3%;
         87
  0;
   G; 2 T; 0 U; 0 Other;
   Score 14.8;
Pred. No. 44
  Mismatches
  INC.
  DΒ
  1,
  2
  Length
  Indels
  ç
  Gaps
  and
```

```
RESULT 84
ADJ96199
   밁
   S
  Matches
   Query Match
13-JAN-1997;
13-JAN-1998;
04-MAR-1999;
12-MAR-1999;
27-APR-1999;
30-APR-1999;
02-AUG-1999;
01-DEC-1999;
03-MAR-20000;
25-AUG-20000;
21-NOV-20000;
  encoding dual-specificity tyrosine-(?)-phosphorylated Kinase 4, DYRK4, antisense oligonucleotide.
  Dobie
   Tumour necrosis factor receptor; TNFR; inflammation; inflammatory bowel disease; encephalitis; attherosclerosis; psoriasis; autoimmune disorder; systemic lugus erythematosus; arthritis; multiple sclerosis; Crohn's disease; autoimmune encephalitis;
  18-APR-2003;
   22-JAN-2004.
   US2004013664-A1
  Homo
   Human TNFR-6alpha
   06-MAY-2004
  ADJ96199
  ADJ96199 standard;
  Sequence 20 BP; 3 A; 3 C; 8
   The
  Example 15;
   syndrome
   New compounds that hybridizes with nucleic acid molecules encoding dualspaceificity tyrosine-(Y)-phosphorylation regulated kinase 4 (DYRK4) and inhibits expression of DYRK4, useful for treating e.g. cancer or Down
   10-MAY-2002;
   invention relates
  sapiens.
  2003-901593/82
  172
   vs. host disease; GVHD; allergy; asthma;
   ₹
  18
  16;
   reverse-transcriptase; primer; ss.
  Similarity
   SISI
   AGATTCCAGGGACTTCAC 189
  AGATTCCAAGGACCTCAC
97US-0035496P.
97US-0006352.
99US-0121774P.
99US-0131964P.
99US-0131964P.
99US-0146371P.
99US-016235P.
2000US-0252131P.
  SEQ ID NO 28; 46pp; English
  Conservative
  2003US-00418242
   PHARM INC
   2002US-00144140.
   (first entry)
  amplifying RT-PCR primer
  DNA;
  6.3%;
   to a compound targeted
  20
  ВP
  G;
6
  Н
   0,
   Score 14.8;
Pred. No. 44
   Mismatches
  T; 0
   U;
  44;
  0 Other
   BB
  1;
  to a nucleic acid molecule
   2
•
  gene therapy; human;
   Length 20;
  Indels
   ٥,
   Gaps
   0
```

```
S
   밁
  Best Loc
Matches
  Query Match
  The present invention relates to novel tumour necrosis factor receptors (TNFR) proteins and their encoding nucleic acids. The invention is usefu for treating and preventing inflammatory disorders such as inflammatory bowel disease, encephalitis, atherosclerosis and psoriasis, autoimmune disorders such as systemic lupus erythematosus, arthritis, multiple sclerosis, Crohn's disease and autoimmune encephalitis, graft vs. host disease (GVHD), allergy and asthma. The invention is also useful in gene therapy. The present sequence is human TNFR-6alpha amplifying RT-PCR primer. The primer is used in the exemplification of the invention.
   Sequence
  Treating or preventing an inflammatory or autoimmune disorder, host disease (GVHD), allergy or asthma comprises administering animal Tumor Necrosis Factor Receptor protein.
   06-JUL-2001; 2001US-0303224P.
24-AUG-2001; 2001US-00935727.
19-APR-2002; 2002US-0373604P.
  Example 28; SEQ ID NO 50; 165pp; English.
   WPI; 2004-121528/12
  Gentz RL,
   (YUGG/)
  (EBNE/)
   (RUBE/)
  (GENT/)
   Local
                        92
 w
   l Similarity
16; Conserv
  FENG P.
   YU G.
NI J.
EBNER R.
FENG P.
  GENTZ R
                      GAGCCTGGCCCCCTCTCA 109
   20 BP;
  GATCCTGGCCCCCCTCTTA
  Yu G,
  Conservative
   N
   z
  ŗ
   ð
  Z.
  88.9%;
   9 C; 3
  ٦
  6.3%;
   Ebner
 20
  0
   G; 6 T; 0 U;
  Score 14.8;
Pred. No. 4
  ×
  Mismatches
  Feng
  ָס
   0
  DB
   Other;
   Ruben
  1:
  اد
   Length
   X.
  Indels
  20
  0
  graft vs
  Gaps
  is useful
  gene
```

```
RESULT 85
ABC227977
XX AEC2277
XX AEC2277
XX AEC227
XX Cardia
XX Cardia
XX Cardia
XX Cardia
XX S5; PC
XX S7
XX S1-JAN
XX S1-JA
   30-JAN-2004; 2004US-00769542.
30-JAN-2004; 2004US-00769744.
22-APR-2004; 2004US-00829674.
22-APR-2004; 2004US-00830477.
10-JAN-2005; 2005US-0642909P.
  cardiant; C-reactive-protein-reducer; Leukotriene-synthesis-antagonist;
ss; PCR; myocardial infarction; cardiovascular disease; FLAP;
   AEC22797;
   AEC22797
  31-JAN-2005; 2005WO-US003312
   18-AUG-2005
   Homo sapiens
  5-lipoxygenase activating protein; primer; genetic marker.
   Human myocardial infarction (MI)
   20-OCT-2005
   WO2005075022-A2
   standard;
   (first entry)
   DNA;
   20
   ВP
  cardiovascular disease;
   gene marker
  PCR
   primer SEQ
   ä
   ĕ
```

Helgadottir

Þ

Hakonarson H,

Gulcher JR,

Gurney

M

(DECO-)

DECODE

GENETICS

EHF.

Example 9; SEQ ID NO 7; 395pp; English

A method of prophylaxis therapy for myocardial infarction (MI) comprises administering to the subject a composition comprising an MI therapeutic agent that inhibits leukotriene synthesis in vivo.

WPI; 2005-648933/66.

Query Match Best Local Matches

16;

Conservative

0

Mismatches

2

Indels

.

Gaps

0

밁 á

18

CAGCTCCCTCATGAGTGG

ه...و

Similarity

6.3%;

Score 14.8; Pred. No. 4

DB 1; Length

Sequence

20

BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

and statin are useful for the manufacture of a medicament for reducing CRP levels in the human subject. The present sequence represents the DNA encoding the 5-lipoxygenase activating protein located in the human myocardial infarction (MI) gene located on chromosome 13q12-13.

The invention relates to a method of prophylaxis therapy for myocardial infarction (MI) comprises administering to the subject a composition comprising an MI therapeutic agent that inhibits leukotriene synthesis vivo. The methods and composition are useful for the prophylactic treatment of myocardial infarction. The leukotriene synthesis inhibitor

synthesis in

```
ঠ
   밁
   17-OCT-2002; 2002US-0419433P.
21-FEB-2003; 2003US-049331P.
17-SEP-2003; 2003US-0503587P.
16-OCT-2003; 2003WO-US032556.
30-JAN-2004; 2004US-00769744.
22-APR-2004; 2004US-00830477.
17-SEP-2004; 2004WO-US030582.
10-JAN-2005; 2005US-0642909P.
31-JAN-2005; 2005WO-US033312.
   72123/c
AEF72123 standard;
                           Prophylaxis therapy for myocardial infarction comprises selecting a human by screening for genetic variation in e.g. 5-lipoxygenase activating protein gene, administering a composition comprising a agent and
   WPI, 2006-124282/13.
  30-MAR-2005; 2005US-00096191.
   US2006019269-A1
   Homo sapiens
   5-lipoxygenase
  prophylaxis;
  Human FLAP gene microsatellite marker-specific PCR primer -
  06-APR-2006
  AEF72123;
   Helgadottir A,
   18
   18
  DECODE
  CAGCTCCCTCATGAGTGG 1
  CAGATCCCTCATGAATGG 35
                  inflammatory marker.
  SNP detection; myocardial infarction;
  (firet
  GENETICS
  activating
   Hakonarson H,
   DNA;
   entry)
   20
   protein;
   ₽₽
   Gulcher JR,
  FLAP; PCR;
   Gurney ME
  primer;
  cardiant;
   SEQ
   ä
```

```
XSSSSSSSSSSXXX
   The invention comprises a method of prophylaxis therapy for myocardial infarction. The method involves selecting a human subject susceptible to myocardial infarction by screening for a genetic variation in either the 5-lipoxygenase activating protein (FLAP) gene or the leukotriene A4 hydrolase (LTA4H) gene. The method further involves administration of a therapeutic agent and monitoring at least one inflammatory marker in the subject before and during the prophylaxis treatment. The method of the invention is useful for prophylaxis therapy for myocardial infarction. The present DNA sequence represents a PCR primer that was used to amplify a microsatellite marker from within the human FLAP gene.
  Sequence
20 BP; 4 A; 5 C; 6
G; 5
T; 0 U; 0 Other;
```

```
Query Match
Best Local S
                  Matches
    18
                 16;
                         Similarity
CAGATCCCTCATGAATGG
                 Conservative
                        6.3%;
    35
                 0;
                        Score 14.8;
Pred. No. 44
                  Mismatches
                              B
                              1;
                 2
                              Length
                  Indels
                  0,
                  Gaps
```

0,

```
RESULT 87
AAQ82294/c
  Chromosome
                    25-MAR-2003
07-SEP-1995
   AAQ82294
  AAQ82294;
  standard;
 11
                    (revised)
(first en
 (locus D11S1131)
  DNA;
                    entry)
   21
STS primer cSRL-4e3-tZ
```

sequence sampled mapping; genomic analysis; complex genome mapping; cosmid library; chromosome 11; sequence tagged site; STS analysis; 88

Synthetic

```
15-JUN-1993;
07-SEP-1993;
    Evans
   22-DEC-1994.
   WO9429486-A1
                           (SALK ) SALK INST BIOLOGICAL
  15-JUN-1994;
GA,
   Smith MW
   93US-00078471.
93US-00117952.
  94WO-US006810
                            STUDIES
```

Sequencing complex genomes, present as fragments in a cosmid library - sequencing end-specific nucleotides of each clone then correlating with spatial relationship of cosmid, esp. for mammalian chromosomes. with Ьy

WPI; 1995-036508/05

Example 4; Page 75; 128pp; English.

Sequences were determined from the ends of chromosome 11-specific cosmids by automated sequencing without intermediate subcloning. A sample of 371 DNA sequence fragments were determined and of these, 277 were suitable for STS primer prediction by computer analysis (using the "Primer" program available from E.Lander, MIT). The STSs and cosmids were mapped by in situ hybridisation, somatic cell hybrid analysis or both. Using this method, 370 STSs specific for human chromosome 11 were generated and most of them were regionally mapped. This procedure illustrates a novel method for sequencing complex genomes, designated "sequence sampled mapping". The sequence sampled mapping method is useful for the complete sequences and elemented based maps, and ultimately, for the AAQ82001-Q82706 for STS primers. (Updated on 25-MAR-2003 to correct PN

Example 9; SEQ ID NO 7; 134pp; English

```
RESULT 88
  밁
                    ફ
   문
  δ
  SXS
   Query Match
Best Local S
Matches 16
  Matches
   Query Match
Best Local (
   specific application is diagnosis of copper toxicosis (CT). The inventic can also be used to create a genetic map of the canine genome; to generate breed-specific profiles; to establish paternity and to identify dogs from DNA fingerprints. The method provides rapid analysis of the target sequences from only a small sample of DNA. Diagnosis can be done at any time in the dog's life. The present sequence is that of a PCR primer of the invention.
   genetic disease; genetic trait; dog; carrier of recessive disease; copper toxicosis; CT; canine genome map; breed-specific profile; DNA fingerprint; dog identification; PCR; primer; ss.
  This invention relates to novel oligonucleotide PCR primers which may be used to identify markers associated with genetic diseases and traits in dogs, in particular to diagnose genetic diseases that are not phenotypically visible and to identify carriers of recessive diseases. A
  Claim 1; Page 18; 40pp; English.
   Sequence 21
  microsatellite repeats,
  (UNMI)
  28-AUG-1997.
   Canis familiaris
   Canine disease marker-related
  Sequence
   field.)
  ä
   New
  WPI; 1997-435082/40
   Brewer GJ,
  22-FEB-1996;
   18-FEB-1997;
   WO9731011-A1
   11-MAR-2004
   ADG77905 standard; DNA;
   dogs
  oligonucleotide primers for diagnosis of genetic diseases and traits dogs - amplify specific regions of the genome containing rosatellite repeats, especially for diagnosing copper toxicosis and
                        145
   18
  74 AGAGCTGGTTGTTTGAAA 91
   16;
  UNIV MICHIGAN
   Similarity
  6.3%;
Similarity 88.9%;
                       CCCCCTTCTCCTTCTGCC 162
   AAAGCTGGTTTTTTGAAA 1
  21
  Venta PJ,
   BP; 0 A; 9 C; 3
   Conservative
  BP; 8
   Conservative
  (first entry)
  96US-0012060P
   97WO-US002396
  Ą
  6.3%;
  σ
  STATE
  Yuzbasiyan-Gurkan V;
   C; 1 G; 7 T; 0 U; 0 Other;
   21
   용
  <u>,</u>
   ç
   G; 9 T; 0
   Score 14.8;
Pred. No. 4;
   Score 14.8;
Pred. No. 4;
   PCR primer 749.
   Mismatches
   Mismatches
   u;
   0 Other;
  DB 1;
  DB 1;
  2
   2
  Length 21;
  Length 21;
  Indels
   Indels
   0
   0;
  Gaps
   Gaps
   invention
   identify
  0
   0
```

RESULT 90
AAS43680
ID AAS43
XX
AC AAS43

AAS43680 standard; DNA; 21

ВP

```
RESULT 89
AAS43670
 밁
                         Ś
  The invention relates to corneodesmosin protein (I) and nucleic acid (II) CC encoding the corneodesmosin gene, where the gene comprises a base constitution, deletion or insertion at one or more positions. (I) and (II) are useful for screening for agents for use in prognosis, diagnosis (C and treatment of individuals having or being susceptible to corneodesmosin-mediated disease, by monitoring the reaction between the molecules and the agents. The nucleotide and amino acid polymorphisms are useful for diagnosing or determining susceptible to corneodesmosin-mediated disease, which facilitates subsequent treatment of the disease for e.g. inflammatory diseases, in particular poriasis. Fragments of (I) care useful in diagnostic, prognostic or therapeutic methods and as creaseful in diagnostic, prognostic or therapeutic methods and as creaseful in diagnostic, prognostic or therapeutic methods and correcting of the disease of corneodesmosin gene. Antibodies which binds to (I) are useful for screening DNA clone libraries for cells secreting the antigen. (II) is useful as a model to investigate the role of corneodesmosin in normal skin function. A843492-A843749 represent corneodesmosin coding
   Matches
  Query Match
   Sequence
  Disclosure;
  Corneodesmosin protein and polynucleotide encoding it, having one or more polymorphisms useful in treating, diagnosing or determining susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
   WPI; 2001-570627/64.
  23-FEB-2000; 2000GB-00004312
   30-AUG-2001.
  Human; single
  18-DEC-2001
   AAS43670;
  AAS43670 standard; DNA; 21
  sequences,
  Olaveson M,
   23-FEB-2001; 2001WO-GB000795
  WO200162788-A2.
   Homo sapiens
  antipsoriatic;
   Corneodesmosin
   Local
                              18
   16; Conserv
 4
                   CAGATCCCTCATGAATGG
   21 BP; 5
   single
   Page 38;
   Lench N,
   Conservative
  (first entry)
  nucleotide polymorphism; SNP; PCR primer; antiinflammatory; corneodesmosin; inflammatory disease; psoriasis; ss.
   PCR primer #140
   A; 5 C; 5
  nucleotide polymorphisms (SNPs)
   6.3%;
   60pp;
  Allen M,
   ВP
  English.
21
                             35
   0; Mismatches
   G; 6 T; 0 U; 0 Other;
  Score 14.8;
Pred. No. 4:
  Tazi-Ahnini
  B
  77
   2;
  Length
  and PCR primers of the
   Indels
  21;
   0
   0
```

```
AAS43
XX
XX
AC
AC
XX
   RESULT 91
   밁
  5
   Matches
   Query Match
Best Local
  The invention relates to corneodesmosin protein (I) and nucleic acid (II) encoding the corneodesmosin gene, where the gene comprises a base substitution, deletion or insertion at one or more positions. (I) and (II) are useful for screening for agents for use in prognosis, diagnosis and treatment of individuals having or being susceptible to corneodesmosin-mediated disease, by monitoring the reaction between the molecules and the agents. The nucleotide and amino acid polymorphisms are useful for diagnosing or determining susceptible to corneodesmosin-mediated disease, by monitoring the reaction between the molecules and the agents. The nucleotide and amino acid polymorphisms are useful for diagnosing or determining susceptible to corneodesmosin-
   mediated disease, which facilitates subsequent treatment of the disease for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I) are useful in diagnostic, prognostic or therapeutic methods and as research tools for e.g. in drug screening. (II) is useful as probes or primers for detecting an allele of the polymorphism or in the regulation of corneodesmosin gene. Antibodies which binds to (I) are useful for screening DNA clone libraries for cells secreting the antigne. (II) is useful as a model to investigate the role of corneodesmosin in normal skin function. AAS43492-AAS43749 represent corneodesmosin coding sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
                               Corneodesmosin PCR primer #148
  18-DEC-2001
  AAS43678 standard;
   Sequence 21
   Disclosure; Page 38; 60pp; English.
  diseases.
  Corneodesmosin protein and polynucleotide encoding it, having one or more polymorphisms useful in treating, diagnosing or determining susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
  WPI; 2001-570627/64.
   Olaveson M, Lench N,
   30-AUG-2001
  Homo sapiens
   Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory; antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
  Corneodesmosin
   18-DEC-2001
   23-FEB-2000; 2000GB-00004312
   23-FEB-2001; 2001WO-GB000795
   WO200162788-A2
  (OXAG-)
  18
   16;
   4
   Similarity
  OXAGEN
   CAGATGCTTCATGAATGG
  CAGATCCCTCATGAATGG 35
   BP; 5 A;
   Conservative
  (first entry)
  (first entry)
  PCR primer #150
  DNA;
  6.3%;
   5 C; 5 G; 6 T; 0 U; 0 Other;
   Allen M,
  21
   21
   0
   Score 14.8;
Pred. No. 4:
   Mismatches
   Tazi-Ahnini
  DB 1; Length 21;
   2;
   Indels
   ٥,
   Gaps
   0
```

Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;

WO200162788-A2 Homo sapiens.

```
RESULT 92
AAS43672
片
   S
  CC (II) are useful for screening for agents for use in prognosis, diagnosis
CC and treatment of individuals having or being susceptible to
CC corneodesmosin-mediated disease, by monitoring the reaction between the
CC corneodesmosin-mediated disease, by monitoring the reaction between the
CC molecules and the agents. The nucleotide and amino acid polymorphisms are
CC useful for diagnosing or determining susceptible to corneodesmosin-
CC mediated disease, which facilitates subsequent treatment of the disease
CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
CC are useful in diagnostic, prognostic or therapeutic methods and as
CC research tools for e.g. in drug screening. (II) is useful as probes or
CC primers for detecting an allele of the polymorphism or in the regulation
CC of corneodesmosin gene. Antibodies which binds to (I) are useful for
CC useful as a model to investigate the role of corneodesmosin in normal
CC skin function. AAS43492-AAS43749 represent corneodesmosin coding
CC terminic single nucleotide polymorphisms (SNPs) and PCR primers of the
   Matches
  Query Match
Best Local
   Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory; antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
   18-DEC-2001
   Sequence 21
   Corneodesmosin protein and polynucleotide encoding it, having one or more polymorphisms useful in treating, diagnosing or determining susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
   Corneodesmosin PCR primer #142.
   AAS43672 standard; DNA; 21
  The invention relates to corneodesmosin protein (I) and nucle encoding the corneodesmosin gene, where the gene comprises a labstitution, deletion or insertion at one or more positions.
   Disclosure; Page 38;
   diseases.
  WPI; 2001-570627/64
   Olaveson M, Lench N,
  23-FEB-2000; 2000GB-00004312
  23-FEB-2001; 2001WO-GB000795
  30-AUG-2001.
  antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss
   Homo sapiens
  (OXAG-)
  Local Similarity
   18
   16;
  4
  OXAGEN LTD
  CAGATCCCTCATGAATGG
  CAGATGCTTCATGAATGG
   Conservative
  BP; 5
  (first entry
   A; 5 C; 5
   6.3%;
   60pp;
   Allen M,
   English
  0;
  21
   35
   G; 6 T; 0 U; 0 Other;
   Score 14.8;
Pred. No. 4;
   Mismatches
   Tazi-Ahnini
  DВ
  ۲.
   <del>بر</del>
   2
  (I) and nucleic acid (II)
  Length
   Indels
  21;
   a base
   <u>.</u>
  Gaps
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0

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RESULT 93
AAS43676
ID AAS43
XX AAS43
AC AAS43
XX LOTE 18-DE
XX COINE
XX Humar
XX Humar
XX Homo
XX Homo
XX Homo
XX Homo
XX Homo
XX 23-FI
XX 23-FI
XX 23-FI
  문
  Ş
  Query Match
Best Local Similarity
   mediated disease, which facilitates subsequent treatment of the disease for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I) are useful in diagnostic, prognostic or therapeutic methods and as research tools for e.g. in drug screening. (II) is useful as probes or primers for detecting an allele of the polymorphism or in the regulation of corneodesmosin gene. Antibodies which binds to (I) are useful for screening DNA clone libraries for cells secreting the antigen. (II) is useful as a model to investigate the role of corneodesmosin in normal skin function. AAS43492-AAS43749 represent corneodesmosin coding sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
   (II) are useful for screening for agents for use in prognosis, diagnosis and treatment of individuals having or being susceptible to corneodesmosin-mediated disease, by monitoring the reaction between the molecules and the agents. The nucleotide and amino acid polymorphisms are useful for diagnosing or determining susceptible to corneodesmosin-
   Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory; antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
   Corneodesmosin protein and polynucleotide encoding it, having one or more polymorphisms useful in treating, diagnosing or determining susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
   The invention relates to corneodesmosin protein (I) and nucleic acid (II) encoding the corneodesmosin gene, where the gene comprises a base substitution, dejetion or insertion at one or more positions. (I) and
                   23-FEB-2000; 2000GB-00004312
  23-FEB-2001; 2001WO-GB000795
  30-AUG-2001
   Homo sapiens
  Corneodesmosin
  18-DEC-2001
  AAS43676
  AAS43676 standard; DNA; 21
  Sequence 21
   (II) are useful
   Olaveson M, Lench N,
  30-AUG-2001.
   (OXAG-) OXAGEN LTD
   23-FEB-2000; 2000GB-00004312
  23-FEB-2001; 2001WO-GB000795
   18
  16;
   4
   CAGATGCTTCATGAATGG 21
   CAGATCCCTCATGAATGG 35
  Conservative
  Page 38; 60pp; English.
  BP; 5
  (first entry)
  PCR primer #146
  >
  6.3%;
  5 C; 5 G; 6 T; 0 U; 0 Other;
   Allen M,
  ВP
  0
  Score 14.8;
Pred. No. 42;
  Mismatches
   Tazi-Ahnini
  DB 1;
  2;
  Length 21;
  Indels
  0
  Gaps
  0
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CC The invention relates to corneodesmosin protein (I) and nucleic acid (II) CC encoding the corneodesmosin gene, where the gene comprises a base CC substitution, deletion or insertion at one or more positions. (I) and CC (II) are useful for screening for agents for use in prognosis, diagnosis CC corneodesmosin-mediated disease, by monitoring the reaction between the CC corneodesmosin-mediated disease, by monitoring the reaction between the CC useful for diagnosing or determining susceptible to corneodesmosin-mediated disease, by monitoring the reaction between the CC useful for diagnosing or determining susceptible to corneodesmosin-cC mediated disease, which facilitates subsequent treatment of the disease CC are useful in diagnostic, prognostic or therapeutic methods and as creaming. (II) is useful as probbes or creasarch tools for e.g. in drug screening. (II) is useful as probbes or CC primers for detecting an allele of the polymorphism or in the regulation of corneodesmosin gene. Antibodies which binds to (I) are useful for CC screening DNA clone libraries for cells secreting the antigen. (II) is screening DNA clone libraries for cells secreting the antigen. (II) is sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the corneodesmosin coding
  Corneodesmosin protein and polynucleotide encoding it, having one or more polymorphisms useful in treating, diagnosing or determining susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
  (OXAG-) OXAGEN LTD
   Page 38;
   Lench N,
   60pp; English
  Allen M,
  Tazi-Ahnini
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Sequence 21 BP; Ç A, 5 C; 5 G; 6 T; 0 U; 0 Other;

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                                Matches
   Query Match
Best Local
               18 CAGATCCCTCATGAATGG 35
4
                                l Similarity
16; Conserv
CAGATGCTTCATGAATGG
                                Conservative
  88.9%;
   6.38;
21
                                0;
   Score 14.8;
Pred. No. 42;
                               Mismatches
   DB 1;
                                Ņ
   Length
                                Indels
   21,
                                <u>,</u>
                               Gaps
                                0
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RESULT 94
AAS43674
ID AAS43
XX AAS44
XX Human
XX Human
XX Homo
X
  WPI; 2001-570627/64
   Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory; antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
   18-DEC-2001
   AAS43674 standard;
   Olaveson M,
   23-FEB-2000; 2000GB-00004312
  23-FEB-2001; 2001WO-GB000795.
  30-AUG-2001.
  WO200162788-A2
   Homo sapiens.
  Corneodesmosin PCR
  OXAGEN
   Lench N,
  (first entry)
  GIT
   primer #144.
  DNA; 21
   Allen M,
  ₽P
   Tazi-Ahnini
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The invention relates to corneodesmosin protein (I) and nucleic acid (II)
CC encoding the corneodesmosin gene, where the gene comprises a base
CC substitution, deletion or insertion at one or more positions. (I) and
CC (II) are useful for screening for agents for use in prognosis, diagnosis
CC and treatment of individuals having or being susceptible to
CC corneodesmosin-mediated disease, by monitoring the reaction between the
CC molecules and the agents. The nucleotide and amino acid polymorphisms are
CC useful for diagnosing or determining susceptible to corneodesmosin-
CC mediated disease, which facilitates subsequent treatment of the disease
CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
CC are useful in diagnostic, prognostic or therapeutic methods and as
CC research tools for e.g. in drug screening. (II) is useful as probes or
CC primers for detecting an allele of the polymorphism or in the regulation
CC of corneodesmosin gene. Antibodies which binds to (I) are useful for
CC screening DNA clone libraries for cells secreting the antigen. (II) is
CC useful as a model to investigate the role of corneodesmosin in normal
CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
conception.
   Query Match
Best Local (
   Matches
New knockdown sequences, useful in lowering the amount of RNA and/or protein production in cells used in drug development process.
   24-APR-2003; 2003WO-EP004362
   24-APR-2003; 2003WO-EP004362
  04-NOV-2004
  WO2004094636-A1
  Unidentified
   ds; RNA production;
  Knock-down target sequence
  27-JAN-2005
  ADU26863 standard; DNA;
  Sequence 21
  Corneodesmosin protein and polynucleotide encoding it, having one or more polymorphisms useful in treating, diagnosing or determining susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
  Arts GJF,
  knock-down target.
   Disclosure; Page 38; 60pp; English
   (GALA-) GALAPAGOS GENOMICS NV. (VSCH/) VAN DER SCHUEREN J.
   Local Similarity
   18
   16;
   4
  CAGATGCTTCATGAATGG
  CAGATCCCTCATGAATGG 35
  Ś
  Lambrecht MJY,
  Conservative
  BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
   (first entry)
  Bergs
  CTL)
  protein production; drug development;
  6.3%;
  21
  #261.
  ВP
  Djokic
   0
   21
   Score 14.8;
Pred. No. 42;
   Mismatches
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   Clasen
   BB
  ŖĮ,
  1; Length 21;
   2
  Indels
   <u>,,</u>
  Gape
   0
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BX PPX BX PPX BX BX BX BX CXX AX CXX

Claim 11; SEQ ID NO 264; 402pp; English

Query Match

Sequence

21 BP; 8 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

6.3%;

Score 14.8;

DB 1;

Length 21;

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RESULT 96
ACL40871/c
ID ACL408
á
   #88888##
   밁
                                     The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or gene ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (C) (b) a carrier. The pharmaceutical composition may also comprise a colon composition composition are selected from ABC4, C20orf103, CACNAID, CDH6, CST, ENPP3, CFLJ11850, GPE54, HAVCR1, SLC6A3, SLC3DA4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CC cancer, stomach cancer, and esophageal cancer. Note: The sequence cancer this patent did not form part of the printed specification, but can be obtained in electronic form cancerly from WIPO at
  Query Match
Best Local Similarity
Matches 16; Conserv
  Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
   Вe X,
  ACL40871 standard; RNA;
   Claim 3; SEQ ID NO 1943; 113pp; English
   WPI; 2005-075568/08.
  20-MAY-2003; 2003US-0471729P
  19-MAY-2004; 2004WO-US015645
  06-JAN-2005
   Synthetic
  Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer;
   C20orf103 siRNA sense sequence,
   24-MAR-2005
  ACL40871;
   Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
  The invention relates to a polynucleotide comprising an RNA sequence. The polynucleotides, vector, libraries, and method are useful in lowering the amount of RNA and/or protein production in cells used in drug development process. The present sequence represents a knock-down target sequence.
                          ftp.wipo.int/pub/published_pct_sequences
  WO2005001092-A2
   short interfering RNA; gene silencing.
   150
   18
   Wei L, Slonim DK,
   TTCTCCTTCTGCCATGAT 167
   cancer.
   TTCTACTTCTGCCATGGT 1
  Conservative
   (first entry)
   6.3%;
   21
  Howes
   ВP
  0;
   Score 14.8;
Pred. No. 4:
   SEQ ID
  Mismatches
  ;HS
  42;
   1943.
   밁
  1;
  2
  Length
  Indels
   21
  0
  1 for
  Gaps
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RESULT 97
ADW85397/c
ID WADW853
XX ADW853
XX ADW853
XX ADW853
XX ADW853
XX MAP3X9
XX MAP3X9
XX MAP3X9
XX MAP3X9
XX MITIAL
XX Uniden
XX U
   ş
  The invention relates to the novel use of a mixed lineage kinase (MLK) CC family kinase inhibitor for treating asthma. Where the asthma is CC associated with a risk factor selected from an at-risk haplotype for CC asthma, at-risk haplotype in MAP3K9 gene, polymorphism in MAP3K9 nucleic CC acid, dysregulation of MAP3K9 mRNA expression, dysregulation of a MAP3K9 CC mRNA isoform, and/or increased MLK1 protein expression. The invention CC further comprises: a method for the diagnosis or identification of CC susceptibility to asthma; a method for the use of a first nucleic acid conclectle for diagnosing asthma or susceptibility to asthma in a sample; a CC method for assessing asthma or susceptibility to asthma in a sample; a CC family kinase nucleic acid inhibitor in a target population or in an CC individual with an at-risk haplotype for asthma, at-risk haplotype in the MAP3K9 gene, polymorphism in the MAP3K9 nucleic acid, dysregulation of CC MAP3K9 gene, polymorphism in the MAP3K9 nucleic acid, dysregulation of CC MAP3K9 mRNA expression, increased MLK1 protein isoform expression; a method for assessing the response to treatment with an MLK1 inhibitor in a target population including an CC individual with an at-risk haplotype for asthma, at-risk population including an CC comprising a sample for the presence or absence of at least one haplotype comprising a cid complise of detection the nation of the population including an CC comprising a cid complied of detection the nation of the population including an CC comprising a cid complied of detection the nation of the population including an CC comprising and the presence of at least one haplotype comprising at least one haplotype comprising and the presence of a cid comprising at least one haplotype comprising and control of the presence of a comprising at least one comprising at least one comprising and control of the 
  밁
  Matches
  Best Local Similarity
  antiarthritic; antipsoriatic; neuroprotective; gastrointestinal-gen.; respiratory disease; chronic obstructive pulmonary disease; chronic bronchitis; inflammation; ss; primer; PCR.
  14-JUL-2003; 2003US-0487072P.
05-APR-2004; 2004US-0559611P.
   ADW85397 standard; DNA; 21
  Disclosure; Fig 12; 640pp; English
  expression or activity
   asthma,
   a medicament
  Use of
  WPI; 2005-122681/13
   Hakonarson H,
  (DECO-) DECODE GENETICS EHF
   14-JUL-2004; 2004WO-US022446
  27-JAN-2005
   WO2005007144-A2
   antiasthmatic; respiratory-gen.;
  mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9;
  MAP3K9 marker amplification
   07-APR-2005
  ADW85397
   nucleic acid capable of detecting the presence or absence of at least specific allele; a reagent kit for assaying the presence of at least haplotype comprising 2 or more alleles comprising: at least one eled nucleic acid capable of detecting at least one specific allele of
   149
  18
   mixed lineage kinase family kinase inhibitor in the manufacture cament for treatment of asthma associated at-risk haplotype for , at-risk haplotype in MAP3K9 gene or increased MLK1 protein
  16;
  CTTCTTGTTCTGCCATGA 1
   CTTCTCCTTCTGCCATGA 166
  Conservative
   (first entry
   Gurney
  88.9%;
   ME,
   Halapi E;
   ВP
  0
  forward primer #1336
  Pred. No. 42;
  Mismatches
   antiinflammatory; antirheumatic;
  2
  Indels
  0
  Gaps
  least
  œ,
  0
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CC the haplotype, and reagents for detection of the label; and a reagent kit CC comprising 2 or more alleles comprising: at least one haplotype CC comprising 2 or more alleles comprising: at least one nucleic acid CC comprising at least one nucleotide sequence that is at least partially CC compilementary to a part of nucleotide sequence of MAPSY9, capable of CC acting as a primer for a primer extension reaction and capable of CC detecting 2 or more specific alleles of the haplotype. The MLK family CC kinase inhibitor has the following activities: antiasthmatic, respiratory components; and gastrointestinal gen. The MLK family kinase control is useful for the treatment of asthma associated with a risk CC factor selected from at-risk haplotype for asthma, at-risk haplotype in CC mAP3X9 gene, polymorphism in MAP3X9 mucleic acid, dysregulation of MAP3X9 gene, polymorphism in MAP3X9 mucleic acid, dysregulation of MAP3X9 gene, polymorphism in MAP3X9 mucleic acid, dysregulation of MAP3X9 cman expression, increased MLK1 biochemical activity and/or increased MLK1 protein sysression; and in diagnosis or identification of susceptibility to asthma. The inhibitor is also useful for the treatment of other respiratory diseases associated with MAP3X9 or other members of the JNK pathway such as chronic obstructive pulmonary disease, chronic psorniatis, multiple sclerosis and inflammatory bowel disease, This complitying a marker of the MAP3X9 kinase, where MAP3X9 is a part of amplifying a marker of the MAP3X9 kinase, where MAP3X9 is a part of the MAP3X9. Mitogen-Activated Protein Kinase (MAPK) signal transduction pathways, œ,

Matches Query Match Local 49 21 16; Similarity CCTTGGTGATGAGTGAGT 66 CCTTGGTGTTAAGTGAGT Conservative 88.9%; 6.3%; 4 0; Score 14.8; Pred. No. 4 Mismatches 42; DB 1; Length 21 2 0, Gaps

0

Sequence 21 BP; 8

?

6 C; 3

G; 4 T; 0 U; 0 Other;

98

밁 Ś

AEC02566 standard; DNA; 21 BP

AEC02566

03-NOV-2005 (first entry)

Human IgE short interfering nucleic acid SEQ ID NO 169

ARESULT 98
ARECOZÓ ID ARECO
XX ARECO
XX ARECO
XX ALUM
DE Humm
XX ALUM
antiallergic; automorphressive; expression; RNA interference; allowers dimmunosuppressive; expression; RNA interference; allowers disease; atopic dermatitis; urticaria; dermatological; dermatological disease; immediate type hypersensitivity; immunosuppressive; asthma; antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory; ear, nose, throat disease; inflammation; respiratory disease; ear, nose, throat disease; inflammation; respiratory disease; gene silencing; antiallergic; antiinflammatory; antiasthmatic; dermatological; immunosuppressive; expression; RNA interference; allergy;

Homo sapiens

WO2005080410-A1

01-SEP-2005

21-FEB-2005; 2005WO-NZ000021

20-FEB-2004; 2004US-0546434P

GENESIS RES & DEV CORP LTD

Watson JD, N Abernethy N, Murison GJ, Webster ဂ္ Grigor MR, Havukkala IJ, Munro Ģ

WPI; 2005-591970/60

. . . .

New composition comprises small interfering nucleic acid molecule (siNA) capable of reducing expression of a target gene that is active in a IgE-mediated disorder, useful for treating, e.g. allergic rhinitis or atopic dermatitis.

Disclosure; SEQ ID NO 169; 178pp; English.

The invention describes a composition comprising a small interfering C nucleic acid molecule (siNA) capable of reducing expression of a target CC gene that is active in a IgE-mediated disorder, a genetic construct that CC expresses the siNA, and a binding agent that specifically binds to a CC target antigen expressed on the surface of the cell. Also described are: C a method for the treatment of an IgE-mediated disorder in a patient; prevention of IgE-mediated disorder in a patient; CC prevention of IgE-mediated disorder in a patient, reduction of CC a specific antigen in a patient; and preventing or reduction of IgE-mediated immune response to a specific antigen in a patient. The composition CC is useful in the preparation of a medicament useful for the treatment of CC an IgE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis, CC urticaria, atopic dermatitis, food allergies, diseases that benefit from CC the reduction of eosinophila in the tissues of the respiratory system, CC or disorders having hypersensitivity immune reaction. This sequence CC represents a siNA for supression of human IgE expression.

Sequence 21 BP; 4 A; 2 C; 9 G; 6 T; 0 U; 0 Other;

Ś Query Match 6.3%; Score 14.8; D Best Local Similarity 88.9%; Pred. No. 42; Matches 16; Conservative 0; Mismatches Query Match Best Local : 1 TGTCTGGGTCATGGGGGC 18 DB 1; Length 21; 2; Indels 0; Gaps <u>.</u>

Search completed: October 2, 2006, 15:45:39 Job time : 0.001 secs

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TGTTTGGGTCATGGAGGC 21

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S-11-060-756-81497
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10-310-914A-116013
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  11-060-756-81484
11-060-756-81500
11-060-756-81511
   11-060-756-81501
   Published Applications NA, Major
   ; Search time 0.001 (without alignments) 1797.376 Million cel
  5.1.9
Biocceleration
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US-10-681-773-779-55
US-10-681-773-779-75
US-10-681-773-778-26
US-10-956-157-111003
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US-10-310-914A-136033
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11939, pp

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11939, pp

129384, pp

129386, pp

1393186, pp

1393186, pp

1393186, pp

139319, pp
   42861,
70955,
77134,
77826,
55282,
131003
  20812,
24075,
41906,
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APPLICANT: Mei, Rui TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms

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ALIGNMENTS

RESULT 1 US-10-891-260-437

Sequence 437, Application US/10891260 Publication No. US20050227244A1 GENERAL INFORMATION:

APPLICANT: Affymetrix, APPLICANT: Matsuzaki,

```
TITLE OF INVENTION: Metilous V.
FILE REFERENCE: 3522.3
CURRENT APPLICATION NUMBER: US/10/891,260
CURRENT FILING DATE: 2004-07-13
PRIOR APPLICATION NUMBER: 10/681,773
PRIOR FILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 10244
SOFTWARE: Patentin version 3.2
SEQ ID NO 437
LENGTH: 33
TYPE: DNA
ORGANISM: homo sapien
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81484
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-81484
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically de
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,91
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1140145
LENGTH: 28
TYPE: RNA
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US-11-060-756-81484/c
US-11-060-756-81484, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
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US-10-310-914A-1140145/c
US-10-914A-1140145, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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   ; ORGANISM: Human
US-10-310-914A-1140145
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  9.8%;
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Acid Arrays for Monitoring
Genes
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Pred.
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Pred. No. 18
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  detectable
  43
  B
  멂
  1:
  1;
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of. Drug

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US-11-060-756-81500
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US-10-310-914A-1072814/c
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publication No. US20060003322A1
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US-11-060-756-81511/c
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  ફ
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US-11-060-756-81500/c
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  ঠ
   APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 81511
  Sequence 81511, Application US/11060756 Publication No. US20050221354A1 GENERAL INFORMATION:
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   GENERAL INFORMATION:
   APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AMI01083 (031996-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
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US-10-310-914A-1072814
   US-11-060-756-81498/c
   US-11-060-756-81487/c
   APPLICANT: Wyeth
APPLICANT: Mounts, Willam Martin
APPLICANT: Mounts, Willam Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AMIO1083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81498
TENES: NOSE AND NO
   Sequence 81498, Application US/11060756 Publication No. US20050221354A1 GENERAL INFORMATION:
   CURRENT FILING DATE: 2005-0:
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3
SEQ ID NO 81487
LENGTH: 25
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   Sequence 81487, Application US/11060756 Publication No. US20050221354A1
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  TITLE OF INVENTION: Target Genes FILE REFERENCE: AM101083 (031896-042000) CURRENT APPLICATION NUMBER: US/11/060,756
  APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
  FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
   APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
  TYPE: DNA
   LENGTH:
  Local Similarity
es 22; Conserv
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   23
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   2005-02-18
  8.8%;
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95.7%;
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2
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  Score 21.4;
Pred. No. 20;
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   Gaps
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Query Match

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Score 20.8;

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Length

25;

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Sequence 116013, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
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  RESULT 11
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  RESULT 10
US-10-310-914A-596177
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US-11-060-756-81501/c
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US-11-060-756-81501
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   SOFTWARE: PatentIn version 3.3
SEQ ID NO 596177
LENGTH: 24
   APPLICANT: Mounts, william Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 81501
  Sequence 81501, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
   Sequence 596177, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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   TYPE: RNA
ORGANISM: Human
-10-310-914A-596177
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   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT EPPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat
  TYPE: DNA
   Local Similarity
  139
   154 CCTTCTGCCATGATTTTAAGATTC 177
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  CTTCTGCCATGATTTTAAGATTCC 178
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  Conservative
  Conservative
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  8.6%;
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  8.8%;
   91.7%;
  Score 20.4; D
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US-11-060-756-81497/c

| Sequence 81497, Application US/11060756 |
| Publication No. US20050221354A1 |
| GENERAL INFORMATION: Molecular Martin APPLICANT: Wyeth |
| APPLICANT: Wyeth |
| TITLE OF INVENTION: Nucleic Acid Arrays for More than 100 |
| TITLE OF INVENTION: Target Genes |
| FILE REFERENCE: AM101083 (031896-042000) |
| CURRENT FILING DATE: 2005-02-18 |
| NUMBER OF SEQ ID NOS: 303284 |
| SOFTMARE: Patentin version 3.2 |
| SEQ ID NO 81497 |
| LENGTH: 25 |
| TYPE: DNA |
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  US-11-060-756-81488/c
; Sequence 81488, Application US/11060756
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  ; ORGANISM: probe US-11-060-756-81488
  US-10-310-914A-116013
  CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 81488
  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUSO1 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: PatentIn version 3.3 SEQ ID NO 116013
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Best Local Similarity
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   APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AMIO1083 (031896-042000)
FILE REFERENCE: AMIO1083 (031896-042000)
  LENGTH: 25
TYPE: DNA
   TYPE: RNA
ORGANISM: Human
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   0; Mismatches
Score
Pred.
   Score 20.4;
Pred. No. 26;
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No. 28;
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RESULT 16
US-11-121-849-630324
; Sequence 630324, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic
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  ; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-628945
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US-11-121-849-628945
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-81505
  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3884.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 628945
   Sequence 81505, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
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Best Local Similarity 88.0%;
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   Sequence 628945, Application US/11121849 Publication No. US20050272080A1
  Query Match
  Matches
   GENERAL INFORMATION: APPLICANT: John Pal
  Matches
   APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
   CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
  NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
   APPLICANT: Wyeth APPLICANT: Moun
  Local Similarity 88.0%;
   195 GCAAATGCTAACGCCATGCTTCTTG 219
  152 CTCCTTCTGCCATGATTTTAAGATT 176
  156
  25
  25
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   1 GCANATACTGACACCATGCTTCTTG 25
  CACCTTCTGCCATGATTGTAAGTTT
   John Palma
  TTCTGCCATGATTTTAAGATTCCAG 180
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  Conservative
               Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
  ; Score 20.2; D; Pred. No. 28; 0; Mismatches
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  Score 20.2;
Pred. No. 28
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RESULT 18

US-10-310-914A-1073215/c

US-10-10-914A-1073215, Application US/10310914A

Publication No. US20060003322A1

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   US-10-310-914A-661150
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   ; ORGANISM: Homo sapien US-11-121-849-630324
  US-10-310-914A-661150/c
  APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable of INVENTION: Bioinformatically detectable of INVENTION: USES thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1073215
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 661150
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LENGTH: 25
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   APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat
  PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
   FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
   TITLE OF INVENTION: Microarrays
                                    TYPE: RNA
                    ORGANISM: Human
  ORGANISM: Human
  TYPE: RNA
  TYPE: DNA
  ENGTH:
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Pred. No. 28;
0; Mismatches
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Pred. No. 30
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Mismatches
  25
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   ۲.
   2
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   Length 25;
   Indels
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Query Match

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Score 19.8;

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**1**;

Length 25;

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; Sequence 81510, Application US/11060756
; Publication No. US20050221354A1
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; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-597791
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   PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 597791
  Sequence 602992, Application US/11121849 Publication No. US20050272080A1 GENERAL INFORMATION:
   GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
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SOFTWARE: Microarray Probe
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PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
   APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
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CURRENT APPLICATION NUMBER: US/11/121,849
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  18
  21;
   21;
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  Similarity
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  CCCTTGGTGATGAGTGAGTTCAC 70
  CAGATCCCTCATGAATGGTTTAG
   CAGATCCCTTATGAATGGTTCAG 23
   Conservative
  Conservative
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  8.4%;
  8.48;
  91.3%;
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   0,
  0
  Score 19.8; I
Pred. No. 31;
0; Mismatches
   Pred. No. 31;
0; Mismatches
   40
  40
  В
  B
   ۲.
  2
   ν
..
   2;
   Length
   Indels
   Indels
  25;
  25;
  0,
   0,
   0,:
   Gaps
  Gaps
   Gaps
  0;
   0
   0
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APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Moi
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81510
   US-11-121-849-595763/c
US-11-121-849-595763/c
Sequence $95763, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:
APPLICANT: John Palma
ITITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
ITITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 595763
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  ; TYPE: DNA; Homo sapien; ORGANISM: Homo sapien US-11-121-849-149128
   RESULT 22
US-11-121-849-149128
   밁
  S
  밁
  ORGANISM: probe US-11-060-756-81510
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  NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe S
SEQ ID NO 149128
  GENERAL INFORMATION:
   Sequence 149128, Application US/11121849 Publication No. US20050272080A1
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  Query Match
  CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
   APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Microarrays
  FILE REFERENCE: 3684.1
  TYPE: DN
   APPLICANT: Wyeth
ORGANISM: Homo sapien
   ENGTH:
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  DNA
  157
  40
   25
  l Similarity
21; Conserv
  N
  TCTGCCATGATTTTAAGATTCCAG 180
  GTGCCATCCCCATAGTAATGAGTG
  greccarecerregreareagre 63
   TCTGCCATGATTGTAAGTTTCCTG 2
   Conservative
  Conservative
  2004-05-03
   8.1%;
   8.1%;
   Sequence Listing Generator V 1.1
  .
   0
   Score 19.2;
Pred. No. 35;
   Score 19.2;
Pred. No. 35;
  Mismatches
   Mismatches
  25
  DB
   Monitoring
  멂
  1;
  Formalin Fixed Paraffin Embedded
  Length
  Length
  Indels
   Expression Profiles of Drug
  25,
  0
   0
  Gaps
  Gaps
  0
   0
  ဒ္ဌ
  ŝ
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  밁
   S
  밁
  Ś
RESULT 26
US-11-121-849-673887
   ई
  ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-595764
  US-11-121-849-668361/c
   RESULT 25
   US-11-121-849-595764/c
   US-11-121-849-595763
   Sequence 595764, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
   Query Match
Best Local (
   Matches
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   LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
-11-121-849-668361
   GENERAL INFORMATION:
  Matches
  APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
  Sequence 668361, Application US/11121849
Publication No. US20050272080A1
   CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1
  PRIOR FILING DATE: 2004-05-0
NUMBER OF SEQ ID NOS: 673904
   SOFTWARE: Microarray Probe EQ ID NO 668361
  PRIOR APPLICATION NUMBER: 60/567,949
  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
  NUMBER OF SEQ ID NOS: 673904
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   24
  25
   64
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   Similarity
  Similarity
  Similarity
  AGTTCACGTGAGAGCTGGTTGTTT
  AGTGAGTTCTTGTGAGAGCTGGCT
   John Palma
  AGTTCTTGTGAGAGCTGGCTGTTT
   AGTTCACGTGAGAGCTGGTTGTTT 87
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   Conservative
  Conservative
  2004-05-03
  87.5%;
  87.5%;
   87.5%;
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Pred. No. 3:
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Pred. No. 35;
   Score 19.2;
Pred. No. 35;
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   Mismatches
  87
   83
  DB 1;
   DB 1;
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  Length 25;
  Length 25;
   Length 25;
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   Indels
  Indels
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  0
   <u>,</u>
  Gaps
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RESULT 27

US-10-310-914A-661230/c

US-10-910-914A-661230, Application US/10310914A

; Publication No. US200600003322A1

; GENERAL INFORMATION:
  RESULT 28
US-10-310-914A-66369
  밁
  Ś
   US-10-310-914A-661230
   밁
  Ś
  ; ORGANISM: Homo sapien US-11-121-849-673887
                               GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200;CBUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILLNG DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
   NUMBER OF SEQ ID NOS: 138402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 661230
SEQ ID NO 66369
LENGTH: 23
  Sequence 66369, Application US/10310914A Publication No. US20060003322A1
  Matches
   Query Match
   NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 673887
LENGTH: 25
  Matches
   Sequence 673887, Application US/11121849 Publication No. US20050272080A1
  Query Match
  GENERAL INFORMATION:
   APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat TITLE OF INVENTION: Bioinformatically détectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06
  CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1
   APPLICANT: John Palma
  TYPE: RNA
ORGANISM: Human
  LENGTH:
  8.1%;
Local Similarity 87.5%;
es 21; Conservative
   Local Similarity
  22
  64 AGTTCACGTGAGAGCTGGTTGTTT 87
  71 GTGAGAGCTGGTTGTTGAAAG 92
  20;
  Conservative
  8.0%;
   0;
  0
   Score 18.8;
   Pred. No.
   Score 19.2;
Pred. No. 3
  Mismatches
  Mismatches
   DB
  ₽B
   1
  ۲.
  ų,
   Length 22;
  Indels
  Indels
  <u>,,</u>
  0,
  Gaps
  Gaps
  0;
  0:
   and
  ΰ
```

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; SEQ ID NO 99099
; LENCTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-99099
RESULT 31
US-10-719-900-570264
  유
   US-10-310-914A-1158304
  밁
  S
   RESULT 29
US-10-310-914A-99099
  밁
  8
  US-10-310-914A-66369
   US-10-310-914A-1158304
   RESULT 30
   APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Batentin version 3.3
SEQ ID NO 1158304
  Sequence 1158304, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
   GENERAL INFORMATION:
   Matches
   Query Match
   Matches
  Query Match
Best Local Similarity
   Sequence 99099, Application US/10310914A Publication No. US20060003322A1
   Matches
   Query Match
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
  APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kyuzat
   LENGTH: 24
TYPE: RNA
ORGANISM: Human
  ORGANISM: Human
   Local
   ocal Similarity
  140 CTGCTCCCCCTTCTCCTTCTGC 161
  137 CACCTGCTCCCCTTCTCCTTC 158
  139 CCTGCTCCCCCTTCTCTG 160
   13;
   l Similarity 59.1
  ccuecuuccccuucaccuucue 24
  |:||:||| |: |:||::|:||
cugcucccgcugcuccuucugc 22
  ceccuecucccccuuceccuuc 22
   Conservative
   Conservative
   8.0%;
  8.0%;
   8.0%;
  ; Score 18.8; D; Pred. No. 38; 7; Mismatches
  7; Mismatches
   6; Mismatches
  Score 18.8;
Pred. No. 38;
   Score 18.8;
Pred. No. 3
   BG
   В
   멂
   1;
   1:
   1:
   <u>۲</u>
   2
   Length 24;
   Length 23;
   Length 23;
   Indels
   Indels
   0
  0
   0
  Gaps
  0
   0
   0
```

```
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detecta
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087,0200,CPUS01
CURRENT APPLICATION UNMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 845546
LENGTH: 25
  맑
   밁
   á
  ; TYPE: DNA; ORGANISM: Mus musculus US-10-719-900-570264
  Ś
   ; ORGANISM: Probe Sequence US-10-956-157-161277
  RESULT 32
US-10-956-157-161277/c
   US-10-310-914A-845546/c
   RESULT 33
   Sequence 161277, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: MOUNTS, WILLIAM
APPLICANT: NOUNTS, WILLIAM
APPLICANT: NOUNTS, WILLIAM
TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
TITLE REPERENCE: 011896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN version 3.2
SEQ ID NO 161277
LENGTH: 25277
   Sequence 845546, Application US/10310914A Publication No. US20060003322A1
  SEQ ID NO 570264
  Sequence 570264, Application US/10719900 Publication No. US20050026164A1
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   Matches
   Query Match
   GENERAL INFORMATION:
  Query Match
   CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
   APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILS REFERENCE: 3528.1
  NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
   TYPE: DNA
  LENGTH:
   Local Similarity
  Local Similarity
   115 CTGCTCCCACTCTTGCATGAGA 136
  22
  17 GCAGATCCCTCATGAATGGTTT 38
   20;
  N
  GCAGATCCTTCATGAATGGCTT
  Conservative
   Conservative
  8.0%;
   90.9%;
  <u>,</u>
   0; Mismatches
   Score 18.8;
Pred. No. 39;
  Score 18.8;
Pred. No. 39;
  Mismatches
   detectable group
   DB
  BB
  1:
   1;
   Length 25;
   Length 25;
  Indels
   Indels
   of novel regulatory genes and
  0,
   0
   Gaps
   0,
  0
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```
APPLICANT: Shen, Mei-Mei

APPLICANT: Kennedy, Giulia

FILE REFERENCE: 3522.2

FULE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-08

NUMBER OF SEQ ID NOS: 124031

SOFTMARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 24075

LENGTH: 25
   ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-24075
   US-10-681-773-24075/c
  RESULT 35
   밁
  S
  RESULT 34
US-10-681-773-20812
   무
  S
   ; ORGANISM: Human
US-10-310-914A-845546
  Best Loc
Matches
   Sequence 24075, Application US/10681773 Publication No. US20040146890A1 GENERAL INFORMATION:
  SEQ ID NO 20812
LENGTH: 25
  Sequence 20812, Application US/10681773 Publication No. US20040146890A1
Query Match
Best Local Similarity
  Query Match
   TYPE: DNA
ORGANISM: Homo sapien
-10-681-773-20812
   GENERAL INFORMATION:
  Best Local Similarity 90.9 Matches 20; Conservative
   APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
FILE REFERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
  Query Match
  APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
APPLICANT: Shen, Mei-Mei
  APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
APPLICANT: Shen, Mei-Mei
   Local
  139 CCTGCTCCCCTTCTCTG 160
   22
  19 AGATCCCTCATGAATGGTTTAGTGC 43
   μ
   Similarity
   AGATCCCTTACGAATGGCTTGGTGC
  Conservative
   7.9%;
   8.0%;
90.9%;
7.9%;
84.0%;
  ; Score 18.6; D; Pred. No. 41; O; Mismatches
  0; Mismatches
   Score 18.8;
Pred. No. 39;
Score 18.6; DB Pred. No. 41;
   25
   DB 1; Length 25;
  BB
                 ۲
               Length 25;
  Length 25;
  Indels
  0;
  Gaps
  Gaps
  0
  0
```

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밁
                          Ś
  ; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-42861
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   ; TYPE: DNA; Homo sapien; ORGANISM: Homo sapien US-10-681-773-41906
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US-10-681-773-42861/c
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   US-10-681-773-41906
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 42861
  NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 41906
LENGTH: 25
  Sequence 42861, Application US/10681773
Publication No. US20040146890A1
GENERAL INFORMATION:
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  Query Match
Best Local Similarity
  Matches
   Query Match
Best Local !
  Sequence 41906, Application US/10681773 Publication No. US20040146890A1
   Matches
  GENERAL INFORMATION:
  APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms:
FILE REFERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR PILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR FILING DATE: 2002-10-08
   APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
APPLICANT: Shen, Mei-Mei
   FILE REFERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR FILING DATE: 2002-10-08
   APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
APPLICANT: Shen, Mei-Mei
APPLICANT: Kennedy, Giulia
   APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
   Match 7.9%;
Local Similarity 84.0%;
25
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  18 CAGATCCCTCATGAATGGTTTTAGTG 42
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  73 GAGAGCTGGTTGTTGAAAGAGCCT
   21;
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AGAACTAGTTGTTGAAAAGAGCCTG
                               AGAGCTGGTTGTTTGAAAGAGCCTG 98
  GAGAACTAGTTGTTGAAAAGAGCCT
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   Conservative
  Conservative
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   0
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Pred. No. 41;
   Score 18.6;
Pred. No. 41;
   Mismatches
  Mismatches
   Mismatches
   25
  97
   DB 1;
  В
  ۲,
   4;
   Length 25;
  Length 25
  Indels
   Indels
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  <u>,,</u>
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   Gaps
  Gaps
  Gaps
   0,
  0
   0
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RESULT 40
US-10-681-773-77826/c
; Sequence 77826, Application US/10681773
  밁
   S
  용
  ঠ
   ; ORGANISM: Homo sapien
US-10-681-773-77134
   US-10-681-773-77134
   RESULT 39
  ; ORGANISM: Homo sapien
US-10-681-773-70955
   US-10-681-773-70955
  APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
FILE REFERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 70955
LENGTH: 25
LENGTH: 25
  Sequence 70955, Application US/10681773
Publication No. US20040146890A1
GENERAL INFORMATION:
APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
APPLICANT: Shen, Mei-Mei
APPLICANT: Kennedy, Giulia
   NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 77134
  Query Match
Best Local
  Sequence 77134, Application US/10681773 Publication No. US20040146890A1
  Query Match 7.9%;
Best Local Similarity 84.0%;
Matches 21; Conservative
  Matches
  GENERAL INFORMATION:
  APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
FILE REFERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR PILING DATE: 2002-05-14
   PRIOR APPLICATION NUMBER: 60/417,190 PRIOR FILING DATE: 2002-10-08
  APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
APPLICANT: Shen, Mei-Mei
APPLICANT: Kennedy, Giulia
  LENGTH: 25
TYPE: DNA
   TYPE: DNA
   16 GGCAGATCCCTCATGAATGGTTTAG 40
   17 GCAGATCCCTCATGAATGGTTTAGT 41
  21;
  1 GCAGATCCCTTACGAATGGCTTGGT 25
  Similarity
  GGCAGATCCCTTACGAATGGCTTGG 25
  Conservative
  7.9%;
  0,
  0; Mismatches
  Score 18.6;
Pred. No. 41;
   Score 18.6;
Pred. No. 41
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   DB 1;
  4.
  4;
   Length 25;
   Length
  Indels
  Indels
  0
  0
  Gaps
  Gaps
  0
  0
```

```
APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in H:
FULE REFERENCE: 3522.2
CURRENT PPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR FILING DATE: 2003-05-14
PRIOR PPLICATION NUMBER: 60/470,475
PRIOR PPLICATION NUMBER: 60/417,190
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR FILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 77826
TYPE: 70.25
TYPE: 70.25
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  5
  ; ORGANISM: Probe Sequence US-10-956-157-55282
  밁
   Ś
   US-10-956-157-131003
   RESULT 42
   US-10-681-773-77826
  US-10-956-157-55282/c
  RESULT 41
   Sequence 131003, Application US/10956157 Publication No. US20050118625A1 GENERAL INFORMATION:
  Sequence 55282, Application US/10956157 Publication No. US20050118625A1 GENERAL INFORMATION:
   NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55282
LENGTH: 25
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  Matches
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  Publication No. US20040146890A1 GENERAL INFORMATION:
   Query Match
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: MOUNTS, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
  APPLICANT: Wyeth
APPLICANT: MOUNTE, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
  LENGTH: 25
   APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
   TYPE: DNA
   ORGANISM: Homo sapien
  Local
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  149 CTTCTCCTTCTGCCATGATTTTAAG 173
   25
  25
   72 TGAGAGCTGGTTGTTTGAAAGAGCC 96
   21;
  Similarity
   Similarity
   CTTCACCTTCCACCATGATTCTAAG
  TGAGAACTAGTTGTTGAAAAGAGCC
  Conservative
   Conservative
  7.9%;
   7.9%;
  0
   0,
  Score 18.6; D
Pred. No. 41;
0; Mismatches
  Score 18.6;
Pred. No. 41;
   Mismatches
  ь
   B
  DВ
  ۲;
   Length
  Length 25;
   in Humans
   25;
   <u>.</u>
  0
   Gaps
  Gaps
   0;
  0
```

```
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AMIJO1083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOPTWARE: Patentin version 3.2
SEQ ID NO 81506
LENGTH: 25
TYPE: DIA
ORGANISM: probe
US-11-060-756-81506
  8
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   밁
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  ; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-131003
   US-10-956-157-199403
  APPLICANT: Mounts, William
TITLE OF INVENTION: HUUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUWAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FILING DATE: 2014-10-04
RUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 199403
LENGTH: 25
TYPE: DNA
ORGANISM: Probe Sequence
  Sequence 81506, Application US/11060756 Publication No. US20050221354A1
   Matches
  SEQ ID NO 131003
  Query Match
Best Local S
  Query Match
  Sequence 199403, Application US/10956157
Publication No. US20050118625A1
   -11-060-756-81506/c
  Matches
  GENERAL INFORMATION:
  Query Match
   SENERAL INFORMATION:
  SOFTWARE: PatentIn version
  APPLICANT: Wyeth APPLICANT: Mount
   APPLICANT: Wyeth APPLICANT: Moun
   ENGTH:
   Local Similarity
   Local
   210 ATGCTTCTTGTTCTGTCTGCAAAAC 234
  154 CCTTCTGCCATGATTTTAAGATTCC 178
                               158 CTGCCATGATTTTAAGATTCCAGGG 182
   1 CCTTCTGCCGTGATTGTCAGTTTCC
  1 ATGCTTCCTGTACAGCCTGCAAAAC 25
   Similarity
   Similarity
   Conservative
  Conservative
   7.9%;
  84.0%;
  84.0%;
  ; Score 18.6; D; Pred. No. 41; O; Mismatches
   Score 18.6; Di
Pred. No. 41;
0; Mismatches
  0
   Score 18.6;
Pred. No. 41;
   0; Mismatches
   25
   몂
  멂
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  1:
  1;
   Length 25;
   Length
  Length 25;
   Indels
  0;
   <u>,</u>
  0
  Gaps
   Gaps
  Gaps
  0
   0
  0,
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  RESULT 47
US-11-121-849-637715
   US-11-121-849-597792
   RESULT 46
US-11-121-849-597792/c
  ; TYPE: DNA; Homo sapien; ORGANISM: Homo sapien US-11-121-849-584812
   RESULT 45
US-11-121-849-584812/c
  Sequence 637715, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
   SEQ ID NO 597792
LENGTH: 25
  GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
  NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 584812
LENGTH: 25
  Best Local Similarity Matches 21; Conserv
   Query Match
   Matches
   Best
   GENERAL INFORMATION:
   Sequence 584812, Application US/11121849 Publication No. US20050272080A1
   Sequence 597792, Application US/11121849 Publication No. US20050272080A1
  Query Match
                               APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
   PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
   FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
  FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
   TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
  APPLICANT: John Palma
   PRIOR FILING DATE: 2004-05-03
  PRIOR APPLICATION NUMBER: 60/567,949
  LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
   Local Similarity 84.(
les 21; Conservative
   25
   24
  25
   67 TCACGTGAGAGCTGGTTGTTTGAAA 91
   CCTCATGAATGGTTTAGTGCCATCC 48
  TCACCTGAGAGCTGATTGCTTAAAA 1
  Conservative
   84.0%;
   84.0%;
   7.98;
   0; Mismatches
   Score 18.6;
Pred. No. 41
   Score 18.6;
Pred. No. 4
  Mismatches
  В
  DB
  ۲,
  1;
  Formalin Fixed
   Length 25;
  Indels
   Indels
  ,
,
   0;
   Paraffin Embedded
   Gaps
  0
   0
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RESULT 49
US-11-121-849-663681/c
  밁
   S
   ; ORGANISM: Homo sapien
US-11-121-849-663681
  US-11-121-849-638121
  RESULT 48
  밁
   S
   US-11-121-849-638121
  PHIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOPTWARE: Microarray Probe Sequence Listing Generator
SEQ ID NO 663681
   GENERAL INFORMATION:
APPLICANT: John Palma
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
PRIOR PILING DATE: 2004-05-03
   NUMBER OF SEQ ID NOS: 67390
SOFTWARE: Microarray Probe
SEQ ID NO 638121
LENGTH: 25
TYPE: DNA
   Sequence 663681, Application US/11121849 Publication No. US20050272080A1
   Sequence 638121, Application US/11121849
Publication No. US20050272080A1
   SEQ ID NO 637715
LENGTH: 25
                Best Local Similarity
  Matches
   Query Match
   GENERAL INFORMATION
  Matches
   Query Match
                                 Query Match
  ORGANISM: Homo sapien -11-121-849-637715
   FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
  APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis
TITLE OF INVENTION: Microarrays
  NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
   PRIOR FILING DATE: 2004-05-03
  TYPE: DNA
  ORGANISM: Homo sapien
   ENGTH: 25
  Match 7.9%;
Local Similarity 84.0%;
  Local Similarity
   24 CCTCATGAATGGTTTAGTGCCATCC 48
   24 CCTCATGAATGGTTTAGTGCCATCC 48
  21;
  CTTCATGAATGTCTTGGTGCCATCC
Conservative
  Conservative
  Conservative
              7.9%;
  673904
  7.9%;
  Sequence Listing Generator V 1.1
  Score 18.6; D
Pred. No. 41;
0; Mismatches
0
              Score 18.6;
Pred. No. 41
  0; Mismatches
  Score 18.6;
Pred. No. 41
Mismatches
  25
  25
                                 DB 1;
   DB 1;
   DB 1;
   of Formalin Fixed Paraffin Embedded
4;
  4.
  4.
                                 Length
   Length 25;
   Length 25;
  Indels
Indels
  Indels
0
  0
  ,
,
  Gaps
Gaps
  Gaps
0
  0
  0
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  밁
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   RESULT 50
US-10-310-914A-131336
  밁
  S
  US-10-310-914A-131349
   RESULT 51
US-10-310-914A-131349
   US-10-956-157-180126
   RESULT 52
   US-10-310-914A-131336
Sequence 180126, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
  Sequence 131349, Application US/10310914A
publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CURRENT APPLICATION UNMERR: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
  Best
  NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 131349
  SEQ ID NO 131336
  GENERAL INFORMATION:
   Sequence 131336, Application US Publication No. US20060003322A1
   Query Match
  Matches
   Query Match
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kruzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
   NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.
  LENGTH: 21
TYPE: RNA
ORGANISM: Human
   ORGANISM: Human
  TYPE: RNA
   LENGTH:
  Local
  Local
  105 TCTCATTCTCCTGCTCCCAC 124
  105 TCTCATTCTCCTGCTCCCAC 124
  25
  79
   13;
  2 UCUCAAUCUCCUGCUCCCAC
   l Similarity
13; Conserv
  1 UCUCAAUCUCCUGCUCCCAC
  Similarity
  TGGTTGTTTGAAAGAGCCTGGCCCC
  TGGCTCTTAGAAAGAGCCTGGCACC 1
   Conservative
  Conservative
  Application US/10310914A
  7.8%;
65.0%;
  7.8%;
   Score 18.4; D
Pred. No. 42;
6; Mismatches
   6
   6
  Score 18.4;
Pred. No. 4
  21
  Mismatches
  103
  40;
   BB
   DB 1;
   <u>ب</u>
   Length 24;
   Length 21;
  Indels
  of novel
   0
   0;
  regulatory genes
   Gaps
   0
   0
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FILE REFERENCE: 031896-043000 (AM 101081)

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CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 180126
LENGTH: 25
TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-180126
   Sequence 453805, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Beoinformatically detectable group of
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-11-06

NUMBER OF SEQ ID NOS: 1388402
  : LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-453805
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 116036
LENGTH: 23
TYPE: RNA
NCANISM: Human
US-10-310-914A-116036
ঠ
  US-10-310-914A-453805
   용
   Ş
  RESULT 53
US-10-310-914A-116036/c
  밁
   १
   RESULT 54
  Sequence 116036, Application US/10310914A publication No. US20060003322A1 GENERAL INFORMATION:
   Query Match
Best Local Similarity
Matches 19; Conserv
   SOFTWARE: PatentIn version 3.3 SEQ ID NO 453805
                                 Matches
   Query Match
Best Local Similarity
   Matches
   Query Match
   216 CTTGTTCTGTCTGCAAAACT 235
134 AGACACCTGCTCCCCCTTCTCCT 156
   23 GCCATCCCCATAGTAATGAGTGA 1
   42 GCCATCCCCTTGGTGATGAGTGA 64
   20;
  -
   Similarity
  CTTGTTCTGTCTGCAAACCT 20
                                 Conservative
   Conservative
  Conservative
  7.7%;
  7.8%;
95.0%;
   7.7%;
65.2%;
  <u>.</u>
  <u>,</u>
  Score 18.4;
Pred. No. 4:
   Score 18.2;
Pred. No. 44;
   Score 18.2;
Pred. No. 4
                                 Mismatches
   Mismatches
  Mismatches
  Ė
   DB 1;
   BB
  ۲.
   Length 23;
  Length 25;
  Length 24;
  Indels
                               Indels
   Indels
  of novel regulatory genes and
                             0,
  <u>.</u>
  0
  Gaps
  Gaps
                             Gaps
  0,
                             ;
  0
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; TYPE: DNA; ORGANISM: Mus musculus US-10-719-900-221757
   밁
 밁
   RESULT 56
US-10-719-900-221757
  ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-106005
   RESULT 55
US-10-681-773-106005/c
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   APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 221757
   NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator
SEQ ID NO 106005
  Sequence 106005, Application US/10681773
Publication No. US20040146890A1
GENERAL INFORMATION:
  Matches
  Query Match 7.7%;
Best Local Similarity 87.0%;
  Sequence 221757, Application US/10719900 Publication No. US20050026164A1
  Matches
  Query Match 7.7%;
Best Local Similarity 87.0%;
   FILE REFERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR FILING DATE: 2002-10-08
  APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
APPLICANT: Shen, Mei-Mei
APPLICANT: Kennedy, Giulia
   APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
   LENGTH:
   ENGTH: 25
                     64 AGTTCACGTGAGAGCTGGTTGTT 86
  24 CTAGTTGTTGAAAAGAGCCTGGC 2
   78 CTGGTTGTTTGAAAGAGCCTGGC 100
  20;
  20;
 μ
   N
   AGCCUCCAGCUCCCCCUUCCCU
AGTTGACGTGATAGCTGGTTCTT 23
  Conservative
  Conservative
  0
  <u>,</u>
  Score 18.2;
Pred. No. 45;
  Score 18.2;
Pred. No. 49
  Mismatches
  Mismatches
   24
   BB
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  ω
••
   Length 25;
   Length 25
  Indels
  Indels
  0
  0,
  Gaps
  0
  0;
```

RESULT 57 US-10-956-157-170117/c

Sequence 170117, Application US/10956157 Publication No. US20050118625A1 GENERAL INFORMATION:

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; ORGANISM: Homo sapien US-11-121-849-297414
   RESULT 59
US-11-121-849-297414/c
  밁
  8
  US-10-310-914A-715048/c

Sequence 715048, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
  Ś
   US-10-310-914A-715048
  밁
   ; ORGANISM: Probe Sequence
US-10-956-157-170117
  APPLICANT: Mounts, William
TITLE OF INVENTION: HUUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUUCLEIC ACID AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FILLING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOPTWARE: Patentin version 3.2
SEQ ID NO 170117
LENGTH: 25
TYPE: DNA. DOCK SCHOOLS
  NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 715048
LENGTH: 25
TYPE: RNA
ORGANISM: Human
  GENERAL INFORMATION
   Sequence 297414, Application US/11121849 Publication No. US20050272080A1
  SEQ ID NO 297414
  Matches
  Query Match
  Matches
   Best Local
  Query Match
   TITLE OF INVENTION: Methods of Genetic Analysis TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1 CURRENT APPLICATION NUMBER: US/11/121,849 CURRENT FILING DATE: 2005-05-03 PRIOR APPLICATION NUMBER: 60/567,949 PRIOR FILING DATE: 2004-05-03 NUMBER OF SEQ ID NOS: 673904 SOPTWARE: Microarray Probe Sequence Listing Gene SOPTWARE: Microarray Probe Sequence Listing Gene
  APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06
   APPLICANT: John Palma
                                      TYPE: DNA
   LENGTH:
   Local Similarity
  23
  70
  23
  62 TGAGTTCACGTGAGAGCTGGTTG 84
  20;
  20;
   Similarity
  CGTGAGAGCTGGTTGTTGAAAG 92
  TGAGTTCACGCAAGATCTGGTTG 1
  Conservative
  Conservative
   7.7%;
87.0%;
   7.7%;
87.0%;
   Sequence Listing Generator V 1.1
  Score 18.2; D
Pred. No. 45;
0; Mismatches
  0; Mismatches
   Score 18.2;
Pred. No. 45;
  DB 1;
  DB 1;
  of Formalin Fixed Paraffin Embedded
  ω
••
  ω
--
  Length 25;
  Length
  Indels
  25;
  0
  0;
  Gaps
  Gaps
  0
  0
```

```
APPLICANT: Wyeth
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 1939
밁
                           Ş
   ; TYPE: DNA; Homo sapiens US-10-847-918-1939
   Ś
  밁
   ; ORGANISM: Human US-10-310-914A-1140091
  US-10-310-914A-1140091/c
; Sequence 1140091, Application US/10310914A
; Publication No. US20060003322A1
  밁
   Ś
  US-10-847-918-1939/c
   RESULT 61
  GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200,CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1140091
LENGTH: 18
TYPE: RNA
  Query Match
Best Local Similarity
  Sequence 1939, Application US/10847918 Publication No. US20050119210A1
  Query Match
Best Local (
  Matches
  GENERAL INFORMATION:
  Matches
   Matches
  Best Local
   Query Match
  LENGTH: 21
                              149 CTTCTCCTTCTGCCATGATTT 169
21 CTTCTTGTTCTGCCATGATTT 1
  18
  45
  23
  19;
  18;
   20;
   5 TGGGTCATGGGGGCAGATCCCTC 27
  Similarity
  Similarity
  ATCCCCTTGGTGATGAGT 62
  Conservative
   Conservative
  Conservative
  7.6%; Dr.
100.0%; Pr
  7.7%;
  7.5%; Score 17.8;
90.5%; Pred. No. 47;
   0,
  Score 18;
Pred. No.
  Score 18.2;
Pred. No. 45;
  Mismatches
   Mismatches
  Mismatches
   42
  DB
   BB
   for
   ١,
   1;
   ۲.
  0
  Diagnosing and
   Length 18
   Length 21;
   Length 25
  0,
  0
   0
  Treating Cancers
   Gaps
   Gaps
  0
  0
   0
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RESULT 62 US-10-847-918-1941

```
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cance
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 1941
LENGTH: 21
TYPE: por
  ; PRIOR FILING DATE: 2003-05-20; NUMBER OF SEQ ID NOS: 14937; SOFTMARE: PatentIn version 3.2; SEQ ID NO 2094; LENGTH: 21; TYPE: RNA; ORGANISM: RNAi-antisense strand US-10-847-918-2094
   밁
   श
   RESULT 63
US-10-847-918-2094
   Ś
  ; TYPE: RNA; CONTINUE STRANT C
   US-10-310-914A-116023/c
Sequence 116023, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of
TITLE OF INVENTION: uses thereof
  Sequence 2094, Application US/10847918 Publication No. US20050119210A1 GENERAL INFORMATION:
   Query Match
Best Local (
   Query Match
   Matches
  Matches
   APPLICANT: Wyeth
APPLICANT: be, Xiaobing
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
   Local Similarity 38.1%; Pred. No. 47
   Local Similarity les 9; Conserv
  149
   150 TrcTccTTcTcccATGATTT 170
   1 UUCUUGUUCUGCCAUGAUUUU 21
   CTTCTCCTTCTGCCATGATTT 169
   CUUCUUGUUCUGCCAUGAUUU 21
   Conservative
   7.5%; Score 17.8;
42.9%; Pred. No. 4
   10; Mismatches
  11; Mismatches
   DB 1;
  멺
   Length 21;
   Length 21;
  Indels
  novel regulatory genes and
  0,
   ٥,
  Gaps
  Cancers
  0;
   ç
```

```
; ORGANISM: Human US-10-310-914A-967563
  RESULT 66
US-10-310-914A-967563/c
  밁
   ; ORGANISM: Human
US-10-310-914A-845545
  RESULT 65
US-10-310-914A-845545/c
   밁
  US-10-310-914A-116023
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 967563
  FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 116023
   Sequence 967563, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
   Query Match 7.5%;
Best Local Similarity 90.5%;
Matches 19; Conservative
  SOFTWARE: PatentIn
SEQ ID NO 845545
LENGTH: 21
   Sequence 845545, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
 Matches
                                     Query Match
   Matches
   Query Match 7.5%;
Best Local Similarity 90.5%;
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
  NUMBER OF SEQ ID NOS: 1388402
  TYPE: RNA
ORGANISM: Human
  LENGTH: 21
  ENGTH: 21
Local Similarity 90.5%; hes 19; Conservative
  140 CTGCTCCCCCTTCTCCTTCTG 160
  21
   21
   19;
   GTCATGGGGGGGGGATCCCTTA 1
   GTCATGGGGGCAGATCCCTCA 28
   Conservative
  version 3.3
Score 17.8; D
Pred. No. 47;
0; Mismatches
   0,
   Score 17.8;
Pred. No. 47
   Score 17.8;
Pred. No. 4
   Mismatches
   Mismatches
                                   DB 1; Length 21;
   BB
   BB
   Length
Indels
   Indels
   Indels
   of novel regulatory genes and
   21;
   21;
 o
,,
   <u>.</u>
   0
 Gaps
   Gaps
   Gaps
 0
   0
   0
```

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RESULT 68
US-10-310-914A-1073155/c
Sequence 1073155, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
  US-10-310-914A-1295208/c

// Sequence 1295208, Application US/10310914A

/ Publication No. US20060003322A1

/ GENERAL INFORMATION:
   RESULT 67
US-10-310-914A-1073142/c
/ Sequence 1073142, Application US/10310914A
/ Publication No. US20060003322A1
  RESULT 69
   뭉
   ঠ
   밁
  S
   밁
  8
  ; ORGANISM: Human
US-10-310-914A-1073155
  US-10-310-914A-1073142
  Best Loc
Matches
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1073155
LENGTH: 21
   Query Match
   SEQ ID NO 1073142
   GENERAL INFORMATION:
  Matches
   Query Match
Best Local
   APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: PatentIn version 3.3
                     APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01
  LENGTH: 21
TYPE: RNA
ORGANISM: Human
  TYPE: RNA
   Local
  140 crecrececerrererrere 160
   21
   20 GATCCCTCATGAATGGTTTAG 40
   21
  19;
   Similarity
   Similarity 90.5%;
   GATCCCTCATGAATGGCTTGG 1
  TGAGAGCTGGTTGTTTGAAAG 92
  Conservative
  Conservative
   90.5%;
  0
  Score 17.8; D
Pred. No. 47;
0; Mismatches
   Score 17.8;
Pred. No. 4
  Mismatches
   47;
   DB
   DB 1;
   ۲.
  2
--
  2.
   Length 21;
   Length 21;
  Indels
  0
  0
  Gaps
  0
  0
                                       and
```

```
; TYPE: DNA
; ORGANISM: Human
US-11-063-391-290
  ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1295208
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  US-10-310-914A-628574
   5
US-10-310-914A-628574
  RESULT 71
  US-11-063-391-290
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Beinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: USes thereof
FILE REFERENCE: 06087.0200.Cepusol
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DAFE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 628574
LENGTH: 282574
TENES BALL
   Sequence 628574, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
  Query Match
Best Local Similarity
Matches 19; Conserv
   CURRENT APPLICATION NUMBER: US/11/063,391
CURRENT FILING DATE: 2005-02-22
NUMBER OF SEQ ID NOS: 980
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 290
LENGTH: 21
   CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1295208
LENGTH: 21
   GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Murison, J Gree
APPLICANT: Grigor, Murray
   Sequence 290, Application US/11063391 Publication No. US20050202077A1
  Matches
   Query Match
  APPLICANT:
   APPLICANT: Abernethy, Nevin
APPLICANT: Webster, Gill
TITLE OF INVENTION: Targeted delivery of RNA interference
TITLE OF INVENTION: molecules
FILE REFERENCE: 11000.1100U
            TYPE: RNA
ORGANISM: Human
  140 CTGCTCCCCCTTCTCTTCTG 160
  al Similarity
19; Conserv
  60 AGTGAGTTCACGTGAGAGCTG
   Munro, Grant
Abernethy, Nev
Webster, Gill
   AATGAGTTCACATGAGAGCTG
   Murison, J Greg
Grigor, Murray R
Havukkala, Ilkka J
  CTGCTCCTCCTTCGCCTTCTG
   Conservative
  Conservative
  90.5%;
  7.5%;
   0
  0
  Score 17.8;
Pred. No. 4
  Score 17.8;
Pred. No. 4
   21
   80
   Mismatches
   Mismatches
  DB 1;
  DB
  ۲.
   2
   Length 21;
  Length
   Indels
  21;
   0
  0,
  Gaps
   Gaps
   0
  0
```

and

```
RESULT 74
US-10-310-914A-399112
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  Ş
  ; SEQ ID NO 281991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-281991
  밁
  S
  US-10-310-914A-1180683/c
; Sequence 1180683, Application US/10310914A
; Publication No. US20060003322A1
  밁
   ঠ
  US-10-956-157-281991
  US-10-310-914A-1180683
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1180683
LENGTH: 22
TYPE: RNA
ORGANISM: Human
ORGANISM: Human
Sequence 399112, Application US/10310914A Publication No. US20060003322A1
  GENERAL INFORMATION:
  Sequence 281991, Application US/10956157 Publication No. US20050118625A1
  Matches
  GENERAL INFORMATION:
  Matches
  Query Match
Best Local
   Matches
   Best Local
  Query Match
  APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTIN
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
  Best Local Similarity
  Query Match
   APPLICANT: Wyeth APPLICANT: Moun
  113 TCCTGCTCCCACTCTTGCATG 133
  153 TCCTTCTGCCATGATTTTAAG 173
  22
  72 TGAGAGCTGGTTGTTTGAAAG 92
  19;
  1 UCCUGCUCCCACUUUUGCUUG 21
   Similarity
  Similarity
  TCCTTCTGCCATGATTGTGAG 2
  Conservative
  Conservative
  Conservative
  7.5%;
  7.5%;
   7.5%;
57.1%;
  Score 17.8; D
Pred. No. 49;
0; Mismatches
  <u>.</u>
  0
   Score 17.8;
Pred. No. 4:
  Score 17.8;
Pred. No. 47
  Mismatches
  Mismatches
  FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
  47
  DB
  멂
  BB
  1;
   Length
  Length 25;
  Length
  0,
  <u>.</u>
  0;
  Gaps
  Gaps
  0
  0
  0
```

```
; APPLICANT: Shiler, Kvuzat; TITLE OF INVENTION: Bioinformatically detecta; TITLE, OF INVENTION: uses thereof; FILE REFERENCE: 06087.0200.CPUS01; CURRENT APPLICATION NUMBER: US/10/310,914A; CURRENT FILING DATE: 2002-12-06; NUMBER OF SEQ ID NOS: 1388402; SOFTWARE: Patentin version 3.3; SEQ ID NO 399112
  멹
  S
   RESULT 75
US-11-121-849-152798/c
   밁
   ş
  RESULT 76
US-10-310-914A-1073186/c
; Sequence 1073186, Application US/10310914A
; Publication No. US20060003322A1
  ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-152798
   US-10-310-914A-399112
                        APPLICANT: Shiler, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087,0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3:3

SEQ ID NO 1073186
  NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator
SEQ ID NO 152798
LENGTH: 25
  Query Match
Best Local
   GENERAL INFORMATION:
APPLICANT: John Palma
   Sequence 152798, Application US/11121849 Publication No. US20050272080A1
   Query Match
Best Local (
  GENERAL INFORMATION:
  Matches
   Matches
  TITLE OF INVENTION: Methods of Genetic Analysis of TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1 CURRENT APPLICATION NUMBER: US/11/121,849 CURRENT FILING DATE: 2005-05-03 PRIOR APPLICATION NUMBER: 60/567,949 PRIOR FILING DATE: 2004-05-03
TYPE: RNA
ORGANISM: Human
   TYPE: RNA
ORGANISM: Human
   ENGTH:
   Local Similarity
   178 CAGGGACTTCACAAGAAGCAA 198
  178 CAGGGACTTCACAAGAAGCAA 198
  25 CATGGCCTTCACAAGAAGCAA 5
   17;
  19;
   4 CAUGGCCUUCACAAGAAGCAA 24
  Similarity
   Conservative
  Conservative
   Kvuzat
Bioinformatically detectable
   7.5%;
81.0%;
  90.5%;
   <u>ب</u>
  Score 17.8;
Pred. No. 49;
   Pred. No. 49;
; Mismatches
   Score 17.8;
Pred. No. 49
  Mismatches
  DB 1;
   멂
   group
  Length 25;
   Formalin
   Length 25;
  Indels .
   Indels
   of novel regulatory genes
   Fixed Paraffin Embedded
  <u>.</u>
   <u>.</u>
  Gaps
   Gaps
  ٥,
   0;
  and
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US-10-310-914A-1073186

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RESULT 77
US-10-310-914A-1295216/c
; Sequence 1295216, Application US/10310914A
; Publication No. US20060003322A1
RESULT 79
   밁
   S
   US-10-681-773-23765/c
  밁
  Ş
  ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1295216
   밁
  ঠ
  ; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-23765
   RESULT 78
  PRIOR APPLICATION NUMBER: 60/417,190
PRIOR FILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 23765
  Sequence 23765, Application US/10681773 Publication No. US20040146890A1 GENERAL INFORMATION:
   SEQ ID NO 1295216
LENGTH: 24
   GENERAL INFORMATION:
   Matches
   Query Match
  Matches
  Query Match
Best Local (
  Matches
  Query Match
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
   APPLICANT: Shen, Mei-Mei
APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Wethods for Genotyping Polymorphisms in Humans
FILE REFERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
   APPLICANT:
   APPLICANT: Matsuzaki, Hajime
  Local
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  155 CTTCTGCCATGATTTTAAGATTCC 178
   42
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  24
   24
  20;
  20;
   20;
   Similarity
  Similarity
  Similarity
   GCCATCCCCTTGGTGATGAGTGAG 65
  GGTCATGGGGGCAGATCCCTCATG 30
   Mei, Rui
  Conservative
   Conservative
  Conservative
  7.5%;
83.3%;
  7.5%;
   7.5%;
   Score 17.6; D
Pred. No. 52;
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  <u>.</u>
  0
   0
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Pred. No. 51;
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  Pred
   Mismatches
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  DB
  BG
   BB
  ۲,
   1;
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  4.
  4;
   4.
  Length 25;
  Length 24;
   Length 24;
  Indels
   Indels
  Indels
   0
  0
  0
  Gaps
  Gaps
   Gaps
  0
  0,
   0
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S
  ; TYPE: DNA; Homo sapien US-10-681-773-38235
  밁
  S
   RESULT 80
US-10-719-900-320328
   밁
  US-10-956-157-55283/c
   ; ORGANISM: Mus musculus 
US-10-719-900-320328
   US-10-681-773-38235/c
   NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 320328
   Sequence 55283, Application US/10956157 Publication No. US20050118625A1 GENERAL INFORMATION:
  Sequence 320328, Application US/10719900
publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION UNMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
   NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 38235
  Sequence 38235, Application US/10681773 Publication No. US20040146890A1 GENERAL INFORMATION:
  Matches
  Query Match
   Query Match
         APPLICANT: Wyeth
APPLICANT: Mounts, William
TITLE OP INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OP INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031895-043000 (AM 101081)
   FILE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR FILING DATE: 2002-10-08
  APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
  APPLICANT:
  APPLICANT: Matsuzaki, Hajime
APPLICANT: Mei, Rui
   TYPE: DNA
  LENGTH:
   ENGTH:
  Local Similarity 83.1
  Local
  178 CAGGGACTTCACAAGAAGCAAATG 201
   152 CTCCTTCTGCCATGATTTTAAGAT 175
   25
  _
  20;
  Similarity
  CAGGGACTTCAAAAGTAGCTATTG 24
   CACCTTCTGCCATGATTGTCAGTT 2
  Shen,
  Conservative
  Mei-Mei
NUMBER: US/10/956,157
   7.5%;
  7.5%;
  Score 17.6; E
Pred. No. 52;
0; Mismatches
  0
  0; Mismatches
  Score 17.6;
Pred. No. 52;
   DB
  DB
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  ۲,
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  Length 25;
  Indels
  Indels
  0
  0
  Gaps
  0
  0
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; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55283
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-55283
   뭉
   र्
  SOPTWARE: PatentIn version 3.2; SEQ ID NO 55284; LENGTH: 25; TYPE: DNA ORGANISM: Probe Sequence US-10-956-157-55284
   В
  ঠ
                  S
   US-10-956-157-123288
  US-10-956-157-55284/c
  RESULT 83
  Query Match
Best Local S
Matches 20
   Sequence 55284, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04
  Sequence 123288, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
   SOFTWARE: PatentIn version 3.2
SEQ ID NO 123288
LENGTH: 25
TYPE: DNA
  Matches
  Query Match
Best Local
   Query Match
  APPLICANT: Wyeth
APPLICANT: Mounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FILING DATE: 2004-10-04
CURRENT FILING DATE: 2004-10-04
RUMBER OF SEQ ID NOS: 319805
  ORGANISM: Probe Sequence
-10-956-157-123288
   CURRENT FILING DATE:
   NUMBER OF SEQ ID NOS: 319805
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   149
  150
   24
   25
                  21
  Similarity
   Similarity
   CTTCACCTTCCACCATGATTCTAA 1
ATCCCTCATGAATGGTTTAGTGCC 44
   CTTCTCCTTCTGCCATGATTTTAA 172
  TTCTCCTTCTGCCATGATTTTAAG 173
  Conservative
  Conservative
   7.5%;
83.3%;
  7.5%;
83.3%;
  7.5%;
  ; Score 17.6; D; Pred. No. 52; O; Mismatches
   Score 17.6; I
Pred. No. 52;
O; Mismatches
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Pred. No. 52;
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  DB 1;
   DB 1;
   DB 1;
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   Length 25;
  Length 25;
   Length
   Indels
   25
   0,
  0
   <u>.</u>.
  Gaps
   Gaps
  Gaps
  0
  0,
   ..
   밁
   Ś
   片
  Ś
   Best
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US-10-843-527-224887/c
Sequence 224887, Application US/10843527
Publication NO. US20050136395A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Exic Schell
APPLICANT: Exic Schell
ITILE OF INVENTION: Methods of Genetic Analysis of
  RESULT 86
  RESULT 85
US-10-843-527-11826
  US-10-956-157-199404
  RESULT 84
US-10-956-157-199404
   밁
  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 11826
LENGTH: 25
   Sequence 11826, Application US/10843527 Publication No. US20050136395A1 GENERAL INFORMATION:
  SOFTWARE: PatentIn version 3.2
SEQ ID NO 199404
LENGTH: 25
   GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts,
  Sequence 199404, Application US Publication No. US20050118625A1
  Matches
  Matches
   Best Local
   Query Match
   Query Match
   TYPE: DNA
ORGANISM: SARS Virus
-10-843-527-11826
  APPLICANT: Michael Mittmann
APPLICANT: Eric Schell
TITLE OF INVENTION: Methods of Genetic Analysis of
FILE REFERENCE: 3602.1
   APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319865
  CURRENT APPLICATION NUMBER: US/10/843,527 CURRENT FILING DATE: 2004-05-10
                                      FILE REFERENCE: 3602.1
   PRIOR APPLICATION NUMBER: 60/469,545 PRIOR FILING DATE: 2003-05-08
   NUMBER OF SEQ ID NOS: 238196
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   N
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   CCTTCTGCCGTGATTGTCAGTTTC 24
   ATTCCTCATGAATTGATTAATGCC 24
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nilarity 83.3%;
Conservative
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US-10-932-182A-168000/c
; Sequence 168000, Application US/10932182A
; Publication No. US20060046253A1
   US-11-036-317-439119/c
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  S
   밁
   ঠ
  ; ORGANISM: SARS Virus
US-10-843-527-224887
   US-10-932-182A-168000
   RESULT 87
   APPLICANT: FÜJIMÜRA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OP INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT PELLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
SQ ID NO 168000
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
ORGANISM: Saccharomyces pastorianus
   FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 439119
LENGTH: 25
  NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 224887
LENGTH: 25
  GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
   TYPE: DNA
ORGANISM: Mus musculus
-11-036-317-439119
  Sequence 439119, Application US/11036317 Publication No. US20050214823A1
  GENERAL INFORMATION:
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   APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
   PRIOR APPLICATION NUMBER: 60/469,545 PRIOR FILING DATE: 2003-05-08
   TYPE: DNA
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  174 ATTCCAGGGACTTCACAAGAAGCA 197
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   24 CAACTCCTTCTCCTTCTCTCTG 1
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  Conservative
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Score
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RESULT 91
US-11-121-849-370/c
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  밁
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  ; ORGANISM: Mus musculus US-11-036-317-706660
   S
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   US-11-036-317-706660
   CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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   PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
  Sequence 706660, Application US/11036317
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  CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
  APPLICANT: Blume, John TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.1
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  TYPE: DNA
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   16 GGCAGATCCCTCATGAATGGTTTA 39
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  20;
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  GGCAGATGTCTGAGGAATGGTTTA
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83.3%;
   7.5%;
83.3%;
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  0
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Sequence 370, Application US/11121849 Publication No. US20050272080A1 GENERAL INFORMATION:

APPLICANT: John Palma

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CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 370
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LENGTH: 25
TYPE: DNA
ORGANISM: Homo saplen
US-11-121-849-370
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   RESULT 93
   ; ORGANISM: Homo sapien
US-11-121-849-588191
   RESULT 92
US-11-121-849-588191
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Publication No. US20050272080A1
GENERAL INFORMATION:
  NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 588191
  Sequence 588191, Application US/11121849 Publication No. US20050272080A1 GENERAL INFORMATION:
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   APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
  APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
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CURRENT FILING DATE: 2005-05-03
CURRENT FILING DATE: 2005-05-03
   PRIOR APPLICATION NUMBER: 60/567,949 PRIOR FILING DATE: 2004-05-03
  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays
                  LENGTH: 25
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  7.5%;
83.3%;
   83.3%;
  ; Score 17.6; D; Pred. No. 52; 0; Mismatches
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US-11-083-784-292730
  US-11-083-784-292730/c
  US-11-121-849-668624/c
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
   NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe S
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   Sequence 292730, Application US/11083784 Publication No. US20050245475A1
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Best Local Similarity
   APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
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PRIOR FILING DATE: 2004-05-03
   GENERAL INFORMATION:
   Sequence 668624, Application US/11121849 Publication No. US20050272080A1
   Best Local
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  Query Match
   APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
  APPLICANT:
   SOFTWARE: Proprietary
  NUMBER OF SEQ ID NOS:
  APPLICANT: Dharmacon,
   TYPE: RNA
7.4%;
Local Similarity 94.7%;
les 18; Conservative
   25 TGGAGGCGGATTCCTCATGAATAG 2
  12 TGGGGGCAGATCCCTCATGAATGG 35
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   Khvorova, Anastasia
Reynolds, Angela
  Leake,
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0

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Gaps

110

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US-11-083-784-1546724/c
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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Publication No. US20050246794A1
  Sequence 1546724, Application US/11083784 Publication No. US20050245475A1
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Best Local Similarity 94.7%;
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-11-101-244-292730
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   PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
  CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
CURRENT FILING UNMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
   APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
   ENERAL INFORMATION:
  TITLE OF INVENTION: Functional and Hyperfunctional sirNA FILE REFERENCE: 13499US
  ENERAL INFORMATION:
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Leake, Devin
Marshall, William
Scaringe, Stephen
   Khvorova, Anastasia
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   Gaps
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  밁
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                              Ś
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   US-11-101-244-1546724/c; Sequence 1546724, Application U; Publication No. US20050246794A1
  US-10-310-914A-1158279
  US-10-310-914A-1158279
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200,CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1158279
LENGTH: 20
  GENERAL INFORMATION:
APPLICANT: Dharmacon,
APPLICANT: Khvorova,
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
   NUMBER OF SEQ ID NOS: 1591911
  FILE REFERENCE: 13499US
  APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
   APPLICANT:
  TYPE: RNA
ORGANISM: Human
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Reynolds,
   Leake, Devin
   7.4%;
ilarity 57.9%;
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```
APPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 115919
LENGTH: 22
TYPE: RNA
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   US-10-310-914A-969089/c
Sequence 969089, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
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US-10-310-914A-1036172
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   US-10-310-914A-115919/c
   US-10-310-914A-969089
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 969089
LENGTH: 22
TYPE: RNA
ORGANISM: Human
ORGANISM: Human
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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  Sequence 115919, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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  22
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  19; Conservative
  Similarity 86.4%;
   Similarity
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GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable gro

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 1087700
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  Ś
  RESULT 103
US-10-310-914A-1087700/c
; Sequence 1087700, Application US/10310914A
; Publication No. US20060003322A1
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  δ
  US-10-310-914A-273857
  US-10-310-914A-1087700
  US-10-310-914A-1036172
   GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: 0802-12-06
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SOFTWARE: PatentIn version 3.3
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   Query Match
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Matches 19; Conserv
  Query Match
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ORGANISM: Human
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  24 CCTCATGAATGGTTTAGTGCCA 45
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RESULT 105 US-10-310-914A-1158289

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APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Beidinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 66335
LENGTH: 24
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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SOFTWARE: Patentin version 3.3
SEQ ID NO 32934
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  Sequence 66335, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087, 0200. CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentn version 3.3
SEQ ID NO 1158289
  Sequence 1158289,
Publication No. U
   Sequence 32934, Application US/10310914A Publication No. US20060003322A1
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  LENGTH: 23
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ORGANISM: Human
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  157 TCTGCCATGATTTTAAGATTCC 178
  22 GTGGGATCTGGTTGTTTAAAAG 1
  71 GTGAGAGCTGGTTGTTGAAAG 92
  l Similarity
19; Conserv
   1 UCUGCCAUGAUUGUAAGUAUCC 22
  h 7.3%;
Similarity 54.5%;
  Conservative
   Conservative
  9, Application US/10310914A
US20060003322A1
   7.3%;
  ; Score 17.2; D; Pred. No. 55; 7; Mismatches
   Score 17.2; D
Pred. No. 56;
0; Mismatches
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   DB 1;
   DB 1;
   <u>د</u>
   Length 24;
   Length 23;
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; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-661149
   멹
   Ś
                  S
  밁
   ş
   ; OTHER INFORMATION: Antisense Oligonucleotide US-10-298-953-44
   뭥
   ; ORGANISM: Human US-10-310-914A-66335
   US-10-298-953-44
  RESULT 108
   Query Match
Best Local S
  Sequence 44, Application US/10298953

Publication No. US20040097444A1

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: MODULATION OF SERINE/THREONINE KINASE 16 EXPRESSION
FILE REFERENCE: HTS-0109
  SEQ ID NO 44
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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CURRENT FILING DATE: 2002-11-16
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   73 GAGAGCTGGTTGTTTGAAAGAG 94
   13;
                   68 CACGIGAGAGCIGGITGITI
   3 GAGAUCUGGUUGUUUAAAAGUG
  Similarity
   Similarity
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   7.1%;
  7.3%;
   90.0%;
   0
  6; Mismatches
   Score 16.8;
Pred. No. 58;
   Score 17.2;
Pred. No. 5
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Pred. No. 58;
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   24
  56
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   BB
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RESULT 110 US-10-310-914A-845542/c

Sequence 845542, Application US/10310914A Publication No. US20060003322A1

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RESULT 112
US-10-310-914A-1242020/c
; Sequence 1242020, Application US/10310914A
  US-10-310-914A-1073095/c
; Sequence 1073095, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
  S
  문
   밁
  ঠ
  ; ORGANISM: Human
US-10-310-914A-1073095
   APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: USES THEREOF
TILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1073095
LENGTH: 20
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Matches
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SEQ ID NO 1242020
LENGTH: 20
   Publication No. US20060003322A1 GENERAL INFORMATION:
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LENGTH: 20
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   GENERAL INFORMATION:
  ORGANISM: Human
-10-310-914A-845542
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
   APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
   APPLICANT: Bentwich, APPLICANT: Shiler, 1
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   140 CTGCTCCCCCTTCTCTTCT 159
  146 CCCCTTCTCCTTCTGCCATG 165
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   20 CCCCTTCGCCTTCTGCCGTG
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   7.1%; Score 16.8;
90.0%; Pred. No. 58
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  Score 16.8;
Pred. No. 58
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  ; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI-BENBE BUTAND
US-10-847-918-1184
   á
   US-10-847-918-1853
   RESULT 114
US-10-847-918-1853/c
   RESULT 113
US-10-847-918-1184/c
   NUMBER OF SEQ ID NOS: 14937
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1853
LENGTH: 21
Type: no.
   Query Match
Best Local S
Matches 18
   APPLICANT: Liu, Wei
APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1184
   Sequence 1853, Application US/10847918 Publication No. US20050119210A1 GENERAL INFORMATION:
  Matches 18;
  APPLICANT: Wyeth
APPLICANT: Be, X.
APPLICANT: Liu, 1
APPLICANT: Sloni
  Matches
   Query Match
  APPLICANT: Wyeth APPLICANT: Be, X APPLICANT: Liu,
   GENERAL INFORMATION:
  Sequence 1184, Application US/10847918 Publication No. US20050119210A1
   Query Match
Best Local Similarity
  PRIOR APPLICATION NUMBER: US 60/471,729 PRIOR FILING DATE: 2003-05-20
   APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE ONTENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
   TYPE: RNA
ORGANISM: RNAi-sense strand
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Local Similarity 90.0%;
171 AAGATTCCAGGGACTTCACA 190
  171 AAGATTCCAGGGACTTCACA 190
   140 CIGCICCCCCTTCTCCTTCT 159
   20 AAGATTCCAGGCGCTTCACA 1
  20 CTGCTTCCCCTTCACCTTCT 1
  18;
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18; Conserv
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Liu, Wei
  Be, Xiaobing
   7.1%;
llarity 90.0%;
Conservative
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  Conservative
   90.0%;
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  Score 16.8;
Pred. No. 59;
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Pred. No. 58;
  Score 16.8;
Pred. No. 59;
  Mismatches
   Mismatches
   DB 1;
   BB
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   Length 21;
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   Gaps
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  0
```

닭

```
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Be, Xiaobing
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 1942
LENGTH: 21
CURGNISM: Homo sapiens
US-10-847-918-1942
   RESULT 117
US-10-847-918-2092/c
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  S
   밁
   ; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-847-918-1944
  US-10-847-918-1944
  US-10-847-918-1942/c
Sequence 2092, Application US/10847918 Publication No. US20050119210A1
  NUMBER OF SEQ ID NOS: 14937
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1944
   Sequence 1944, Application US/10847918 Publication No. US20050119210A1
   Query Match 7.1%;
Best Local Similarity 90.0%;
Matches 18; Conservative
   Sequence 1942, Application US/10847918 Publication No. US20050119210A1
   Matches
  Query Match
  GENERAL INFORMATION:
   APPLICANT: Liu, Wei
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR APPLICATION NUMBER: US 60/471,729
PRIOR TILING DATE: 2003-05-20
  APPLICANT: Wyeth APPLICANT: Be, 3
  LENGTH:
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Local Similarity 45.0%;
les 9; Conservation
  149 CTTCTCCTTCTGCCATGATT 168
   149 CTTCTCCTTCTGCCATGATT 168
   20 CTTCTTGTTCTGCCATGATT 1
   CUUCUUGUUCUGCCAUGAUU 21
   Be, Xiaobing
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   9; Mismatches
   Score 16.8;
Pred. No. 59;
  Score 16.8;
Pred. No. 59;
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   Gaps
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APPLICANT: Slonim, Donna

APPLICANT: Howes, Steve

TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers

FILE REFERENCE: 031896-026000 (AM101264)

CURRENT APPLICATION NUMBER: US/10/847,918

CURRENT FILING DATE: 2004-05-19

PRIOR APPLICATION NUMBER: US 60/471,729

PRIOR APPLICATION NUMBER: US 60/471,729

PRIOR FILING DATE: 2003-05-20

NUMBER OF SEQ ID NOS: 14937

SOFTWARE: Patentin version 3.2

SEQ ID NO 2092

LENGTH: 21
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; ORGANISM: Homo sapiens
US-10-847-918-2092
   Ş
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US-10-310-914A-828967/c
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   US-10-310-914A-1009274/c
   US-10-310-914A-828967
Sequence 1009274, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1009274
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087,0200,CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 828957
LENGTH: 21
  Sequence 828967, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
  Query Match
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   Query Match
  Matches
  TYPE: RNA
ORGANISM: Human
  Local
   139 CCTGCTCCCCCTTCTCCTTC 158
   150 TTCTCCTTCTGCCATGATTT 169
   20
   21 TICTTGTTCTGCCATGATTT 2
  18;
  18;
  Similarity
   cerecrééecerrerecre 1
  Conservative
  Conservative
  7.18;
  90.0%;
  ,.
  0; Mismatches
  Score 16.8;
Pred. No. 59;
  Score 16.8;
Pred. No. 59;
  Mismatches
   B
   DB
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  Gaps
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  0
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밁
   ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-74338
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; ORGANISM: Human
US-10-310-914A-1371246
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US-10-310-914A-1009274
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 74338
LENGTH: 23
LENGTH: 23
LENGTH: 23
LENGTH: 23
LENGTH: 23
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 66087.0200.CepUs01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1371246
LENGTH: 21
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Best Local :
  Best Local
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   137 CACCTGCTCCCCCTTCTCCT 156
   179 AGGGACTTCACAAGAAGCAA 198
                            208 CCATGCTTCTTGTTCTGTCT 227
22
  20
   20
   18;
   l Similarity
18; Conserv
   Similarity 90.0%;
18; Conservative
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   Conservative
  7.1%;
90.0%;
  90.0%;
   0;
   0;
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Pred. No. 59
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   Score 16.8; D
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Pred. No. 59;
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   Mismatches
   DB 1;
   DB 1;
   DB 1; Length 21;
   Length 21;
   Length 23;
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   Gaps
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RESULT 122

and

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  Ś
  US-10-310-914A-287417/c
   RESULT 124
  US-10-708-204-3803
  밁
   ; OTHER INFORMATION: synthetic oligonucleotide
US-10-416-122-2
  US-10-708-204-3803
  RESULT 123
  Sequence 287417, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
   SOPTWARE: PatentIn version 3.2
SEQ ID NO 3803
LENGTH: 23
TYPE: RNA
ORGANISM: Homo Sapiens
  Sequence 2, Application US/10416122
Publication No. US20040072199A1
GENERAL INFORMATION:
   APPLICANT: Brem, Gottfried
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF
TITLE OF INVENTION: DNA-CONTAINING SAMPLES BY MEANS OF OLIGONUCLEOTIDES
FILE REFERENCE: KLAUSI.001APC
CURRENT APPLICATION NUMBER: US/10/416,122
CURRENT FILING DATE: 2003-10-24
PRIOR APPLICATION NUMBER: PCT/EP01/12880
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 14
NUMBER OF SEQ ID NOS: 14
  Matches
  Query Match
Best Local :
   GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
  Sequence 3803, Application US/10708204 Publication No. US20050222399A1
   Query Match
Best Local Similarity
Matches 18; Conserv
  SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 2
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
  CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE TITLE OF INVENTION: THEREOF FILE REFERENCE: 55033
   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
   LENGTH: 24
  140 crecrececricicite 159
  57 ATGAGTGAGTTCACGTGAGAGCT 79
  ψ
  Similarity
   AUCAGUGAGCUCAGGAGAGAGCU 23
  crrecreerrererrer
   Conservative
   7.0%;
  7.1%;
   Score 16.6;
Pred. No. 6;
  Score 16.8;
Pred. No. 61
  24
   Mismatches
  Mismatches
   DB 1;
  DB 1;
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  Length 24;
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  DISEASE AND USES
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RESULT 126
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US-10-310-914A-651766, Application US/10310914A
Publication No. US20060003322A1
   US-10-310-914A-360372/c

; Sequence 360372, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:
                 Ś
   밁
  S
   밁
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  US-10-310-914A-287417
  US-10-310-914A-360372
  GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06
  NUMBER OF SEQ IB NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 651766
LENGTH: 23
TYPE: RNA
  SEQ ID NO 360372
   Matches
   NUMBER OF SEQ ID NOS: 13884
SOFTWARE: PatentIn version
SEQ ID NO 287417
   Query Match
   Matches
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  -10-310-914A-651766
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
  NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
  CURRENT FILING DATE:
   TYPE: RNA
ORGANISM: Human
  ORGANISM: Human
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ORGANISM: Human
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  ENGTH: 23
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les 19; Conserv
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  Local
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   100 CCCCCTCTCATTCTCCTGCTCCC 122
65 GTTCACGTGAGAGCTGGTTGTTT 87
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   7.0%;
82.6%;
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CCUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
· CURRENT FILING DATE: 2002-12-06
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable gro
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION UNMER: US/10/310,914A
CURRENT FILING DATE: 2002-12-66
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 967480
LENGTH: 23
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; Sequence 967480, Application US/10310914A
; Publication No. US20060003322A1
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   ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-819312
   US-10-310-914A-819312/c
; Sequence 819312, Application US/10310914A
; Publication No. US20060003322A1
  뮍
  á
  US-10-310-914A-967480
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILLING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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  103 CCTCTCATTCTCCTGCTCCCACT 125
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  65 GTTCACGTGAGAGCTGGTTGTTT 87
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US-10-310-914A-1053329/c
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| GENERAL INFORMATION:
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   ঠ
  RESULT 130
US-10-310-914A-115988/c
  밁
   S
  US-10-310-914A-115988
   US-10-310-914A-1186008
   APPLICANT: Bentalci, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1053329
LENGTH: 18
TYPE: RNA
ORGANISM: Human
ORGANISM: Human
   Best Loc
Matches
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 115988
   Sequence 115988, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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  NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1186008
  Query Match
   Query Match
   Matches
   Best Local Similarity
   Query Match
  LENGTH: 23
TYPE: RNA
ORGANISM: Human
  LENGTH: 18
TYPE: RNA
ORGANISM: Human
   Local
   Local Similarity
wes 17; Conserv
                          146
   19;
  18
  75 GAGCTGGTTGTTGAAAG
  23
   76 AGCTGGTTGTTTGAAAGAGCCTG 98
   17;
   Similarity
                            CCCCTTCTCCTTCTGCCA 163
   Conservative
   Conservative
   Conservative
   94.4%;
   6.9%;
   7.0%;
82.6%;
   Score 16.4; D
Pred. No. 62;
0; Mismatches
   92
   ٥,
   Score 16.4;
Pred. No. 62
   0; Mismatches
   Score 16.6;
Pred. No. 64;
   Mismatches
   62,
  DB
   멂
   DB
   1.
  ۲,
   1;
  Length 18;
  Length 18;
  Length
   Indels
   0;
   0
   0;
   Gaps
   Gaps
   Gaps
   0
   0
   0
```

```
Junen, Shawn

APPLICANT: McSwiggen, James

APPLICANT: Sirna Therapeutics, Inc.

TITLE OF INVENTION: Inhibition of Gene Expression Using Duplex Forming

TITLE OF INVENTION: Oligonucleotides

FILE REFERENCE: 03-1070 (400.139)

CURRENT APPLICATION NUMBER: US/10/727,780A

CURRENT FILING DATE: 2003-12-03

NUMBER OF SEQ ID NOS: 772

SOFTWARE: Patentin version 3.3

SEQ ID NO 425

LENGTH: 19

TYPE: RND
  밁
  Ş
   US-10-310-914A-1053330/c
; Sequence 1053330, Application US/10310914A
; Publication No. US20060003322A1
  밁
   Ś
  RESULT 134
US-11-083-784-134328/c
  US-10-310-914A-1053330
   US-10-727-780A-425
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILIS DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1053330
   GENERAL INFORMATION:
   Sequence 134328, Application US/11083784 Publication No. US20050245475A1
   Matches
   Query Match
   GENERAL INFORMATION
   Best Local Similarity Matches 17; Conserv
  Query Match
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
   LENGTH: 19
TYPE: RNA
  FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
   ORGANISM: Human
   ocal
  146 CCCCTTCTCCTTCTGCCA 163
   148 CCTTCTCCTTCTGCCATG
   18
  19
  l Similarity
17; Conserv
   Conservative
   Conservative
   6.98;
   6.98;
   165
   0
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   Score 16.4;
Pred. No. 63;
  Score 16.4;
Pred. No. 6
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  63;
   DB 1;
  BB
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   Length 19;
   Indels
   Indels
   0
   0
   Gaps
   0
   0
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and

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US-11-083-784-863172/c
; Sequence 863172, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
  밁
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   RESULT 136
   ; ORGANISM: Homo sapiens
US-11-083-784-134365
  US-11-083-784-134365/c
   밁
  ; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-134328
   PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 134365
  Query Match 6.9%;
Best Local Similarity 94.4%;
Matches 17; Conservative
  Sequence 134365, Application US/11083784 Publication No. US20050245475A1
   SOFTWARE: Proprietary
SEQ ID NO 134328
  Query Match 6.9%;
Best Local Similarity 94.4%;
Matches 17; Conservative
   APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirna
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PELLING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
APPLICANT: Dharmacon,
   PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
   FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
  APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
   NUMBER OF SEQ ID NOS: 1591911
   NPPLICANT: Scaringe, Stephen
   LENGTH: 19
   105 TCTCATTCTCCTGCTCCC 122
  107 TCATTCTCCTGCTCCCAC 124
  18 TCTCAATCTCCTGCTCCC 1
   19 TCAATCTCCTGCTCCCAC 2
   Marshall, William
  Stephen
  0; Mismatches
  0;
  Score 16.4;
Pred. No. 63;
   Score 16.4;
Pred. No. 6
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  DB 1;
   DB 1;
  1.
   Length 19;
  Length 19
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  0;
  Gaps
  Gaps
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  0
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RESULT 138
US-11-083-784-1250582
; Sequence 1250582, Application US/11083784
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  á
  ; ORGANISM: Homo sapiens
US-11-083-784-914575
   á
   ; ORGANISM: Homo sapiens US-11-083-784-863172
   US-11-083-784-914575/c
  SOFTWARE: Proprietary
SEQ ID NO 914575
LENGTH: 19
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  NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 863172
LENGTH: 19
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  Query Match
Best Local (
  Sequence 914575, Application US/11083784 Publication No. US20050245475A1
   Matches
   Query Match
Best Local Similarity
  FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
  APPLICANT:
   APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anasta:
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
  CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
   PRIOR APPLICATION NUMBER: 60/426,137 PRIOR FILING DATE: 2002-11-14
  PRIOR APPLICATION NUMBER: 60/426,137 PRIOR FILING DATE: 2002-11-14
  NUMBER OF SEQ ID NOS: 1591911
   APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
  APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
  APPLICANT:
  FILE REFERENCE: 13499US
   TYPE: RNA
   TYPE: RNA
  150 TTCTCCTTCTGCCATGAT 167
   105 TCTCATTCTCCTGCTCCC 122
  19
  19 TCTCATTCTCCTGCTTCC
   l Similarity
17; Conserv
  TITTCCTTCTGCCATGAT 2
   Leake, Devin
  Leake, Devin
   Khvorova, Anastasia
Reynolds, Angela
   Conservative
   Conservative
   6.9%;
  6.9%;
  Anastasia
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  N
   <u>.</u>
   Score 16.4;
Pred. No. 63;
  Score 16.4;
Pred. No. 63;
  Mismatches
   Mismatches
   DB
  DB
   1; Length 19;
  1; Length 19;
   1;
   Indels
   Indels
   0
   0;
   Gaps
   Gaps
   0
   0
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1250582
RESULT 140
US-11-101-244-134365/c
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-134328
   RESULT 139
US-11-101-244-134328/c
  밁
  S
   ; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1250582
  PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 134328
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Best Local :
   Sequence 134328, Application US/11101244 Publication No. US20050246794A1
  Matches
   Query Match
Best Local Similarity 55.6%;
Matches 10. Conservative
  GENERAL INFORMATION:
   GENERAL INFORMATION:
  Publication No. US20050245475A1
  APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
  APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
  APPLICANT: Dharmacon,
APPLICANT: Khvorova,
APPLICANT: Reynolds,
APPLICANT: Leake, Dev
  TITLE OF INVENTION: Functional and Hyperfunctional sirNA FILE REFERENCE: 13499US
   APPLICANT:
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  107 TCATTCTCCTGCTCCCAC 124
  19
  70 CGTGAGAGCTGGTTGTTT 87
  10; Conservative
  17;
   6.9%;
Similarity 94.4%;
   Khvorova, Anastasia
Reynolds, Angela
  Marshall, William
Scaringe, Stephen
  Conservative
   Devin
  0
   Score 16.4;
Pred. No. 6
   Score 16.4;
Pred. No. 63
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  DB 1; Length 19;
  DB 1; Length 19;
  Indels
  Indels
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  Gaps
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  0
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  ; ORGANISM: Homo sapiens US-11-101-244-863172
  ; ORGANISM: Homo sapiens US-11-101-244-134365
  US-11-101-244-863172/c
   SOFTWARE: Proprietary
SEQ ID NO 863172
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SEQ ID NO 134365
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  Query Match 6.9%;
Best Local Similarity 94.4%;
   Sequence 134365, Application US/11101244 Publication No. US20050246794A1
  GENERAL INFORMATION
  PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
  FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
  APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anas
APPLICANT: Reynolds, Ange
APPLICANT: Leake, Devin
  PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
  FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
   APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
  NUMBER OF SEQ ID NOS: 1591911
  APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
  APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
   PRIOR FILING DATE: 2002-11-14
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  TYPE: RNA
  LENGTH:
  LENGTH: 19
  6.9%;
Local Similarity 94.4%;
(es 17; Conservation)
                                      105 TCTCATTCTCCTGCTCCC 122
  105 TCTCATTCTCCTGCTCCC 122
19
   18 TCTCAATCTCCTGCTCCC 1
  Khvorova, Anastasia
Reynolds, Angela
   Leake, Devin
   Conservative
   0; Mismatches
  Score 16.4;
Pred. No. 63;
  Score 16.4;
Pred. No. 6
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   Length 19;
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;
   Gaps
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RESULT 142 US-11-101-244-914575/c ; Sequence 914575, Application US/11101244

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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILLNG DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILLNG DATE: 2002-11-14
US-10-310-914A-313831
US-10-310-914A-313831, Application US/10310914A
; Sequence 313831, Application US/10310914A
; Publication No. US20060003322A1
   吊
  ঠ
   US-11-101-244-1250582
   RESULT 143
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   ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-914575
   ; ORGANISM: Homo sapiens
US-11-101-244-1250582
  APPLICANT: Dharmacon, I
APPLICANT: Khvorova, I
APPLICANT: Reynolds, I
APPLICANT: Leake, Devi
APPLICANT: Marshall, V
APPLICANT: Scaringe, S
   PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1250582
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SOFTWARE: Proprietary
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  Sequence 1250582, Application U Publication No. US20050246794A1
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  Publication No. US20050246794A1
  Query Match
   APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Ennctional and Hyperfunctional sirNA
   FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
   ENGTH:
  6.9%;
Local Similarity 94.4%;
hes 17; Conservation
  Match 6.9%;
Local Similarity 55.6%;
   150 TICTCCTTCTGCCATGAT 167
   INFORMATION
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  70 CGTGAGAGCTGGTTGTTT 87
   10;
   CGUGAGAUCUGGUUGUUU 18
   Conservative
  Application US/11101244
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Pred. No. 6
   Pred. No. 6
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  Length 19;
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   Gaps
   Gaps
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; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 313831
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-313831
  ; TYPE: RNA; Homo Sapiens US-10-708-204-3346
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  US-10-310-914A-59888/c
   RESULT 146
  US-10-708-204-3346/c
  RESULT 145
US-10-310-914A-59888
                                APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION USES US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILLNG DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 59888
LENGTH: 21
TYPE: RNA
TYPE: RNA
   Sequence 3346, Application US/10708204
Publication No. US20050222399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE /
  NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3346
   GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
   GENERAL INFORMATION:
  Sequence 59888, Application US/10310914A Publication No. US20060003322A1
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Best Local Similarity
  Matches
   Query Match
  FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
                   ORGANISM: Human
   LENGTH: 21
  Local Similarity
nes 18; Conserv
   140 ÇTÇÇTÇÇÇÇTTÇTÇÇTT 157
   135 GACACCTGCTCCCCCTTCTCC 155
  21 GACCCCTGTTCTCCCTTCTCC
  3 cuecuccccceucuccuu
  Conservative
   Conservative
   6.9%;
  6.9%;
  20
   9
  0; Mismatches
  Score 16.2;
Pred. No. 6
  Score 16.4;
Pred. No. 65;
   Mismatches
  68;
  몂
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  Length 21;
   Length 21;
  Indels
  0
   0
  Gaps
   DISEASE AND USES
   0
  0
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RESULT 149
US-10-310-914A-612161
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   US-10-310-914A-174457

Sequence 174457, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
  밁
  र्
  NUMBER OF SEQ ID NOS: 1388402
SOUTWARE: PatentIn version 3.3
SEQ ID NO 95531
LENGTH: 21
TYPE: RNA
ORGANISM: Human
  US-10-310-914A-95531/c
  문
   ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-174457
   RESULT 148
   RESULT 147
Sequence 612161, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
  SOFTWARE: PatentIn version 3.3 SEQ ID NO 174457
   Sequence 95531, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
  Query Match
Best Local (
   Query Match
Best Local
  Matches
  Query Match
  APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 066097.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402
   -10-310-914A-9553:
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kyuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06607.0200.CFUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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   142 GCTCCCCCTTCTCCTTCTGCC 162
  21
   79
  2
  94 GCCTGGCCCCCCTCTCATTCTC 114
   l Similarity
  Similarity
   Similarity
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   Conservative
   6.9%;
   ; Score 16.2; D
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  1;
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   Length 21;
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  Gaps
  0
   0
   <u>..</u>
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   Ş
   밁
  ફ
   RESULT 151
US-10-310-914A-969044/c
   US-10-310-914A-628516
   US-10-310-914A-628516
  US-10-310-914A-612161
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 969044
FENCETT 31
   SOFTWARE: PatentIn version 3.3 SEQ ID NO 628516 LENGTH: 21
  SOFTWARE: PatentIn version 3.3
SEQ ID NO 612161
LENGTH: 21
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   Sequence 969044, Application US/10310914A Publication No. US20060003322A1
   Matches
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  Sequence 628516, Application US Publication No. US20060003322A1
  Best Local Similarity Matches 12; Conserv
   Best Local Similarity
  Query Match
  APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT FILING DATE: 0502-12-06 CURRENT FILING DATE: 2002-12-06 NUMBER: 05 SEQ ID NOS: 1388402
  APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
  APPLICANT: Bentwich,
ORGANISM: Human
10-310-914A-969044
   ORGANISM: Human
   TYPE: RNA
   TYPE: RNA
ORGANISM: Human
  TYPE:
   108 CATTCTCCTGCTCCCACTCTT 128
  24 CCTCATGAATGGTTTAGTGCC 44
   Ь
  CCUCAUGAAUAGCUUGGUGCC
   Conservative
   Conservative
  Application US/10310914A
   6.9%;
57.1%;
  6.9%;
   Score 16.2;
Pred. No. 68;
  Score 16.2;
Pred. No. 6
   Mismatches
   Mismatches
   DB 1;
  DВ
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   Length 21;
  Length 21;
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  Gaps
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   and
  and
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RESULT 154
US-10-310-914A-97305/c
US-10-310-914A-97305/c
; Sequence 97305, Application US/
; Publication No. US20060003322A1
; GENERAL INFORMATION:
   US-10-310-914A-1111794/c
; Sequence 1111794, Application US/10310914A
; Publication No. US20060003322A1
  á
  밁
   S
   RESULT 153
US-10-310-914A-1227944
  몽
   S
  밁
  US-10-310-914A-1111794
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTMARE: Patentin version 3.3
SEQ ID NO 111794
   Sequence 1227944, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
  Query Match
Best Local Similarity
  GENERAL INFORMATION:
   Matches
   Query Match
  Query Match
  ORGANISM: Human
-10-310-914A-1227944
APPLICANT: Bentwich,
  APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT PEPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06
  SOFTWARE: PatentIn version 3.3
  NUMBER OF SEQ ID NOS: 1388402
  LENGTH: 21
TYPE: RNA
ORGANISM: Human
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   140 CTGCTCCCCCTTCTCTTCTG 160
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   22
  72
  18;
   18;
   Similarity
  Similarity
   TCCCTCATGAATGGTTTAGTG 42
  TGAGAGCTGGTTGTTTGAAAG 92
  Conservative
   6.9%;
llarity 57.1%;
Conservative
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  6.9%;
85.7%;
   6.98;
   US/10310914A
   Score 16.2; D
Pred. No. 68;
6; Mismatches
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Pred. No. 68;
   Score 16.2;
Pred. No. 68;
  Mismatches
   Mismatches
   DB
  В
  DB 1;
  1;
   ω
--
   Length 21;
  Length 21;
  Length
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US-10-310-914A-360369/c

Sequence 360369, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kyuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes (
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS. 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 360369
  ; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 97305
LENGTH. ?
   밁
   á
  RESULT 156
US-10-310-914A-875345
   밁
   Ş
                                    US-10-310-914A-875345
  US-10-310-914A-360369
  US-10-310-914A-97305
  NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 875345
LENGTH: 22
TYPE: RNA
  Sequence 875345, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
   Query Match
Best Local
   Matches
   Matches
Query Match
   Query Match
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
  LENGTH: 22
TYPE: RNA
ORGANISM: Human
  TYPE: RNA
ORGANISM: Human
  ORGANISM: Human
  ENGTH: 22
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   143 CTCCCCCTTCTCCTTCTGCCA 163
   102
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   21 CTCCCCCTCCCCCTTCTCCCA 1
   18;
   Similarity
   CCCTCTCATTCTCCTGCTCCC 122
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   Conservative
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  6.9%;
   0,
   Score 16.2; D
Pred. No. 69;
0; Mismatches
   Score 16.2;
Pred. No. 6
  Score 16.2;
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Length 22;
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   Length
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   Gaps
   0,
   0
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뭉
  5
  ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-910065
   문
   S
  RESULT 157
US-10-310-914A-910065/c
  Sequence 910065, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
  Query Match
Best Local (
   SEQ ID NO 910065
LENGTH: 22
  Sequence 521, Application US/10092900A Publication No. US20040043382A1
  Matches
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   Best Local Similarity
  APPLICANT:
   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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  APPLICANT:
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  APPLICANT:
   PPLICANT:
   PPLICANT:
   PPLICANT:
  PPLICANT:
   PPLICANT:
   143 CTCCCCCTTCTCCTTCTGCCA 163
  21 CTCCTTCTTCTCCTTCTTCCA 1
  18;
   53
  Similarity
   Padigaru, Muralidhara
Spytek, Kimberly A.
Shenoy, Suresh G.
Taupier Jr., Raymond
   GGUGAGGAGGGAGCUCACGUG 22
   GGTGATGAGTGAGTTCACGTG 73
  Guo, Xiaojia Sasha
Tchernev, Velizar T.
Fernandes, Elma R.
  Patturajan, Meera
Gangolli, Esha A.
Vernet, Corine A.M.
Lepley, Denise M.
Rieger, Daniel K.
                            Leite, Mario W.
Zhong, Haihong
Alsobrook, John P.
   Gerlach,
  Zerhusen, Bryan D.
Gusev, Vladimir Y.
  Anderson, David W.
Spaderna, Steven K.
  Casman, Stacie J.
Malyankar, Uriel M.
  Catterton, Elina
  Kekuda, Ramesh
  Conservative
  Conservative
  Weizhen
  Carol E.A.
  Charles E.
  Linda
  Valerie
  6.9%;
  71.4%; Pred. No.
   Raymond J.
   Score 16.2; D
Pred. No. 69;
0; Mismatches
  0
  Mismatches
   69;
  BG
  1; Length 22;
  ω
--
   group of
  Indels
  novel regulatory genes
   0
  <u>.</u>
  Gaps
   0
  0
   and
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밁
  US-10-310-914A-596179
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US-10-310-914A-596179
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  US-10-092-900A-521
  PRIOR APPLICATION NUMBER: USSN 60/274,322
PRIOR FILING DATE: 2001-03-08
PRIOR PELICATION NUMBER: USSN 60/283,675
PRIOR PELICATION NUMBER: USSN 60/283,675
PRIOR PELICATION NUMBER: USSN 60/338,092
PRIOR PELICATION NUMBER: USSN 60/274,281
PRIOR APPLICATION NUMBER: USSN 60/274,281
PRIOR APPLICATION NUMBER: USSN 60/274,191
PRIOR PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/274,191
PRIOR APPLICATION NUMBER: USSN 60/274,191
PRIOR APPLICATION NUMBER: USSN 60/325,681
PRIOR APPLICATION NUMBER: USSN 60/325,681
PRIOR PILING DATE: 2001-03-08
  PRIOR APPLICATION NUMBER: USSN 60/304,354
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: USSN 60/279,995
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: USSN 60/294,899
PRIOR APPLICATION NUMBER: USSN 60/287,424
PRIOR APPLICATION NUMBER: USSN 60/287,424
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
   GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 596179
LENGTH: 23
TYPE: RNA
ORGANISM: Human
ORGANISM: Human
   Sequence 596179, Application US/10310914A
Publication No. US20060003322A1
   Query Match 6.9%; Score 16.2;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches
   Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 768
SEQ ID NO 521
   Matches
  Query Match
   FILE REFERENCE: 21402-290C
CURRENT APPLICATION NUMBER: US/10/092,900A
CURRENT FILING DATE: 2002-03-07
  TITLE OF INVENTION: No. US20040043382Alel Proteins and Nucleic Acids Encoding Same
   TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: probe
  LENGTH: 23
  Local
  100 cccccrcrcarrerecrecre 120
  20 GATCCCTCATGAATGGTTTAG 40
ω
   1 Similarity 61.9
13; Conservative
  N
  cceccrcrccrrcrcccecrc 22
  61.9%;
   Ş
  Score 16.2; D
Pred. No. 70;
5; Mismatches
  Mismatches
  See File Wrapper or PALM
  DB 1;
  DB 1;
   ω
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   Length 23;
  Length 23;
   Indels
   Indels
   0,
   <u>,</u>
   Gaps
   Gaps
   0
   <u>..</u>
   and
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Ś
  US-11-083-784-508230/c
   뭐
  US-10-310-914A-1037134/c
; Sequence 1037134, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
  밁
   ঠ
   ; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1171021
  US-10-310-914A-1171021/c
  US-10-310-914A-1037134
  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 66087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1037134
LENGTH: 18
   APPLICANT: Shiler, Kyuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1171021
   Sequence 508230, Application US/11083784 
Publication No. US20050245475A1
   Sequence 1171021, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
   GENERAL INFORMATION:
   Matches
  Query Match
Best Local Similarity
   Query Match
Best Local :
            APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
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   APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat
  TYPE: RNA
ORGANISM: Human
   rocal
APPLICATION NUMBER: US/10/714,333
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  154 CCTTCTGCCATGATTTTAAGA 174
   18
   16;
  21 CCTTCTACCATGACTGTAAGA 1
  l Similarity
18; Conserv
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   Conservative
  Conservative
  6.8%; Score 16; 100.0%; Pred. No.
  Pred. No. 70;
0; Mismatches
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   Mismatches
  . DB 1;
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   0;
  Length 18
  Length 23;
   Indels
  Indels
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  ٥,
  Gaps
   Gaps
   0
  0
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   ; ORGANISM: Homo sapiens US-11-101-244-508230
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US-11-101-244-508230/c
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   ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-508230
   US-09-791-942-85
   GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Robert Rothlein
APPLICANT: Takashi Kei Kishimoto
APPLICANT: Lex M. Cowsert
NUMBER OF SEQ ID NOS:
SEQ ID NO 85
  Sequence 85, Application US/09791942 Patent No. US20020147166A1
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  SEQ ID NO 508230
LENGTH: 19
   SOFTWARE: Proprietary
SEQ ID NO 508230
   Best Local
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   Sequence 508230, Application US/11101244 Publication No. US20050246794A1
  Matches
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CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 66/426,137
PRIOR APPLICATION NUMBER: 66/426,137
PRIOR APPLICATION NUMBER: 66/426,137
PRIOR PILING DATE: 2002-11-14
  APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
                                 CURRENT APPLICATION NUMBER: US/09/791,942
CURRENT FILING DATE: 2001-02-22
   FILE REFERENCE:
   NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
  TITLE OF INVENTION:
  APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
   APPLICANT:
   APPLICANT:
  NUMBER OF SEQ ID NOS: 1591911
   PRIOR APPLICATION NUMBER: 60/426,137 PRIOR FILING DATE: 2002-11-14
   PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
   TYPE: RNA
  ENGTH:
   INFORMATION:
  105 TCTCATTCTCCTGCTC 120
   105 TCTCATTCTCCTGCTC 120
   19
   19 TCTCATTCTCCTGCTC 4
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16; Conserv
  16;
   Reynolds, Angela
   Leake, Devin
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  Conservative
   ON: ANTISENSE MODULATION OF TALIN EXPRESSION RTS-0099
   100.0%;
   100.0%;
   6.8%;
  0,
   Score 16;
Pred. No.
  0
   Score 16; pred. No.
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  Mismatches
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  <u>,</u>
  0
  Length 19;
  Length 19
  Indels
  Indels
  0
  <u>.</u>
  Gaps
  Gaps
  0
  0
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문
  밁
   ફ
   RESULT 166
US-10-476-264-285/c
  ; OTHER INFORMATION: Antisense Oligonucleotide US-09-791-942-85
   US-10-415-463-85
   SEQ ID NO 85
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
   Query Match
Best Local Similarity
  Sequence 285, Application US/10476264 Publication No. US20050123910A1
   Matches
   Matches
  Query Match
  SENERAL INFORMATION:
   APPLICANT: Lex M. COWBERT
TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
FILE REFERENCE: RTSP-0198
CURRENT APPLICATION NUMBER: US/10/415,463
CURRENT FILING DATE: 2003-11-13
  GENERAL INFORMATION:
  PRIOR APPLICATION NUMBER: GB0110044.5
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: GB0110046.0
PRIOR ETLING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: GB0124594.3
PRIOR FILING DATE: 2001-10-12
  TITLE OF INVENTION: Enzyme and SNP marker FILE REFERENCE: 16721-002US1
CURRENT APPLICATION NUMBER: US/10/476,264
CURRENT FILING DATE: 2003-10-24
  PRIOR APPLICATION NUMBER: 09/702,251
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 89
  APPLICANT: Isis Pharmaceuticals, Inc
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
  PRIOR APPLICATION NUMBER: PCT/GB02/01887
PRIOR FILING DATE: 2002-04-24
  APPLICANT: Cookson, William Osmond Charles Michael APPLICANT: Moffat, Miriam Fleur
   ORGANISM: Artificial Sequence FEATURE:
   Local Similarity
nes 16; Conserv
             APPLICATION NUMBER: GB0124575.2 FILING DATE: 2001-10-12
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SEQ ID NOS:
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   Application US/10415463
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   Gaps
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Search completed: October Job time: 0.001 secs
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  Ś
   ; ORGANISM: Human US-10-310-914A-1037133
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US-10-310-914A-1037133/c
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  US-10-476-264-285
   Sequence 1037133, Application US/10310914A
Publication No. US20060003322A1
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kyuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1037133
LENGTH: 22
TYDE: NAM
  Query Match
Best Local Similarity
Matches 16; Conserva
   SEQ ID NO 285
LENGTH: 20
   Matches
   Query Match
   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
   OTHER INFORMATION: Primer
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   191 AGAAGCAAATGCTAAC 206
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   18
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100.0%; Pred. No.
               2, 2006, 15:43:17
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. 72;
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   Length 20;
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   Gaps
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